



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 206082

TO: Celine Qian
Location: REM/3D21/2C70
Art Unit: 1636
Thursday, November 02, 2006
Case Serial Number: 10/702319

From: Dwayne Hill
Location: Biotech-Chem Library
REM-1A41
Phone: (571)272-8972

Dwayne.Hill@uspto.gov

Search Notes

Examiner Qian,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Dwayne Hill
STIC Biotech/Chem Library
(571)272-8972

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ACCESS DB # 206082
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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 10/30/06
Art Unit: 1636 Phone Number: 2-0777 Serial Number: 107702,319
Location (Bldg/Room#): 3021 (Mailbox #): 2070 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Compositions and Methods for the modification of gene expression
Inventors (please provide full names): PERERA, Ranjan et al.

Earliest Priority Date: 11/6/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 113, also search
fragments of SEQ ID NO: 113 (nt 1019-1675, 1019-1643)
& 41-3070),
and a 20 mer search of SEQ ID NO: 113.
For both commercial & interference database.

Thanks.

Print
☒

Log ☐

113-3070 NA

10/31

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:09:33 ; Search time 16931 Seconds
(without alignments)
11595.215 Million cell updates/sec

Title: US-10-702-319A-113
 Perfect score: 3070
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 20

Total number of hits satisfying chosen parameters: 206339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl: *

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14: gb_om:*
15: gb_ba:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query # |        | DB | ID       | Description |
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| 2          | 1255  | 40.9    | 2096   | 2  | BD262168 | Compositi   |
| 3          | 1255  | 40.9    | 2096   | 2  | AR360953 | Sequence    |
| 4          | 774   | 25.2    | 1630   | 2  | BD224383 | Materials   |
| 5          | 774   | 25.2    | 1630   | 2  | AR216433 | Sequence    |
| 6          | 774   | 25.2    | 1630   | 2  | AR432835 | Sequence    |
| 7          | 272   | 8.9     | 661    | 2  | BD262120 | Compositi   |
| 8          | 272   | 8.9     | 661    | 2  | AR360905 | Sequence    |
| 9          | 189   | 6.2     | 1452   | 4  | EGOMTRN  | E.gunnii OM |
| 10         | 163   | 5.3     | 3022   | 4  | AF168777 | Eucalyptu   |
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| 12         | 111   | 3.6     | 407    | 2  | AR216432 | Sequence    |
| 13         | 111   | 3.6     | 407    | 2  | AR432834 | Sequence    |
| 14         | 111   | 3.6     | 421    | 2  | AR074115 | Sequence    |
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| 16         | 111   | 3.6     | 421    | 2  | BD224300 | Materials   |
| 17         | 111   | 3.6     | 421    | 2  | BD273002 | Materials   |
| 18         | 111   | 3.6     | 421    | 2  | AR216350 | Sequence    |

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| 23 | 41  | 1.3 | 221362 | 12  | AC134084     | AC134084 Rattus no  |                   |
| 24 | 41  | 1.3 | 226317 | 12  | AC1334081    | AC1334081 Rattus no |                   |
| 25 | 41  | 1.3 | 235954 | 12  | AC094907     | AC094907 Rattus no  |                   |
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| 29 | 40  | 1.3 | 294315 | 12  | AC114243     | AC114243 Rattus no  |                   |
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| 31 | 39  | 1.3 | 144678 | 6   | AL772294     | Mouse DNA           |                   |
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| 33 | 39  | 1.3 | 192583 | 6   | AL671782     | Mouse DNA           |                   |
| 34 | 39  | 1.3 | 204904 | 6   | AC124029     | Mus muscu           |                   |
| 35 | 39  | 1.3 | 207840 | 6   | AC160395     | Mus muscu           |                   |
| 36 | 39  | 1.3 | 212662 | 6   | AC103663     | Mus muscu           |                   |
| 37 | 39  | 1.3 | 214018 | 12  | AC094045     | Rattus no           |                   |
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| 44 | 38  | 1.2 | 170810 | 12  | CT025599     | Mus muscu           |                   |
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## ALIGNMENTS

|            |                                                                                                                                                               |             |     |        |                 |
|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|-----|--------|-----------------|
| RESULT 1   | AR360987                                                                                                                                                      | 3070 bp     | DNA | linear | PAT 17-AUG-2003 |
| LOCUS      | Sequence 113 from patent US 6596925.                                                                                                                          |             |     |        |                 |
| DEFINITION | AR360987                                                                                                                                                      |             |     |        |                 |
| ACCESSION  | AR360987                                                                                                                                                      |             |     |        |                 |
| VERSION    | AR360987.1                                                                                                                                                    | GI:33768497 |     |        |                 |
| KEYWORDS   | Unknown.                                                                                                                                                      |             |     |        |                 |
| SOURCE     | Unknown.                                                                                                                                                      |             |     |        |                 |
| ORGANISM   | Unclassified.                                                                                                                                                 |             |     |        |                 |
| REFERENCE  | 1 (bases 1 to 3070)                                                                                                                                           |             |     |        |                 |
| AUTHORS    | Perera,J.R., Bagleton,C. and Rice,S.J.                                                                                                                        |             |     |        |                 |
| TITLE      | Compositions and methods for the modification of gene expression                                                                                              |             |     |        |                 |
| JOURNAL    | Patent: US 6596925-A 113 22-JUL-2003; and Rubicon Forests<br>Genesis Research & Development Corp. Ltd. and Rubicon Forests<br>Holdings Ltd.; Parnell;<br>NZX; |             |     |        |                 |
| FEATURES   | Location/Qualifiers                                                                                                                                           |             |     |        |                 |
| source     | 1..3070                                                                                                                                                       |             |     |        |                 |
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|            | /mol_type="genomic DNA"                                                                                                                                       |             |     |        |                 |
| ORIGIN     |                                                                                                                                                               |             |     |        |                 |
|            | Query Match 100.0%; Score 3070; DB 2; Length 3070;                                                                                                            |             |     |        |                 |
|            | Best Local Similarity 100.0%; Pred. No. 0;                                                                                                                    |             |     |        |                 |
|            | Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                 |             |     |        |                 |
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|            |                                                                                                                                                               |             |     |        |                 |
| Db         | 1 AGCACCATCAGCAAAAATAGATGGGATAGTGGGACACACCTGTTTCAGTTTGATTC 60                                                                                                 |             |     |        |                 |
|            |                                                                                                                                                               |             |     |        |                 |
| Qy         | 61 CTTTGAGTACCTACACTGATAGCTTGATCAATAAGATGGGATAATAGATTCCACGAGG 120                                                                                             |             |     |        |                 |
|            |                                                                                                                                                               |             |     |        |                 |
| Db         | 61 CTTTGAGTACCTACACTGATAGCTTGATCAATAAGATGGGATAATAGATTCCACGAGG 120                                                                                             |             |     |        |                 |
|            |                                                                                                                                                               |             |     |        |                 |
| Qy         | 121 GATAAAAAGGTGGGAGATAGGGGATCTCCCGTCTGATCGCTCGGTAGGTTGAAAAATA 180                                                                                            |             |     |        |                 |
|            |                                                                                                                                                               |             |     |        |                 |
| Db         | 121 GATAAAAAGGTGGGAGATAGGGGATCTCCCGTCTGATCGCTCGGTAGGTTGAAAAATA 180                                                                                            |             |     |        |                 |
|            |                                                                                                                                                               |             |     |        |                 |
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Genesis Research & Development Corp. Ltd. and Rubicon Forests Holdings Ltd.; Parnell;  
NZX;

Location/Qualifiers  
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FEATURES  
source

ORIGIN

Query Match 40.9%; Score 1255; DB 2; Length 2096;

Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1655; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 3  
AR360953 LOCUS 2096 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 60 from patent US 6596925.  
ACCESSION AR360953  
VERSION AR360953.1 GI:33768463  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2096)  
Perera,J.R., Bagleton,C. and Rice,S.J.  
AUTHORS  
TITLE Compositions and methods for the modification of gene expression  
JOURNAL Patent: US 6596925-A 60 22-JUL-2003;

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Db 1754 CTTTCGCGACTCAGTCATCGAGTTCCTGAAGACCGCTTGATCTGCTCTCTGTGTGAT 1813
QY 2788 GTTCATGTTCTTGGATTTCAGAGGTCGTGAAGGCGCTTCTTCACAGTTCGCTCGG 2847
Db 1814 GTTCATGTTCTTGGATTTCAGAGGTCGTGAAGGCGCTTCTTCACAGTTCGCTCGG 1873
QY 2848 CATAACCAAGTCTTCTCATAAAGGAAACAATAAGACGACTGTATGATGGCGCAAGTG 2907
Db 1874 CATAACCAAGTCTTCTCATAAAGGAAACAATAAGACGACTGTATGATGGCGCAAGTG 1933
QY 2908 GAAGTTACAAGATTGTTGTTTATGCTATAAAGTTTTCAGTCTTCTGCATACTGATTT 2967
Db 1934 GAAGTTACAAGATTGTTGTTTATGCTATAAAGTTTTCAGTCTTCTGCATACTGATTT 1993
QY 2968 CACAGATGTCTAACGAAACGGGTATATGAGTGTGCTCAATGATGAATTTGTGATAT 3027
Db 1994 CACAGATGTGTAAACGAAACGGGTATATGAGTGTGCTCAATGATGAATTTGTGATAT 2053
QY 3028 TCTGTCTCTTTTTCAGTAAATCACTTCGAAACAAAAA 3070
Db 2054 TCTGTCTCTTTTTCAGTAAATCACTTCGAAACAAAAA 2096

RESULT 4
BD224383 1630 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD224383
VERSION BD224383.1 GI:33034153
KEYWORDS JP 2002527058-A/107.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 1630)
Blokberg, L.N. and Havukkala, I.J.
Materials and methods for the modification of plant lignin content
TITLE Patent: JP 2002527058-A 107 27-AUG-2002;
JOURNAL GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS LTD
COMMENT OS Eucalyptus grandis
PN JP 2002527058-A/107
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PD 27-AUG-2002
PF 06-OCT-1999 JP 2000575991
PR 09-OCT-1998 US 09/169789,14-JUL-1999 US 60/143811 PI
LEONARD NATHAN BLOKBERG, ILKA JAAKKO HAVUKKALA PC
C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/02,C12N9/04,C12N9/PC
C12N9/24,
PC C12N9/88,C12N15/00,C12N5/00
CC Materials and methods for the modification of plant lignin CC

FH Key source Location/Qualifiers
FT source 1..1630 /organism='Eucalyptus grandis'.
FT source 1..1630 /organism='Eucalyptus grandis'
/ncbi_type='genomic DNA'
/db_xref='taxon:71139'

FEATURES
source
ORIGIN
Query Match 25.2%; Score 774; DB 2; Length 1630;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1864 CAGTCCCGACCCAGAACCCCGAGGACCCGCTCATGCTCGACCGGATCTTCGGGTGCTG 1923
Db 264 CAGTCCCGACCCAGAACCCCGAGGACCCGCTCATGCTCGACCGGATCTTCGGGTGCTG 323
QY 1924 GCCAGTACTCGTGTCTCAGTGCACCTCCCGACCTCCCGATGGCAGGTTCGAGCGG 1983
Db 324 GCCAGTACTCGTGTCTCAGTGCACCTCCCGACCTCCCGATGGCAGGTTCGAGCGG 383
QY 1984 CTCTAGCGTCTAGCGCGCGTGTGCAAGTCTTGGTCAAGAACGAGACGCGGTCTCCATC 2043
Db 384 CTCTAGCGTCTAGCGCGCGTGTGCAAGTCTTGGTCAAGAACGAGACGCGGTCTCCATC 443
QY 2044 GCCGCACTCAACTTGATGAACCCAGGACAAATCTCTCATGGAAGCTGGTATTACCTGAAA 2103
Db 444 GCCGCACTCAACTTGATGAACCCAGGACAAATCTCTCATGGAAGCTGGTATTACCTGAAA 503
QY 2104 GATCGCGTCTTGAAGCGCGGATCCCATTTCAACAGCGCTACGGGATGACCGGTTCCGAG 2163
Db 504 GATCGCGTCTTGAAGCGCGGATCCCATTTCAACAGCGCTACGGGATGACCGGTTCCGAG 563
QY 2164 TATCATGGCACCGACCGCGATTTCAACAAGATCTTTAAACCGGGAATGTCTGATCACTCC 2223
Db 564 TATCATGGCACCGACCGCGATTTCAACAAGATCTTTAAACCGGGAATGTCTGATCACTCC 623
QY 2224 ACCATTACTATGAAGAAGATACCTGGAACATACAAAGGCTTCGAGGCGCTTCGAGACCGTG 2283
Db 624 ACCATTACTATGAAGAAGATACCTGGAACATACAAAGGCTTCGAGGCGCTTCGAGACCGTG 683
QY 2284 GTCGATGTCGAGCGCGGCTGCGGCGCGTCTCAGCATGATCGTTCGCAATATCCCATCA 2343
Db 684 GTCGATGTCGAGCGCGGCTGCGGCGCGTCTCAGCATGATCGTTCGCAATATCCCATCG 743
QY 2344 ATGAAGGATCAACTTCGACCC - GCCCAAGGATTTGAAGACGCCGCCCTTCCTGGT 2402
Db 744 ATGAAGGATCAACTTCGACCCCTCTCAGTGTGAAGACGCTCCACCCCTTCCTGGT 803
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Db 804 GTCAGCAGCTCGAGCGGACATGTTTCGTGAGCGGTTCCAAAGGAGATGCAATTTTCATG 863
QY 2463 AGTGATATGTCATGCTGAGTACGACCATTTGGCGAGTTCCTCAAGACTGCTAC 2522
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QY 2523 GATCGCGTCCCAACCAATGGAAGTGTGTCAGAGTGCCTACTCCCTGTGATCCCA 2582
Db 924 GATCGCGTCCCAACCAATGGAAGTGTGTCAGAGTGCCTACTCCCTGTGATCCCA 983
QY 2583 GACACGAGCTAGCGACCAAGATGTGATCCCATGCTGATCATGTTGGGCCCAAC 2642
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|    |      |                                                                  |      |
|----|------|------------------------------------------------------------------|------|
| QY | 2044 | GCCGCACTCAACTTGATGAACACAGGACAAAATCCTCATGGAAAGCTGGTATTACCTGAAA    | 2103 |
| DB | 444  |                                                                  |      |
|    | 444  | GCCGCACTCAACTTGATGAACACAGGACAAAATCCTCATGGAAAGCTGGTATTACCTGAAA    | 503  |
| QY | 2104 | GATGCGGTCTTGAAGCGCGAATCCCATTTCAACAAGCGGTACGGGATGACCGGTTTCGAG     | 2163 |
| DB | 504  | GATGCGGTCTTGAAGCGCGAATCCCATTTCAACAAGCGGTACGGGATGACCGGTTTCGAG     | 563  |
| QY | 2164 | TATCATNGGCACCGACCGCGGATTTCAACAAGATCTTTAAACCGGGGAATGTCTGTACTCTCC  | 2223 |
| DB | 564  | TATCATNGGCACCGACCGCGGATTTCAACAAGATCTTTAAACCGGGGAATGTCTGTACTCTCC  | 623  |
| QY | 2224 | ACCAATTACTATGAAGAGATACCTGGAAACATACAAGGGCTTCGAGGGCTCGAGACCGTG     | 2283 |
| DB | 624  | ACCAATTACTATGAAGAGATACCTGGAAACATACAAGGGCTTCGAGGGCTCGAGACCGTG     | 683  |
| QY | 2284 | GTCGATGTCGAGGCGGCATCTGGGCGGTCTCAGCATGATCGTTTGCAAAATACCCATCA      | 2343 |
| DB | 684  | GTCGATGTCGAGGCGGCATCTGGGCGGTCTCAGCATGATCGTTTGCAAAATACCCATCG      | 743  |
| QY | 2344 | ATGAAAGGGATCAACTTTCGACC-GCCGCCAACGGATTGAAGACGCCCAACCCCTTCCTGGT   | 2403 |
| DB | 744  | ATGAAAGGGATCAACTTTCGACCCTCGCTCAGTGATTGAAGACGCTCCACCCCTTCCTGGT    | 803  |
| QY | 2403 | GTCGAAGCAGTCGAGGCGGCATGTTTCGTTCAGCGTTTCCAAAGGCGAGATGCCATTTTCATG  | 2463 |
| DB | 804  | GTCGAAGCAGTCGAGGCGGCATGTTTCGTTCAGCGTTTCCAAAGGCGAGATGCCATTTTCATG  | 863  |
| QY | 2463 | AAGTGGATATGCCATGACTCGAGGTGACGACCATTTTCGCGGAAGTTTCCTCAAGAACTGCTAC | 2523 |
| DB | 864  | AAGTGGATATGCCATGACTCGAGGTGACGACCATTTTCGCGGAAGTTTCCTCAAGAACTGCTAC | 923  |
| QY | 2523 | GATGCGCTTCCCAACAATGGAAGAGTGATCGTTTCGAGAGTCGGTACTCCCTGTGTACCCA    | 2583 |
| DB | 924  | GATGCGCTTCCCAACAATGGAAGAGTGATCGTTTCGAGAGTCGGTACTCCCTGTGTACCCA    | 983  |
| QY | 2583 | GACACGCGCTTAGCGACCAAGATGTGATCCACATCGACTGCATCATGTGTGCCCCACAAC     | 2643 |
| DB | 984  | GACACGCGCTTAGCGACCAAGATGTGATCCACATCGACTGCATCATGTGTGCCCCACAAC     | 1043 |
| QY | 2643 | CCAGCGGGAAAGAGAGACACAGAAGAGTTTCGAGGCAATTTGGCCAAAGGGCCCGGATTT     | 2703 |
| DB | 1044 | CCAGCGGGAAAGAGAGACACAGAAGAGTTTCGAGGCAATTTGGCCAAAGGGCCCGGATTT     | 1103 |
| QY | 2703 | CAGGGCTTCCAGTCACTGTGCTGGCTTTTCGSCACTCAGCTCATGGAGTTCCTGAAGACC     | 2763 |
| DB | 1104 | CAGGGCTTCCAGTCACTGTGCTGGCTTTTCGSCACTCAGCTCATGGAGTTCCTGAAGACC     | 1163 |
| QY | 2763 | GCTTGATCTGCTCCTCTGTGGTGATGTTCAAGGTTCTTGGATTTGGAAGGTCGTGAAGGA     | 2823 |
| DB | 1164 | GCTTGATCTGCTCCTCTGTGGTGATGTTCAAGGTTCTTGGATTTGGAAGGTCGTGAAGGA     | 1223 |
| QY | 2823 | GCCCTTTTCTCAGAGTGGCTTCGACATACCAAGTTCTTCTCATAAAGGAAACAATAAG       | 2883 |
| DB | 1224 | GCCCTTTTCTCAGAGTGGCTTCGACATACCAAGTTCTTCTCATAAAGGAAACAATAAG       | 1283 |
| QY | 2883 | AAAGCGACTGTATGATGGCCCAAGTGAAGTTTCAAGATTTGTGTTTTATGCTATAAAG       | 2943 |
| DB | 1284 | AAAGCGACTGTATGATGGCCCAAGTGAAGTTTCAAGATTTGTGTTTTATGCTATAAAG       | 1343 |
| QY | 2943 | TTTTTGATCTTCTGCACTATGATTTTCAAGATGTGTAAAGAAACCGCGTATATGATGT       | 3003 |
| DB | 1344 | TTTTTGATCTTCTGCACTATGATTTTCAAGATGTGTAAAGAAACCGCGTATATGATGT       | 1403 |
| QY | 3003 | GCCCTGAATGATGAAATTTGTATATCTGTCTTCTTTTTCAGTAAATCACTTCGACAAA       | 3063 |
| DB | 1404 | GCCCTGAATGATGAAATTTGTATATCTGTCTTCTTTTTCAGTAAATCACTTCGACAAA       | 1463 |
| QY | 3063 | A 3063                                                           |      |
| DB | 1464 | A 1464                                                           |      |

|                       |            |                                                                    |               |           |                 |
|-----------------------|------------|--------------------------------------------------------------------|---------------|-----------|-----------------|
| RESULT 5              | AR216433   | 1630 bp                                                            | DNA           | linear    | PAT 25-SEP-2002 |
| LOCUS                 | AR216433   | Sequence 107 from patent US 6410718.                               |               |           |                 |
| DEFINITION            | AR216433   |                                                                    |               |           |                 |
| ACCESSION             | AR216433   |                                                                    |               |           |                 |
| VERSION               | AR216433.1 | GI:23314913                                                        |               |           |                 |
| KEYWORDS              |            | Unknown.                                                           |               |           |                 |
| SOURCE                |            | Unknown.                                                           |               |           |                 |
| ORGANISM              |            | Unclassified.                                                      |               |           |                 |
| REFERENCE             |            | 1 (bases 1 to 1630)                                                |               |           |                 |
| AUTHORS               |            | Bloksberg, L.N. and Havukkala, I.                                  |               |           |                 |
| TITLE                 |            | Materials and methods for the modification of plant lignin content |               |           |                 |
| JOURNAL               |            | Patent: US 6410718-A 107 25-JUN-2002;                              |               |           |                 |
|                       |            | Genesis Research & Development Corporation Ltd. and Fletcher       |               |           |                 |
|                       |            | Challenge Forests Ltd.;;                                           |               |           |                 |
| NZX;                  |            |                                                                    |               |           |                 |
| FEATURES              |            | Location/Qualifiers                                                |               |           |                 |
| source                |            | 1..1630                                                            |               |           |                 |
|                       |            | /organism="unknown"                                                |               |           |                 |
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| ORIGIN                |            |                                                                    |               |           |                 |
| Query Match           |            | 25.2%;                                                             | Score 774;    | DB 2;     | Length 1630;    |
| Best Local Similarity |            | 99.4%;                                                             | Pred. No. 0;  |           |                 |
| Matches 1194;         |            | Conservative                                                       | 0; Mismatches | 6; Indels | 1; Gaps 1;      |
| QY                    | 1864       | CAGCTCCCGACCCAGAAACCCCGAGGACCCGTCATGCTCGACCGGATCTTCGGGCTGCTG       | 1923          |           |                 |
| Db                    | 264        | CAGCTCCCGACCCAGAAACCCCGAGGACCCGTCATGCTCGACCGGATCTTCGGGCTGCTG       | 323           |           |                 |
| QY                    | 1924       | GCACGTACTTCGGTGTCTACGTGCACCCCTCCGCGACCTCCCGGATGCGAAGTTCGAGCGG      | 1983          |           |                 |
| Db                    | 324        | GCACGTACTTCGGTGTCTACGTGCACCCCTCCGCGACCTCCCGGATGCGAAGTTCGAGCGG      | 383           |           |                 |
| QY                    | 1984       | CTCTACGGTTAGCGCGGTGTGCAGATTCTTGGTCAAGACGAGGACGGGTCTCCATC           | 2043          |           |                 |
| Db                    | 384        | CTCTACGGTTAGCGCGGTGTGCAGATTCTTGGTCAAGACGAGGACGGGTCTCCATC           | 443           |           |                 |

```
RESULT 6
AR432835
LOCUS AR432835 1630 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 107 from patent US 6653528.
ACCESSION AR432835
VERSION AR432835.1 GI:40195438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1630)
Blokberg, L.N. and Havukkala, I.
Pinus radiata nucleic acids encoding O-methyl transferase and
methods for the modification of plant lignin content therewith
Patent: US 6653528-A 107 25-NOV-2003;
Genesis Research & Development Corporation Limited and Rubicam
Forests Industries Limited; Parnell;
NZX;
FEATURES
source Location/Qualifiers
1..1630
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 25.2%; Score 774; DB 2; Length 1630;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
1;
QY 1864 CAGCTCCCGACCCAGAACCCCGAGGACCCCGTCATGCTCGACCGGATCTTCGGCGTCTG 1923
DB 264 CAGCTCCCGACCCAGAACCCCGAGGACCCCGTCATGCTCGACCGGATCTTCGGCGTCTG 323
QY 1924 GCAGCTACTCCGTGCTCAGCTGCACCTCCCGGACCTCCCGATGCGCAAGTTCGAGCG 1983
DB 324 GCAGCTACTCCGTGCTCAGCTGCACCTCCCGGACCTCCCGATGCGCAAGTTCGAGCG 383
QY 1984 CTCTAGGCTTAGCGCGGTGTCAGTCTCTGTCAGAACGAGGACGGGTCTCCATC 2043
DB 384 CTCTAGGCTTAGCGCGGTGTCAGTCTCTGTCAGAACGAGGACGGGTCTCCATC 443
QY 2044 GCGGCACTCAACTGTATGAACACGAGCAAAATCCTCATGAAAGCTGGTATTACCTGAA 2103
DB 444 GCGGCACTCAACTGTATGAACACGAGCAAAATCCTCATGAAAGCTGGTATTACCTGAA 503
QY 2104 GATGCGGTCTTGAAGCGGGAATCCCATTCAAAGCGGTACGGGATGACCGGTTCGAG 2163
DB 504 GATGCGGTCTTGAAGCGGGAATCCCATTCAAAGCGGTACGGGATGACCGGTTCGAG 563
QY 2164 TATCATGGACCGACCGCGGATTCACAGATCTTTAACCGGGGAATGTCGTATCACTCC 2223
DB 564 TATCATGGACCGACCGCGGATTCACAGATCTTTAACCGGGGAATGTCGTATCACTCC 623
QY 2224 ACATTTACTATGAAGATACCTGGAACATACAGGGCTTCGAGGGCTTCGAGACCGTG 2283
DB 624 ACATTTACTATGAAGATACCTGGAACATACAGGGCTTCGAGGGCTTCGAGACCGTG 683
QY 2284 GTCGATGTCGAGGCGGCATCTGGGGCGTCTCAGCATGATGTCGTCACCAATACCATCA 2343
DB 684 GTCGATGTCGAGGCGGCATCTGGGGCGTCTCAGCATGATGTCGTCACCAATACCATCG 743
QY 2344 ATGAAGGGATCAACTTCGACC-GCCCAACGGATTGAACAGCGCCACCCCTTCCTGGT 2402
DB 744 ATGAAGGGATCAACTTCGACCCTTCGACCTGCTCAGCATGATTGAAGACGCTCCACCCCTTCCTGGT 803
QY 2403 GTCAAGCAGCTCGAGGCGGCATGTTGTCGTCAGCGTTCGAAGGAGATGTCATTTTCATG 2462
DB 804 GTCAAGCAGCTCGAGGCGGCATGTTGTCGTCAGCGTTCGAAGGAGATGTCATTTTCATG 863
QY 2463 AAGTGGATATGCCATGATCGAGTACGACCATTTGCGCGAAGTTCCTCAAGAACTGCTAC 2522
DB 864 AAGTGGATATGCCATGATCGAGTACGACCATTTGCGCGAAGTTCCTCAAGAACTGCTAC 923
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QY 2523 GATGCGCTTCCCAACAATGAAAGGTGATCGTTGTCAGAGTGGGTACTCCTCTGTGTACCCA 2582
DB 924 GATGCGCTTCCCAACAATGAAAGGTGATCGTTGTCAGAGTGGGTACTCCTCTGTGTACCCA 983
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DB 984 GACACGAGCTTAGCGACCAAGAATGTATGCCATCGATCGATCATGTTTGGCCCAAC 1043
QY 2643 CCAGCGGGAAGAGAGAGACACAGAAGGAGTTGCGAGGATTCGCCAAAGGGCGGATTT 2702
DB 1044 CCAGCGGGAAGAGAGAGACACAGAAGGAGTTGCGAGGATTCGCCAAAGGGCGGATTT 1103
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DB 1404 GCTGGAATGATGGAATTTGATGATTTCTGCTCTTTTTCAGTAAATCACTTCGAACAA 1463
QY 3063 A 3063
DB 1464 A 1464
RESULT 7
LOCUS BD262120 661 bp DNA linear PAT 17-JUL-2003
DEFINITION Composition and methods for the modification of gene expression.
ACCESSION BD262120
VERSION BD262120.1 GI:33071888
KEYWORDS JP 2002539834-A/12.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 661)
Perera, R., Rice, S.J. and Eagleton, C.K.
Composition and methods for the modification of gene expression
Patent: JP 2002539834-A 12 26-NOV-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS INDUSTRIES LTD
OS Eucalyptus grandis (flooded gum)
PN JP 2002539834-A/12
PD 26-NOV-2002 JP 200608755
PR 25-MAR-1999 US 09/276599, 30-JUL-1999 US 60/146591 PI
RANJAN PERERA, STEPHEN J RICE, CLARE KATHERINE EAGLETON PC
C12N15/09, A01H5/00, C07K14/415, C12N5/10, C12Q1/02, C12Q1/68, PC
C12N15/00,
PC C12N5/00
CC Composition and methods for the modification of gene CC
expression
FH Key Location/Qualifiers
FT 5'UTR (1)..(654)
FT TATA_signal (537)..(543)
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|---------------------------|--------------------------------------------------------------------|-------------------|
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| FEATURES                  | Location/Qualifiers                                                |                   |
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|                           | /organism="Eucalyptus grandis"                                     |                   |
|                           | /mol_type="genomic DNA"                                            |                   |
|                           | /db_xref="taxon:71139"                                             |                   |
| ORIGIN                    |                                                                    |                   |
| Query Match               | 8.9%; Score 272; DB 2; Length 661;                                 |                   |
| Best Local Similarity     | 99.7%; Pred. No. 2.8e-141;                                         |                   |
| Matches 322; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;                                 |                   |
| Qy                        | 1116 CATGTTGACAAAAGCGCTGATTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT | 1175              |
| Db                        | 98 CATGTTGACAAAAGCGCTGATTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT   | 157               |
| Qy                        | 1176 GACGATGGCCCTCAGGGGAAATTAAGGCGCAACCCAGATTGCAAGAGCACAAGAGCA     | 1235              |
| Db                        | 158 GACGATGGCCCTCAGGGGAAATTAAGGCGCAACCCAGATTGCAAGAGCACAAGAGCA      | 217               |
| Qy                        | 1236 CGACCCAACTTCTTACACAGATCATCCAGATCGGCCAGTAAGGGTAATTAATTAAT      | 1295              |
| Db                        | 218 CGATCAACCTTCTTACACAGATCATCCAGATCGGCCAGTAAGGGTAATTAATTAAT       | 277               |
| Qy                        | 1296 TAACAAATAGCTCTTGATACCGGAACTCGGTATTTCTCTCACTTCCATAAACCCCTGATT  | 1355              |
| Db                        | 278 TAACAAATAGCTCTTGATACCGGAACTCGGTATTTCTCTCACTTCCATAAACCCCTGATT   | 337               |
| Qy                        | 1356 AATTGTTGGGAAAGCGAGCAGCAACCCACAAAGGTCAGATGTCATCCACGAGAGAGA     | 1415              |
| Db                        | 338 AATTGTTGGGAAAGCGAGCAGCAACCCACAAAGGTCAGATGTCATCCACGAGAGAGA      | 397               |
| Qy                        | 1416 GAGAGAGAGAGAGAGAGAGAG 1438                                    |                   |
| Db                        | 398 GAGAGAGAGAGAGAGAGAGAG 420                                      |                   |
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| AR360905                  | Sequence 12 from patent US 6596925.                                | PAT 17-AUG-2003   |
| LOCUS                     | AR360905                                                           | 661 bp DNA linear |
| DEFINITION                | AR360905.1 GI:33768415                                             |                   |
| ACCESSION                 | AR360905.1                                                         |                   |
| VERSION                   | Unknown.                                                           |                   |
| KEYWORDS                  | Unknown.                                                           |                   |
| SOURCE                    | Unknown.                                                           |                   |
| ORGANISM                  | Unknown.                                                           |                   |
| REFERENCE                 | 1 (bases 1 to 661)                                                 |                   |
| AUTHORS                   | Perera,J.R., Eagleston,C. and Rice,S.J.                            |                   |
| TITLE                     | Compositions and methods for the modification of gene expression   |                   |
| JOURNAL                   | Patent: US 6596925-A 12 22-JUL-2003;                               |                   |
|                           | Genesis Research & Development Corp. Ltd. and Rubicon Forests      |                   |
|                           | Holdings Ltd.; Parnell;                                            |                   |
|                           | NZ;                                                                |                   |
| FEATURES                  | Location/Qualifiers                                                |                   |
| source                    | 1..661                                                             |                   |
|                           | /organism="unknown"                                                |                   |
|                           | /mol_type="genomic DNA"                                            |                   |
| ORIGIN                    |                                                                    |                   |
| Query Match               | 8.9%; Score 272; DB 2; Length 661;                                 |                   |
| Best Local Similarity     | 99.7%; Pred. No. 2.8e-141;                                         |                   |
| Matches 322; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;                                 |                   |
| Qy                        | 1116 CATGTTGACAAAAGCGCTGATTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT | 1175              |
| Db                        | 98 CATGTTGACAAAAGCGCTGATTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT   | 157               |
| Qy                        | 1176 GACGATGGCCCTCAGGGGAAATTAAGGCGCAACCCAGATTGCAAGAGCACAAGAGCA     | 1235              |
| Db                        | 158 GACGATGGCCCTCAGGGGAAATTAAGGCGCAACCCAGATTGCAAGAGCACAAGAGCA      | 217               |



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Query Match 6.2%; Score 189; DB 4; Length 1452;
Best Local Similarity 99.3%; Pred. No. 2.7e-94;
Matches 289; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2388 CCACCCTTCTCGTGTCAAGCACGTCGAGGCGACATGTCGTTCAGCGTTCACAAAGGGA 2447
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QY 2448 GATGCCATTTTCATGAAGTGATATGCCATGACTGGAGTGACGACCATTCGCGAAGTTC 2507
DB 861 GATGCCATTTTCATGAAGTGATATGCCATGACTGGAGTGACGACCATTCGCGAAGTTC 920

QY 2508 CTCGAAGACTGCTACGATGGCTTCCACAAATGGAAGTGATGCTTCGAGATCGGTA 2567
DB 921 CTCGAAGACTGCTACGATGGCTTCCACAAATGGAAGTGATGCTTCGAGATCGGTA 980

QY 2568 CTCCTGTGTACCCAGACAGCGAGCTAGCGACCAAGATGTGATCCACATCGACTGCATC 2627
DB 981 CTCCTGTGTACCCAGACAGCGAGCTAGCGACCAAGATGTGATCCACATCGACTGCATC 1040

QY 2628 ATGTTGGCCACACACCCAGCGGGAAGAGAGGACACAGAGGAGTTCGAG 2678
DB 1041 ATGTTGGCCACACACCCAGCGGGAAGAGAGGACACAGAGGAGTTCGAG 1091

RESULT 10
AF168777
LOCUS
DEFINITION
Eucalyptus globulus caffeic acid O-methyltransferase (COMT2) gene,
partial cds.
AF168777
VERSION
AF168777.1 GI:5739366
KEYWORDS
SOURCE
ORGANISM
Eucalyptus globulus
Eucalyptus globulus
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 3022)
De Melis, L.E., Whiteman, P.H. and Stevenson, T.W.
Molecular cloning and sequence analysis of genomic DNA fragments
amplified enzymatically for phenylalanine ammonia lyase and caffeic
acid O-methyltransferase from Eucalyptus globulus
Unpublished
2 (bases 1 to 3022)
De Melis, L.E., Whiteman, P.H. and Stevenson, T.W.
Direct Submission
Submitted (14-JUL-1999) Applied Biology & Biotechnology, RMIT
University, GPO Box 2476V, Melbourne, Vic 3001, Australia
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us-10-702-319a-113.olig.rge
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Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2859 GCGAAGTTCTCTCAAGAACTGCTACGATGGCTTCCCAACAATGGAAGGTGATCGTTGCA 2918

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DB 2919 GAGTGGTACTCCCTGTGTGTACCCAGACACGAGCCCTAGCGACCAAGAATGTGATCCACATC 2978

QY 2619 GACTGCATCATGTTGGCCCAACACCCAGCGGGAAGAGAGGA 2661
DB 2979 GACTGCATCATGTTGGCCCAACACCCAGCGGGAAGAGAGGA 3021

RESULT 11
BD224382
LOCUS
DEFINITION
Materials and methods for the modification of plant lignin content.
BD224382
ACCESSION
BD224382.1 GI:33034152
VERSION
JP 2002527058-A/106.
KEYWORDS
Eucalyptus grandis
ORGANISM
Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 407)
Blokberg, L.N. and Havukkala, I.J.
Materials and methods for the modification of plant lignin content
Patent: JP 2002527058-A 106 27-AUG-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS LTD
OS Eucalyptus grandis
PN JP 2002527058-A/106
PD 27-AUG-2002
PF 06-OCT-1999 JP 2000575991
PR 09-OCT-1998 US 09/169789,14-JUL-1999 US 60/143811 PI
LEONARD NATHAN BLOKBERG, ILKKA JAAKKO HAVUKKALA PC
C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/02,C12N9/04,C12N9/PC
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CC Materials and methods for the modification of plant lignin
content
FH Key Location/Qualifiers
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DB 297 ATGCTCGACCGGATCTTCGGCTGCTGGCCAGCTACTCGTGTACGTGACGCTCCGCGC 356

QY 1957 GACCTCCCGGATGCAAGTTCGAGCGGCTCTACGGCTTAGCGCCGCTGTC 2007
DB 357 GACCTCCCGGATGCAAGTTCGAGCGGCTCTACGGCTTAGCGCCGCTGTC 407

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Thu Nov 2 13:35:49 2006

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LOCUS AR216432 407 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 106 from patent US 6410718.  
ACCESSION AR216432  
VERSION AR216432.1 GI:23314912  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 407)  
AUTHORS Bloksberg,L.N. and Havukkala,I.  
TITLE Materials and methods for the modification of plant lignin content  
JOURNAL Patent: US 6410718-A 106 25-JUN-2002;  
Genesis Research & Development Corporation Ltd. and Fletcher  
Challenge Forests Ltd.;  
NZX;  
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LOCUS AR432834 407 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 106 from patent US 6653528.  
ACCESSION AR432834  
VERSION AR432834.1 GI:40195437  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 407)  
AUTHORS Bloksberg,L.N. and Havukkala,I.  
TITLE Pinus radiata nucleic acids encoding O-methyl transferase and  
methods for the modification of plant lignin content therewith  
JOURNAL Patent: US 6653528-A 106 25-NOV-2003;  
Genesis Research & Development Corporation Limited and Rubicam  
Forests Industries Limited; Parnell;  
NZX;  
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Query Match 3.6%; Score 111; DB 2; Length 407;  
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LOCUS AR074115 421 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 24 from patent US 5952486.  
ACCESSION AR074115  
VERSION AR074115.1 GI:10000875  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 421)  
AUTHORS Bloksberg,L.N., Havukkala,I. and Grierson,A.W.  
TITLE Materials and methods for the modification of plant lignin content  
JOURNAL Patent: US 5952486-A 24 14-SEP-1999;  
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Qy 1957 GACCTCCCGGATGCGAAGGTCGAGCGGCTTACGGCTTAGCGCGGTGTGC 2007  
Db 371 GACCTCCCGGATGCGAAGGTCGAGCGGCTTACGGCTTAGCGCGGTGTGC 421

RESULT 15  
BD005663  
LOCUS BD005663 421 bp DNA linear PAT 31-JAN-2002  
DEFINITION Materials and methods for the modification of plant lignin content.  
ACCESSION BD005663  
VERSION BD005663.1 GI:18634034  
KEYWORDS JP 2001500378-A/24.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 421)  
AUTHORS Bloksberg,L.N., Grierson,A.W. and Havukkala,I.J.  
TITLE Materials and methods for the modification of plant lignin content  
JOURNAL Patent: JP 2001500378-A 24 16-JAN-2001;  
GENESIS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS  
LTD  
COMMENT  
OS Unidentified  
PN JP 2001500378-A/24  
PD 16-JAN-2001  
PF 10-SEP-1997 JP 1998513535  
PR 11-SEP-1996 US 08/713000  
PI LEONARD NATHAN BLOKSBERG,ALISTAIR WALLACE GRIERSON, PI ILKKA  
JAAKKO HAVUKKALA  
PC C12N15/53,C12N15/54,C12N15/52,C12N15/60,C12N15/82,A01H5/00 CC  
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ORIGIN  
Query Match 3.6%; Score 111; DB 2; Length 421;  
Best Local Similarity 100.0%; Pred. No. 3.5e-50;  
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| Db | 371  | GACCTCCCCGATGGCAAGGTCGAGCGGCTCTACGGCTTAGCGCGGTTGTC        | 421  |

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Job time : 16938 secs

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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:27:09 ; Search time 17309.4 Seconds  
(without alignments)  
11193.945 Million cell updates/sec

Title: US-10-702-319A-113\_COPY\_41\_3070

Perfect score: 3030

Sequence: 1 cacctgttcagtttgattcc.....acttcgaacaaaaaaaaa 3030

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb env.\*

2: gb pat.\*

3: gb ph.\*

4: gb pi.\*

5: gb pr.\*

6: gb ro.\*

7: gb sts.\*

8: gb sv.\*

9: gb un.\*

10: gb vi.\*

11: gb ov.\*

12: gb htg.\*

13: gb in.\*

14: gb om.\*

15: gb ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2          | 2020.4 | 66.7        | 2096   | 2     | BD262168 Compositi |
| 3          | 2020.4 | 66.7        | 2096   | 2     | AR360953 Sequence  |
| 4          | 1429.6 | 47.2        | 1630   | 2     | BD224383 Materials |
| 5          | 1429.6 | 47.2        | 1630   | 2     | AR216433 Sequence  |
| 6          | 1429.6 | 47.2        | 1630   | 2     | AR432835 Sequence  |
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| 9          | 676    | 22.3        | 1876   | 2     | AX773024           |
| 10         | 676    | 22.3        | 1876   | 4     | AF220491           |
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| 12         | 671.6  | 22.2        | 1408   | 4     | D0001169           |
| 13         | 664    | 21.9        | 1393   | 4     | AB086104           |
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| 15         | 651.8  | 21.5        | 1268   | 4     | PACOMT1            |
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| 17         | 638.2  | 21.1        | 661    | 2     | AR360905           |
| 18         | 631    | 20.8        | 1503   | 2     | AR637756           |

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| 24 | 613   | 20.2 | 1486 | 4 | CBU86760   |
| 25 | 605.4 | 20.0 | 1331 | 4 | SSNCAFMEH  |
| 26 | 603.8 | 19.9 | 1370 | 2 | AR366728   |
| 27 | 603.8 | 19.9 | 1370 | 2 | AR382609   |
| 28 | 601.6 | 19.9 | 1380 | 4 | AF454632   |
| 29 | 601.6 | 19.9 | 1386 | 4 | AF454631   |
| 30 | 598.8 | 19.8 | 1377 | 4 | AF139533   |
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| 32 | 577.6 | 19.1 | 1187 | 4 | AF154918   |
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## ALIGNMENTS

RESULT 1  
AR360987  
LOCUS AR360987 3070 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 113 from patent US 6596925.  
ACCESSION AR360987  
VERSION AR360987.1 GI:33768497  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3070)  
Perera,J.R., Eagleton,C. and Rice,S.J.  
AUTHORS Compositions and methods for the modification of gene expression  
TITLE Patent: US 6596925-A 113 22-JUL-2003;  
JOURNAL Genesis Research & Development Corp. Ltd. and Rubicon Forests Holdings Ltd.; Parnell;  
NZX;

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|        | Best Local Similarity | 100.0%;                                                        | Pred. No. 0;  |           |              |
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| Qy     | 61                    | GATTAATGATTCACAGAGGATAAAAGTAGGAGATAGGGGATCTCCCGCTGTATG         | 120           |           |              |
| Db     | 101                   | GATAATGATTCACAGAGGATAAAAGTAGGAGATAGGGGATCTCCCGCTGTATG          | 160           |           |              |
| Qy     | 121                   | CCTCGGTAGTTTCAAAATAGGCAAAAGTTTCGCCGTTGATTTGACAGCAAAAGACACC     | 180           |           |              |
| Db     | 161                   | CCTCGGTAGTTTCAAAATAGGCAAAAGTTTCGCCGTTGATTTGACAGCAAAAGACACC     | 220           |           |              |
| Qy     | 181                   | GTCCTTATGATTCATGATTCATTTGATTCACCATGATAGGGTGAATTCCTAGAGTGAGGAGA | 240           |           |              |

Db 221 GTCGTTATGCATGCATGATCCATTGTTACCAATGATGGGTGAAATCCTAGAGTGAGAGA 280  
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361 ATTAATAATATTGCTCCTGAATTTGACGTCCACTGACAAAAGCGCTTTGCTCCTCGAAAATA 420  
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Qy 1321 GGTGGAAAGCGACAGCCAAACCAAAAGGTCAATGTCAATCCACGAGAGAGAGAG 1380  
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Qy 1741 AGCCGCCATTCGAGATTCGACCTTCTCGAGATCATATGSCAAAGACGGGCGGGCGGTTCC 1800  
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RESULT 2  
BD262168  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD262168  
Composition and methods for the modification of gene expression.  
BD262168  
BD262168.1 GI:33071936  
Eucalyptus grandis  
Eucalyptus grandis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; Myrtales; Myrtaceae; Eucalyptus.  
1 (bases 1 to 2096)  
Perera, R., Rice, S.J. and Bagleton, C.K.  
Composition and methods for the modification of gene expression  
Patent: JP 2002539834-A 60 26-NOV-2002;  
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE  
FORESTS INDUSTRIES LTD  
OS Eucalyptus grandis (flooded gum)  
PN JP 2002539834-A/60  
PD 26-NOV-2002  
PF 24-FEB-2000 JP 2000608755  
PR 25-MAR-1999 US 09/276599, 30-JUL-1999 US 60/146591 PI  
RAJAN PERERA, STEPHEN J RICE, CLARE KATHERINE EAGLETON PC  
C12N15/09, A01H5/00, C07K14/415, C12N5/10, C12Q1/02, C12Q1/68, PC  
C12N15/00,  
PC C12N5/00  
CC Composition and methods for the modification of gene CC

expression  
FH Key Location/Qualifiers  
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/mol\_type="genomic DNA"  
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ORIGIN  
Query Match 66.7%; Score 2020.4; DB 2; Length 2096;  
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Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;  
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LOCUS AR360953  
DEFINITION Sequence 60 from patent US 6596925.  
ACCESSION AR360953  
VERSION AR360953.1 GI:33768463  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2096)  
AUTHORS Perera,J.R., Eagleton,C. and Rice,S.J.  
TITLE Compositions and methods for the modification of gene expression  
JOURNAL Patent: US 6596925-A 60 22-JUL-2003;  
Genesis Research & Development Corp. Ltd. and Rubicon Forests  
Holdings Ltd.; Parnell;  
NZX;  
FEATURES  
source Location/Qualifiers  
1..2096  
/organism="unknown"  
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ORIGIN  
Query Match 56.7%; Score 2020.4; DB 2; Length 2096;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;  
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## RESULT 4

BD224383  
LOCUS BD224383 1630 bp DNA linear PAT 17-JUL-2003  
DEFINITION Materials and methods for the modification of plant lignin content.  
ACCESSION BD224383  
VERSION BD224383.1 GI:33034153  
KEYWORDS JP 2002527058-A/107.  
SOURCE Eucalyptus grandis

## ORGANISM

Eucalyptus grandis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; Myrtales; Myrtaceae; Eucalyptus.

## REFERENCE

1. (bases 1 to 1630)  
Bloksberg, L.N. and Havukkala, I.J.  
Materials and methods for the modification of plant lignin content  
Patent: JP 2002527058-A 107 27-AUG-2002;  
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE  
FORESTS LTD

## COMMENT

OS Eucalyptus grandis  
PN JP 2002527058-A/107  
PD 27-AUG-2002  
PF 06-OCT-1998 JP 2000575991  
PR 09-OCT-1998 US 09/169789, 14-JUL-1999 US 60/143811 PI  
LEONARD NATHAN BLOKSBERG ILKKA JAAKKO HAVUKKALA PC  
C12N15/09, A01H5/00, C12N5/10, C12N9/00, C12N9/02, C12N9/04, C12N9/PC  
10, C12N9/24,  
PC C12N9/88, C12N15/00, C12N5/00  
CC Materials and methods for the modification of plant lignin CC

## FEATURES

source  
FT  
Key Location/Qualifiers  
1..1630  
/organism="Eucalyptus grandis"  
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## ORIGIN

Query Match 47.2%; Score 1429.6; DB 2; Length 1630;  
Best Local Similarity 99.0%; Pred. No. 0;







Db 191 CAAGCGCCCATGAGCTCGACCTCTCGAGATCATGGCCAAAGCCGGCGCGGCTT 250  
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## RESULT 8

AF006009 1300 bp mRNA linear PLN 24-SEP-1997  
LOCUS Clarkia breweri caffeic acid O-methyltransferase (COMT) mRNA,  
DEFINITION complete cds.

ACCESSION AF006009

VERSION AF006009.1 GI:2240206

KEYWORDS

SOURCE

ORGANISM

Clarkia breweri

Clarkia breweri

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Myrtales; Onagraceae; Clarkia.

1 (bases 1 to 1300)

Wang,J. and Pichersky,E.

Nucleotide Sequence of S-Adenosyl-L-Methionine:Caffeic Acid

3-O-Methyltransferase from Clarkia breweri (Accession No. AF006009)

(PCR97-104)

Plant Physiol. 114, 1567 (1997)

2 (bases 1 to 1300)

Wang,J. and Pichersky,E.

Characterization of (Is)oenol O-Methyltransferase Involved in

Floral Scent Production in Clarkia breweri

Unpublished

3 (bases 1 to 1300)

Wang,J. and Pichersky,E.

Direct Submission

Submitted (29-MAY-1997) Biology, University of Michigan, 830 North

University Avenue, Ann Arbor, MI 48109, USA

JOURNAL

Location/Qualifiers

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## ORIGIN

Query Match 22.3%; Score 676.6; DB 4; Length 1300;  
Best Local Similarity 76.5%; Pred. No. 6.1e-172;  
Matches 859; Conservative 0; Mismatches 254; Indels 10; Gaps 2;

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LOCUS AX773024 1876 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 1 from Patent WO03046163.
ACCESSION AX773024
VERSION AX773024.1 GI:32485193
KEYWORDS .
SOURCE Fragaria x ananassa
ORGANISM Fragaria x ananassa
 Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
REFERENCE 1
 Schwab,W., Kaldenhoff,R. and Wein,M.
 Multifunctional caffeic acid O-methyltransferase
 Patent: WO 03046163-A 1 05-JUN-2003;
 Bayerische Julius-Maximilians-Universitaet Wuerzburg (DB)
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Best Local Similarity 77.0%; Pred. No. 8.2e-172;
Matches 850; Conservative 0; Mismatches 250; Indels 4; Gaps 2;
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## RESULT 10

AF220491 1876 bp mRNA linear PLN 27-JAN-2000  
LOCUS Fragaria x ananassa O-methyltransferase (omt1) mRNA, complete cds.  
DEFINITION AF220491  
ACCESSION AF220491  
VERSION AF220491.1 GI:6760442  
KEYWORDS  
SOURCE Fragaria x ananassa  
ORGANISM Fragaria x ananassa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
1 (bases 1 to 1876)  
Kaldenhoff R., Wein, M. and Schwab, W.  
Isolation and characterization of a O-methyltransferase from  
strawberry  
Unpublished  
JOURNAL  
REFERENCE 2 (bases 1 to 1876)  
AUTHORS Kaldenhoff, R., Wein, M. and Schwab, W.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-2000) Botanik I, Julius-von-Sachs-Institut fuer  
Biowissenschaften, Julius-von-Sachs-Platz 2, Wuerzburg 97082,  
Germany

## FEATURES

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## gene

## CDS

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ORIGIN  
Query Match 22.3%; Score 676; DB 4; Length 1876;  
Best Local Similarity 77.0%; Pred. No. 8.2e-172;  
Matches 850; Conservative 0; Mismatches 250; Indels 4; Gaps 2;  
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DEFINITION Sequence 3 from Patent WO03046163.
ACCESSION AX773026
VERSION AX773026.1 GI:32485194
KEYWORDS
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Fragaria x ananassa
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.

REFERENCE
1 Schwab,W., Kaldenhoff,R. and Wein,M.
AUTHORS Multifunctional caffeic acid o-methyltransferase
TITLE Patent: WO 03046163-A 3 05-JUN-2003;
JOURNAL Bayerische Julius-Maximilians-Universitaet Wuerzburg (DB)
FEATURES
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ORIGIN
Query Match 22.3%; Score 675.8; DB 2; Length 1098;
Best Local Similarity 76.8%; Pred. No. 1e-171;
Matches 838; Conservative 0; Mismatches 252; Indels 1; Gaps 1;

Qy 1639 CCGGCTCCGAGACCCAGATGACCCCGACCCCAAGTCTCGGACGAGCGCAACCTCTCG 1698
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Db 548 ACTCCACCAATTACTATGAAGAATCTTTGAGACTTACAAAGGCTTCGAGGGCCTCAAT 607

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Db 608 CCAATCGTGTGTCGGTGGCGGCAACCGAGCTGTGTGTAACATGATCGTTTCCAAGTACC 667

Qy 2299 CATCAATGAAGGATCAACTTCGAC- CGCCCCAACGGAATGAAGACGCCCCACCCCTTC 2357
Db 668 CTTGATCAAGGCGCATCAACTTCGACTTCGCTCATGTTATCGAAGATGCTCCTCAATATC 727

Qy 2358 CTGGTCTCAAGCACTGTCGGAGGCGCATGTTGTCAGCGTTCCAAAGGAGATGCCATTT 2417
Db 728 CTGGTCTTCAACACGTTGGAGGGGACATGTTGTAAGTGTACCAAGGGAATGCAATTT 787

Qy 2418 TCATGAAGTGGATATGCCATGACTGAGTGACGACCATTTGCGGAAAGTTCCTCAAGAACT 2477
Db 788 TCATGAAGTGGATATGTCAGACTGAGTGACGAGCATTTGCATAAATCTTGAAGAACT 847

Qy 2478 GCTACGATGCGCTTCCCAACAATGGAAAGTGTGTCGAGAGTGGCTACTCCCTGTGT 2537
Db 848 GCTACGCTGCGCTTCCAGACGATGGCAAGTGTGTTCTGCTGAGTGCATTTCTTCTGTG 907

Qy 2538 ACCGACGACGAGCTTAGGACCAAGATGTGATCCACATCGACTGCATCATGTTGGCCC 2597
Db 908 CACGACGACTAGCTTGGCCACCAAGGGAGTGTGTCATATGATGATGATGTTGGCGC 967

Qy 2598 ACAACCCGCGGGAAGAGAGACACAGAGGAGTTCGAGGCAATTTGGCCAAAGGGCGCG 2657
Db 968 ACAACCTCGCGCAAGAGAGACCGAGCAAGAAATTTGAAGCCCTGGCTTAAGGGTCTG 1027

Qy 2658 GATTTCAAGGCTTCCAAAGTCAATGCTGCTGCTTTCGGCACTCACGTCATGAGTCTGA 2717
Db 1028 GATTTCAAGGCAATTCGCTGCTGCTGATGCTTTCAACACCTATGTCATTGAGTTCTTA 1087

Qy 2718 AGACCGCTTGA 2728
Db 1088 AGAAGATCTGA 1098

RESULT 12
DQ001169
LOCUS DQ001169 1408 bp mRNA linear PLN 01-SEP-2005
DEFINITION Acacia mangium x Acacia auriculiformis caffeic acid
O-methyltransferase mRNA, complete cds.
ACCESSION DQ001169
VERSION DQ001169.1 GI:68159361
KEYWORDS
SOURCE
ORGANISM
Acacia mangium x Acacia auriculiformis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Mimosoideae; Acaciae;
Acacia.
REFERENCE
1 (bases 1 to 1408)
AUTHORS Sukganah,A., Wickneswari,R. and Choong,C.Y.
TITLE Full length of Acacia mangium x Acacia auriculiformis hybrid cDNA
clones encoding cinnamoyl-CoA reductase (CCR) and caffeic acid
O-methyltransferase (COMT)
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 1408)
AUTHORS Choong,C.Y., Wickneswari,R. and Sukganah,A.
TITLE Direct Submission
JOURNAL Submitted (07-APR-2005) School of Environmental and Natural
Resource Sciences, Universiti Kebangsaan Malaysia, Faculty of
Science and Technology, Bangi, Selangor 43600, Malaysia
FEATURES
Location/Qualifiers
source
1. 1408
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```

ORIGIN

|                       |                 |                                                               |           |              |
|-----------------------|-----------------|---------------------------------------------------------------|-----------|--------------|
| Query Match           | 22.2%;          | Score 671.6;                                                  | DB 4;     | Length 1408; |
| Best Local Similarity | 75.8%;          | Pred. No. 1.4e-170;                                           |           |              |
| Matches 844;          | Conservative 0; | Mismatches 269;                                               | Indels 1; | Gaps 1;      |
| Qy                    | 1639            | CCGGCTCGAGACCCAGATGACCCCGACCCAGTCTCGGACGACGAGCGCAACCTCTTCG    | 1698      |              |
| Db                    | 79              | CAGCGCGGAGACTCAGATAACCCCTACCCATGTCAACGACGAGGAGCAACCTCTTCG     | 138       |              |
| Qy                    | 1699            | CCATGACGTCGGGAGCGCTCCGTCCTCCATGCTCCATGCTTAAGCCGCCATCGATCG     | 1758      |              |
| Db                    | 139             | CCATGACGTCGGGAGCGCTCCGTCCTCCATGCTCCATGCTTAAGCCGCCATCGATCG     | 198       |              |
| Qy                    | 1759            | ACCTCTCGAGATCATGCGGACGAGCGGCGCGCTTCTCTCCACGCGGGAATTCG         | 1818      |              |
| Db                    | 199             | ATCTACTCGAGATCATGCGGAGCGGCGCTTCTCTCCACGCGGGAATTCG             | 258       |              |
| Qy                    | 1819            | CGGACAGCTCCGACCCAGAACCCGAGGACCGCTCATGCTCGACCGGATCTTCGGC       | 1878      |              |
| Db                    | 259             | CCTCCAGCTTCCGACCAAGAACCCGAGGACCGCTCATGCTCGACCGGATCTTCGGC      | 318       |              |
| Qy                    | 1879            | TGCTGGCAGTACTCTCGTGTCTCAGTGCACGCTCCGACCTCCCGATGCGGAGTTCG      | 1938      |              |
| Db                    | 319             | TGTTGGCTGTACAACTCTCTCAGTCTCTCCCTCCGAAACCTCCCGACCGGAGATCG      | 378       |              |
| Qy                    | 1939            | AGCGGCTCTAGCGCTTACGCGCGGTGTGCAAGTCTTCTGGTCAAGAACGAGGACGGGTCT  | 1998      |              |
| Db                    | 379             | AGAGGCTCTAGCGCTTACGCGCGGTGTGCAAGTCTTCTGGTCAAGAACGAGGACGGGTCT  | 438       |              |
| Qy                    | 1999            | CCATGCGCGCACTCAACTTGTATGACACCGAGCAAAATCTCATGAAAGCTGGTATTACC   | 2058      |              |
| Db                    | 439             | CTATCGCTCCCTCAACCTCATGAATCAGGACAAAGTCTCTCATGAGAGCTGGTACTACT   | 498       |              |
| Qy                    | 2059            | TGAAGATGCGGTCTTGAAGCGGAAATCCATTCMAAGCGGTACGGGATGACCGGT        | 2118      |              |
| Db                    | 499             | TGACAGACAGTCTTGAAGGAGGATTCATTCATCAACAGGCAATGGCATGACATCGT      | 558       |              |
| Qy                    | 2119            | TCGAGTATCATGGCACCGACCGGATTCACAAAGATCTTTAAACCGGGAATGCTGTATC    | 2178      |              |
| Db                    | 559             | TTGAGTACACCGCAAGATGCGAGGTTCACAAAGTGTTTTAAACGAGGATGCGGAC       | 618       |              |
| Qy                    | 2179            | ACTCCACATTAATATGAAGAGATATCTGGAACACATACAGGGCTTCGAGGGCTTCGAGA   | 2238      |              |
| Db                    | 619             | ACTCCACATTAATATGAAGAGATATCTGGAACACATACAGGGCTTCGAGGGCTTCGAGA   | 678       |              |
| Qy                    | 2239            | CCGTGGTCGATGTCGGAGCGGCACTCGGGCGGTGCTCAGCATGATGCTTCCCAATACC    | 2298      |              |
| Db                    | 679             | CTCTCGTCGATGTCGGTGGCGGCACTCGGGCGGTGCTCAGCATGATGCTTCTAAGTACC   | 738       |              |
| Qy                    | 2299            | CATCAATGAAGAGGATCAACTTCGACC--GCCCAACGATTTGAAGCGCCACCCCTTC     | 2357      |              |
| Db                    | 739             | CTTCAATGAAGGATTAACCTTTGACCTGGCCCCATGTCAATGAAGAGGCTCCCTCTTTTC  | 798       |              |
| Qy                    | 2358            | CTGTGTGTCAGACGTCGGAGCGGACATGTTCTGTCAGCGGTTCCAAAGGAGATGCAATTT  | 2417      |              |
| Db                    | 799             | CAGGTGTTGACATGTTGTCGGGACATGTTCTGTCAGTGTTCCTCAAAAGCTGACGCTGTTT | 858       |              |

|    |      |                                                               |      |  |
|----|------|---------------------------------------------------------------|------|--|
| Qy | 2418 | TCATGAAGTGGATATGCGCATGACTGGAGTGCACGACCATTCGCGAAGTTCCTCAAGAACT | 2477 |  |
| Db | 859  | TCATGAAGTGGATATGCGCATGACTGGAGTGCACGACCATTCGCGAAGTTCCTCAAGAACT | 918  |  |
| Qy | 2478 | GCTACGATGCGCTTCCCAACAATGGAAGTGTGTTGGTGGAGTGGTACTCCTCTGTGT     | 2537 |  |
| Db | 919  | GCTACGATGCGCTTCCCAACAATGGAAGTGTGTTGGTGGAGTGGTACTCCTCTGTGT     | 978  |  |
| Qy | 2538 | ACCAGACACGAGCTAGCGACCAAGAAATGTGATCCACATCGACTGATGATGTTGCC      | 2597 |  |
| Db | 979  | CTCGGACTCGAGCTTGGCGACCAAGGGGTGGTCCACATTCAGCTCATGCTGGCTC       | 1038 |  |
| Qy | 2598 | ACAACCCAGCGGGAAGAGAGGACACAGAAGAGTTCGAGGCAATTCGCCAAAGGGCCG     | 2657 |  |
| Db | 1039 | ATAACCCAGGTGGCAAGAGAGGACTGAGAAAGAGTTCGAGGCTTCGCCCAAGGGCTG     | 1098 |  |
| Qy | 2658 | GATTCAGGGCTTCCAAAGTCAATGTCGTCGCGCTTTCGGCACTCAGCTCATGAGTTCCTGA | 2717 |  |
| Db | 1099 | GCTTCCAAAGTTCGCGTGTGTTGTTGCTCTGCTCACTCTATATCATGGAATTCCTCA     | 1158 |  |
| Qy | 2718 | AGACCGCTTCATGCTCTCTCTGTTGGTGTGATGTC                           | 2751 |  |
| Db | 1159 | AGAACCTTAACCTGTTCTCTTTATTTCGATC                               | 1192 |  |

|            |                                                                     |                                                                       |      |                 |
|------------|---------------------------------------------------------------------|-----------------------------------------------------------------------|------|-----------------|
| RESULT 13  |                                                                     |                                                                       |      |                 |
| AB086104   |                                                                     | 1393 bp                                                               | mRNA | linear          |
| LOCUS      | Rosa chinensis var. spontanea RCOMT2                                | mRNA for caffeic acid                                                 |      | PLN 21-JAN-2006 |
| DEFINITION | O-methyltransferase, complete cds.                                  |                                                                       |      |                 |
| ACCESSION  | AB086104                                                            |                                                                       |      |                 |
| VERSION    | AB086104.1                                                          | GI:32440932                                                           |      |                 |
| KEYWORDS   |                                                                     |                                                                       |      |                 |
| SOURCE     | Rosa chinensis var. spontanea                                       |                                                                       |      |                 |
| ORGANISM   | Rosa chinensis var. spontanea                                       |                                                                       |      |                 |
| REFERENCE  | 1                                                                   | Wu, S., Watanabe, N., Mita, S., Ueda, Y., Shibuya, M. and Ebizuka, Y. |      |                 |
| AUTHORS    | Two O-methyltransferases isolated from flower petals of Rosa        |                                                                       |      |                 |
| TITLE      | chinesis var. spontanea involved in scent biosynthesis              |                                                                       |      |                 |
| JOURNAL    | J. Biosci. Bioeng. 96 (2), 119-128 (2003)                           |                                                                       |      |                 |
| PUBMED     | 16233496                                                            |                                                                       |      |                 |
| REFERENCE  | 2                                                                   | (bases 1 to 1393)                                                     |      |                 |
| AUTHORS    | Wu, S. and Watanabe, N.                                             |                                                                       |      |                 |
| TITLE      | Direct Submission                                                   |                                                                       |      |                 |
| JOURNAL    | Submitted (03-JUN-2002) Naoharu Watanabe, Shizuoka University,      |                                                                       |      |                 |
|            | Department of Applied Biological Chemistry, Faculty of Agriculture, |                                                                       |      |                 |
|            | 836 Ohya, Shizuoka, Shizuoka 422-8529, Japan                        |                                                                       |      |                 |
|            | (E-mail: acwat@agr.shizuoka.ac.jp, Tel: 81-54-238-4870,             |                                                                       |      |                 |
|            | Fax: 81-54-238-4870)                                                |                                                                       |      |                 |
| FEATURES   | Location/Qualifiers                                                 |                                                                       |      |                 |
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|            | O-methylation of caffeic acid to form ferulic acid"                 |                                                                       |      |                 |
|            | /codon_start=1                                                      |                                                                       |      |                 |
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|            | ERLYGLPVCVKFLTKNEDGVSIAALCLMNQKVLVESWYHLKDAVLDDGIPFNKAYGM           |                                                                       |      |                 |

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ORIGIN

|                           |        |                                                               |           |              |
|---------------------------|--------|---------------------------------------------------------------|-----------|--------------|
| Query Match               | 21.98; | Score 664;                                                    | DB 4;     | Length 1393; |
| Best Local Similarity     | 74.84; | Pred. No. 1.6e-168;                                           |           |              |
| Matches 859; Conservative | 0;     | Mismatches 285;                                               | Indels 4; | Gaps 2;      |
| QY                        | 1626   | AGAAATGGTTTCGACCGGCTCCGAGACCCAGATACACCCGACCAAGTCTCGACGACGAG   | 1685      |              |
| DB                        | 76     | AAAATGGTTTCAACCGG---CGAGACTCAGATGACTCCGACCCCAAGTCTCCGACGAGGA  | 132       |              |
| QY                        | 1686   | GCGAACCTCTTTCGCATGCGAGCTGGCGAGCGCTCCGTCTCCCATGTCCTTAAGGCC     | 1745      |              |
| DB                        | 133    | GCCAACTCTTGGCCATGCAATCGCCAGCGCTCCGTCTCCCATGTCCTCAAGGCC        | 192       |              |
| QY                        | 1746   | GCCATCGAGATCGACCTCTCGAGATCATGCCAAGACGGCGCGGCTTCCTCTCC         | 1805      |              |
| DB                        | 193    | GCCATTGAGCTCGACCTCTTGGAGATCATGCCCAAGGCCGACCCGAGCGTTCCTCTCC    | 252       |              |
| QY                        | 1806   | ACGGGGAAATCGCGGCACAGCTCCCGACCAAGAACCCCGAGGCACCCGTCATGCTCGAC   | 1865      |              |
| DB                        | 253    | CCTAATGACCTAGCTCTCAGCTTCCGACCAAGAACCCCGAAGCTCCGGTCATGCTGAC    | 312       |              |
| QY                        | 1866   | CGGATCTTCCGGCTGCTGGCGAGTACTCCGTGCTCAGCTGCGACCCCTCCGCGACCTCCC  | 1925      |              |
| DB                        | 313    | CGGATGCTTGGCTTCTGGCCAGCTACTCCATTCTAACCTACTCTCTTGGCTACACTTCCG  | 372       |              |
| QY                        | 1926   | GATGGCAAGTCGAGCGGCTTACGGCTTAGCGCGGCTGTCAGTCTTGGTCAAGAAC       | 1985      |              |
| DB                        | 373    | GACGGCAAGTTGAGAGGCTCTACGGTTTGGGACCTGTGTGTAATTTTGACCAAGAAC     | 432       |              |
| QY                        | 1986   | GAGGACGGGCTCTCCATCGCGCACTCAACTTGATGAACAGGACAAATCTCATGGAA      | 2045      |              |
| DB                        | 433    | GAAATGGTGTCTCCATTGCTGCTCTCTGCTCATGAACCAAGACAGGCTCTGTCGAG      | 492       |              |
| QY                        | 2046   | AGCTGGTATTACCTGAAGATGCGGCTCTTGAAGCGGGAATCCCATTCACAAAGGCGTAC   | 2105      |              |
| DB                        | 493    | AGCTGGTATCATCTAAAGGATGCAAGTCTTCTGATGGTGGGATTCATTTAAAGGCGCTAT  | 552       |              |
| QY                        | 2106   | GGGATGACCGGTTGCGATCATGCGACCCAGCCCGGATTCACCAAGATCTTTAAACGG     | 2165      |              |
| DB                        | 553    | GGAATGACTGTCTTTGATTCATGGAACCTGACCTTAGATTCACCAAGGCTTTCACAAAG   | 612       |              |
| QY                        | 2166   | GGAATGCTGATCACTCCACCACTACTATGAAGAGATACCTGGAACATACAAAGGCTTC    | 2225      |              |
| DB                        | 613    | GGAATGGCTGACCACTCCACCACTTACCATGAAGAAATCCCTTGAGACTTATAAAGGCTTT | 672       |              |
| QY                        | 2226   | GAGGCGCTCGAGACCGTGGTGCATGTCGAGCGGCGCACTGGGGCGGTGCTCAGCATGATC  | 2285      |              |
| DB                        | 673    | GAGGCGCTCACATCCATCCATGTCGAGCGGCGCACCGGAGCTGTGTTTAAACATGATC    | 732       |              |
| QY                        | 2286   | GTTGCCAATACCACTCATGAAGGATCAACTTCGAC-CGCCCCACCGATTGAAGAC       | 2344      |              |
| DB                        | 733    | GTTCCTAAGTACCTTCGATCAAGGCGATCAACTTTGACTTGCCTCATGTGATCGAAGAT   | 792       |              |
| QY                        | 2345   | GCCCCACCCCTTCCTGGTGTCAAGCACGTCGGAGCGCACATGTTGTCGAGCGTTCCAAAG  | 2404      |              |
| DB                        | 793    | GCTCTCTCAATATCTTGGTGTGCAACATGTTGGAGGGACATGTTTGTAAAGTGTACCGAAA | 852       |              |
| QY                        | 2405   | GGAGATGCCATTTTCATGAAGTGGATATGCCATGACTGGATGACGACCATTTGGCGGAG   | 2464      |              |
| DB                        | 853    | GGAGATGCCAATTTTTCATGAAGTGGATATGTCACGACTGGAGTGACGACACTGCTTGAAA | 912       |              |
| QY                        | 2465   | TTCTCTCAAGAACTGCTAGATCGCTTCCCAACAATGGAAGGTCATCGTTGCGAGATGC    | 2524      |              |
| DB                        | 913    | TTCTTGAAGAATATGCTATGACGGCTTCCAGCAATGGAAGTGAATCTTGGTGAAGTGC    | 972       |              |
| QY                        | 2525   | GTACTCCCTGTGTACCCAGACACGAGCCCTAGCGACCAAGAATGTGATCCATCGACTGC   | 2584      |              |
| DB                        | 973    | ATTCTGCGGTAGCAGCGGACACTAGCTCGCCACCAAGGGAGTTGTCATATCGACGTG     | 1032      |              |

|            |                                                                                                                                                                                                                                                                                                                                                                                                       |                                                               |      |        |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|------|--------|
| QY         | 2585                                                                                                                                                                                                                                                                                                                                                                                                  | ATCATGTTGGCCCAACCCAGCGGGAAAGAGAGGACACACAGGAGTTCGAGGCATTTG     | 2644 |        |
| DB         | 1033                                                                                                                                                                                                                                                                                                                                                                                                  | ATCATGTTGGCTCACACCCCGGTGGCAAGAGAGGACGGGGCAGAGTTTGAAGCCCTG     | 1092 |        |
| QY         | 2645                                                                                                                                                                                                                                                                                                                                                                                                  | GCCAAAGGGCGCGGATTTTCAGGGCTTCCAAGTCATGTCGTGCGCTTTCGGCACTCACGTC | 2704 |        |
| DB         | 1093                                                                                                                                                                                                                                                                                                                                                                                                  | GCTAAGGGGTCTGGATTTCAAGGCATTTCGAGTAGCATGTAATGCTTTCAACACCTATGTC | 1152 |        |
| QY         | 2705                                                                                                                                                                                                                                                                                                                                                                                                  | ATGGAATTCCTCAAGACCGCTTGATCTGCTCTCTGCTGATGTTTCATGGTTCTTGGAT    | 2764 |        |
| DB         | 1153                                                                                                                                                                                                                                                                                                                                                                                                  | ATCGAGTTTCTCAAGAAGATCTGAGTACTGCTACTTGGCTTAGTTGATGTTTGTATGCT   | 1212 |        |
| QY         | 2765                                                                                                                                                                                                                                                                                                                                                                                                  | TTGAAAGG 2772                                                 |      |        |
| DB         | 1213                                                                                                                                                                                                                                                                                                                                                                                                  | GTCAATAAG 1220                                                |      |        |
| RESULT 14  |                                                                                                                                                                                                                                                                                                                                                                                                       |                                                               |      |        |
| LOCUS      | RCH439740                                                                                                                                                                                                                                                                                                                                                                                             | 1339 bp                                                       | mRNA | linear |
| DEFINITION | Rosa chinensis mRNA for caffeic acid O-methyltransferase (cont1 gene).                                                                                                                                                                                                                                                                                                                                |                                                               |      |        |
| ACCESSION  | AJ439740                                                                                                                                                                                                                                                                                                                                                                                              |                                                               |      |        |
| VERSION    | AJ439740.1                                                                                                                                                                                                                                                                                                                                                                                            | GI:27527919                                                   |      |        |
| KEYWORDS   | caffeic acid O-methyltransferase; comt1 gene.                                                                                                                                                                                                                                                                                                                                                         |                                                               |      |        |
| SOURCE     | Rosa chinensis                                                                                                                                                                                                                                                                                                                                                                                        |                                                               |      |        |
| ORGANISM   | Rosa chinensis                                                                                                                                                                                                                                                                                                                                                                                        |                                                               |      |        |
| REFERENCE  | 1 (bases 1 to 1339)                                                                                                                                                                                                                                                                                                                                                                                   |                                                               |      |        |
| AUTHORS    | Scalliet,G., Journot,N., Jullien,P.F., Baudino,S., Magnard,J.L., Channellere,S., Verne,P., Dumas,C., Bendahmane,M., Cock,M. and Huguency,P.                                                                                                                                                                                                                                                           |                                                               |      |        |
| TITLE      | Biosynthesis of the major scent components 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene by novel rose O-methyltransferases                                                                                                                                                                                                                                                                        |                                                               |      |        |
| JOURNAL    | PEBS Lett. 523 (1-3), 113-118 (2002)                                                                                                                                                                                                                                                                                                                                                                  |                                                               |      |        |
| PUBMED     | 12123815                                                                                                                                                                                                                                                                                                                                                                                              |                                                               |      |        |
| REFERENCE  | 2 (bases 1 to 1339)                                                                                                                                                                                                                                                                                                                                                                                   |                                                               |      |        |
| AUTHORS    | Cock,J.J.Mark.                                                                                                                                                                                                                                                                                                                                                                                        |                                                               |      |        |
| TITLE      | Direct Submission                                                                                                                                                                                                                                                                                                                                                                                     |                                                               |      |        |
| JOURNAL    | Submitted (25-MAR-2002) RDP, ENSL, 46, allée d'Italie, Lyon cedex 07 69364, France                                                                                                                                                                                                                                                                                                                    |                                                               |      |        |
| FEATURES   | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                   |                                                               |      |        |
| source     | 1..1339                                                                                                                                                                                                                                                                                                                                                                                               |                                                               |      |        |
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| gene       | 1..1339                                                                                                                                                                                                                                                                                                                                                                                               |                                                               |      |        |
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| CDS        | 52..1149                                                                                                                                                                                                                                                                                                                                                                                              |                                                               |      |        |
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## ORIGIN

| Query Match           | 21.9%          | Score 663.2                                                      | DB 4     | Length 1339 |
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| Matches 842           | Conservative 0 | Mismatches 258                                                   | Indels 4 | Gaps 2      |
| Qy                    | 1626           | AGAAATGGGTTTCGACCGCGCTCCGAGACCCAGATGACCCCGACCCCAAGTCTCGGACGACGAG | 1685     |             |
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| Db                    | 286            | CGGATGCTTCGGCTTCTGGCCAGCTACTCCATTTCAACCTACTCTTTCGGGTACACTTCGG    | 345      |             |
| Qy                    | 1926           | GATGGCAAGTTCGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCCTTGGTCAAGAAC     | 1985     |             |
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| Db                    | 526            | GGAATGACTGCTTTTGTATTCATATGGAACTTGACCTTAGATTCAACAAGGTCTTCAACAAG   | 585      |             |
| Qy                    | 2166           | GGAATGTCTGATCACTCCACCATTAATCATGNAAGAAGATATCGGNAACAATACAGGGGCTTC  | 2225     |             |
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| Db                    | 646            | GAGGGCTTCACATCCATCTGTGATGTTCGAGGCGGCACTGGGAGCTGTTGTTTACATGATC    | 705      |             |
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| Db                    | 706            | GTTTCTAAGTACCCCTTCGATCAAGGGCATCAACTTTGACTTTGCTCATGTGATCGAAGAT    | 765      |             |
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 DEFINITION X83217  
 ACCESSION X83217.1 GI:602587  
 VERSION caffeic acid O-methyltransferase.  
 KEYWORDS Prunus dulcis (almond)  
 SOURCE Prunus dulcis  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.

REFERENCE 1 Garcia-Mas,J., Messeguer,R., Arus,P. and Puigdomenech,P.  
 The Electronic Plant Gene Register  
 JOURNAL Plant Physiol. 108 (3), 1341-1343 (1995)  
 PUBMED 12228545  
 2 (bases 1 to 1268)  
 Puigdomenech,P.  
 AUTHORS Direct Submission  
 TITLE Submitted (05-DEC-1994) P. Puigdomenech, Dept. Genetica Molecular  
 JOURNAL CID-CSIC, Jordi Girona 18-26, 08034 Barcelona, SPAIN

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gene  
 CDS

ORIGIN  
 Query Match 21.5%; Score 651.8; DB 4; Length 1268;  
 Best Local Similarity 75.7%; Pred. No. 3.3e-165;  
 Matches 820; Conservative 0; Mismatches 262; Indels 1; Gaps 1;

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Qy 1707 CTGCGGAGCGCCTCCGTGCTCCCATGGTCTCTAAAGCGCGCCATCGAGATCGACCTCCTC 1766

Job time : 17311.4 secs

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Db 453 GCAGTTCTTGAAGGTGGCAITTCATTCNAAGGGCTTATGGAATGACTGCTTTTGAATAT 512
Qy 2127 CATGSCACGACCCCGGATTCNAAGATCTTTAAACCGGGGAATGTCTGATCACTCCACC 2186
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Db 693 AAGGGCATTAACCTTCGACTTGGCTCATGTCAATGAAGATGCTCTCAATATCCCGGTGTG 752
Qy 2366 AAGCAGTCGGAGGCGACATGTTCTGACGTTCCAAAGGAGATGCCATTTTCATGAAG 2425
Db 753 GAGCATGTTGGGGAGACATGTTTAAAGTGTTCAAAAGGAGATGCAATTTTCATGAAG 812
Qy 2426 TGGATATGCCATGACTGGAGTCACGACCAATTCGCGGAAGTTCTCAAGAACTGCTACGAT 2485
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Db 1113 TGA 1115
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GenCore version 5.1.9

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(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 104899840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description |
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| 2          | 3030   | 100.0       | 3070   | 10 | ADH75529    |
| 3          | 3030   | 100.0       | 3070   | 14 | ADW80563    |
| 4          | 2020.4 | 66.7        | 2096   | 3  | AAC62810    |
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| 7          | 2020.4 | 66.7        | 2096   | 14 | ADW80510    |
| 8          | 1429.6 | 47.2        | 1630   | 3  | AAH68014    |
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| 10         | 676    | 22.3        | 1876   | 9  | AAH60735    |
| 11         | 638.2  | 21.1        | 661    | 3  | AAC62762    |
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| 13         | 638.2  | 21.1        | 661    | 10 | ADH75428    |
| 14         | 638.2  | 21.1        | 661    | 14 | ADW80462    |
| 15         | 631    | 20.8        | 1501   | 6  | ABK48067    |
| 16         | 631    | 20.8        | 1501   | 10 | ADD93899    |
| 17         | 629.4  | 20.8        | 1503   | 2  | AAX26295    |
| 18         | 618.2  | 20.4        | 1368   | 2  | AAQ38448    |

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|----|-------|------|------|----|-----------|
| 19 | 613   | 20.2 | 1486 | 10 | AAAD47178 |
| 20 | 611.4 | 20.2 | 1486 | 2  | AAV71042  |
| 21 | 603.8 | 19.9 | 1370 | 6  | AAAD27040 |
| 22 | 603.8 | 19.9 | 1370 | 10 | ADI29673  |
| 23 | 603.8 | 19.9 | 1370 | 12 | ADJ96483  |
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| 26 | 589   | 19.4 | 1380 | 4  | AAAD11127 |
| 27 | 589   | 19.4 | 1380 | 14 | ADZ14865  |
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| 30 | 564.6 | 18.6 | 1092 | 12 | ADN73604  |
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| 33 | 556.6 | 18.4 | 1314 | 10 | ADI29687  |
| 34 | 556.6 | 18.4 | 1314 | 12 | ADJ96497  |
| 35 | 555.6 | 18.3 | 1341 | 2  | AAQ77692  |
| 36 | 554.2 | 18.3 | 1098 | 4  | AAAD19546 |
| 37 | 534.4 | 17.6 | 1460 | 2  | AAX35662  |
| 38 | 534   | 17.6 | 534  | 13 | ADQ88319  |
| 39 | 529.2 | 17.5 | 1124 | 13 | ADX32385  |
| 40 | 523   | 17.3 | 1418 | 2  | AAX35663  |
| 41 | 523   | 17.3 | 1507 | 6  | ABSS4111  |
| 42 | 519.8 | 17.2 | 1431 | 2  | AAQ38450  |
| 43 | 485   | 16.0 | 485  | 13 | ADQ88320  |
| 44 | 478.8 | 15.8 | 1244 | 2  | AAQ38449  |
| 45 | 475.4 | 15.7 | 1452 | 10 | ADC68550  |

## ALIGNMENTS

## RESULT 1

ABK17109  
ID ABK17109 standard; cDNA; 3070 BP.

XX AC ABK17109;

XX DT 26-MAR-2002 (first entry)

XX DE Eucalyptus grandis promoter polynucleotide #51.

XX KW Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;  
temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;  
PCR primer.

XX OS Eucalyptus grandis.

XX PN WO200198485-A1.

XX PD 27-DEC-2001.

XX PF 20-JUN-2001; 2001WO-NZ000115.

XX PR 28-JUN-2000; 2000US-00598401.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PI (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.

XX PI Perera R, Rice S, Eagleton C, Lasham A;

XX DR WPI; 2002-114583/15.

XX PT Novel polynucleotide promoter sequences from Pine and Eucalyptus useful  
for modifying expression of endogenous and/or heterologous  
polynucleotides in transgenic plants.

XX PS Claim 1; Page 103-104; 121pp; English.

XX CC The invention relates to isolated promoter sequences from Pinus radiata  
and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,  
flower-, pollen-, bud-, meristem-specific promoters or temporally







[illegible]

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| QY | 241  | TAGTCCTTTAGAAAGTCCCAATTCACCCCTATCATAGGCTTTCTGCATATCCAATTTAAGA   | 300  |
| DB | 281  | TAGTCCTTTAGAAAGTCCCAATTCACCCCTATCATAGGCTTTCTGCATATCCAATTTAAGA   | 340  |
| QY | 301  | ACAGCCGGNAATTGACGTCTACATTTTCTGACTTTTAAATTGATGTAGAACCTCTTAGACT   | 360  |
| DB | 341  | ACAGCCGGNAATTGACGTCTACATTTTCTGACTTTTAAATTGATGTAGAACCTCTTAGACT   | 400  |
| QY | 361  | ATTAAAATAATTGCTCGAAATTTGACGTCCACTGCACAAAGCGTTTGTCTCTGGAANAATA   | 420  |
| DB | 401  | ATTAAAATAATTGCTCGAAATTTGACGTCCACTGCACAAAGCGTTTGTCTCTGGAANAATA   | 460  |
| QY | 421  | AGTACAGCAGGTAGGGCTTTAAGCGAATTGGCAATCACCTTAGAATGATCTTATATGCG     | 480  |
| DB | 461  | AGTACAGCAGGTAGGGCTTTAAGCGAATTGGCAATCACCTTAGAATGATCTTATATGCG     | 520  |
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| DB | 521  | TAATTTACAAGACTGATGGSGCGGTATCGGTCTAAATTGTTCAAGGATGTGGTACCCTTGGGT | 580  |
| QY | 541  | ATTAGGCTATGATGGTTTCGATTGAGATTCGGTGGTATGATGCCAGAAITAAAAAAGTGC    | 600  |
| DB | 581  | ATTAGGCTATGATGGTTTCGATTGAGATTCGGTGGTATGATGCCAGAAITAAAAAAGTGC    | 640  |
| QY | 601  | TGCACTGATGAGAAATAGTTTCATCCTCGAGTATATCCCAATGATCTGGTAGAAGAGTCCA   | 660  |
| DB | 641  | TGCACTGATGAGAAATAGTTTCATCCTCGAGTATATCCCAATGATCTGGTAGAAGAGTCCA   | 700  |
| QY | 661  | TTCAAGGCATCTGGACCGGGGGCTTGGTAAGTCCCAGTTGGAAAGTAGCCCTCTCTAACT    | 720  |
| DB | 701  | TTCAAGGCATCTGGACCGGGGGCTTGGTAAGTCCCAGTTGGAAAGTAGCCCTCTCTAACT    | 760  |
| QY | 721  | TCCTTCTTGGTAAACAGAGCTATTAGGGACATATTCATCTCATTAGTAACAACCTTAAGGA   | 780  |
| DB | 761  | TCCTTCTTGGTAAACAGAGCTATTAGGGACATATTCATCTCATTAGTAACAACCTTAAGGA   | 820  |
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| DB | 1001 | GTAATTTTTGTCCCCCAGCTCAGGCATTTAAATTCGAGAGCACATCGCCCCAAAATTTCT    | 1060 |
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| QY | 1261 | AATAGCTCTTGTACCGGGAACCTCCGTATTTCTCTCATTCCATAAACCCTGATTAATTT     | 1320 |
| DB | 1301 | AATAGCTCTTGTACCGGGAACCTCCGTATTTCTCTCATTCCATAAACCCTGATTAATTT     | 1360 |
| QY | 1321 | GGTGGGAAAGCGACAGCCAAACCCACAAAGGTTCAGATGTCATCCACGAGACGAGAGAG     | 1380 |



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Db 2441 AAAGGAGATGCCATTTTTCATGAAGTGATGATATGCCATGACTGAGTGCAGACCATTTGGC 2500
Qy 2461 GAAGTTCTCTCAAGACTCTGATGCGCTTCCCAACAATGAAGAGTGATCGTTGCAGA 2520
Db 2501 GAAGTTCTCTCAAGAACTCTGATGCGCTTCCCAACAATGAAGAGTGATCGTTGCAGA 2560
Qy 2521 GTGGCTACTCTCTGTGTACCCAGACACAGAGCTTAGCGACCAAGAAATGTGATCCACATCGA 2580
Db 2561 GTGGCTACTCTCTGTGTACCCAGACACAGAGCTTAGCGACCAAGAAATGTGATCCACATCGA 2620
Qy 2581 CTGCATCATGTGTGGCCCAACAACCCAGCGGGGAAAGAGAGGACACAGAAGGAGTTGAGGC 2640
Db 2621 CTGCATCATGTGTGGCCCAACAACCCAGCGGGGAAAGAGAGGACACAGAAGGAGTTGAGGC 2680
Qy 2641 ATTGGCCAAAGGGCGGATTTTCAGGGCTTCCAAAGTCAATGCTGCGCTTTTCGGCACTCA 2700
Db 2681 ATTGGCCAAAGGGCGGATTTTCAGGGCTTCCAAAGTCAATGCTGCGCTTTTCGGCACTCA 2740
Qy 2701 CGTCATGAGTTCTCTGAAGACCGCTTGATCTGCTCCTCTGTGTGATGTTTCATGTTCTT 2760
Db 2741 CGTCATGAGTTCTCTGAAGACCGCTTGATCTGCTCCTCTGTGTGATGTTTCATGTTCTT 2800
Qy 2761 GGATTTGAAAGGTCGTGAAGAGGCGCTTTTCTCAGATGCGCTTCGGCATACCAAGTTCT 2820
Db 2801 GGATTTGAAAGGTCGTGAAGAGGCGCTTTTCTCAGATGCGCTTCGGCATACCAAGTTCT 2860
Qy 2821 TCTCATAAAGGAACATAGAGCGGACTGTATGATGCGCGCAAGTGAAGTTACAGAT 2880
Db 2861 TCTCATAAAGGAACATAGAGCGGACTGTATGATGCGCGCAAGTGAAGTTACAGAT 2920
Qy 2881 TTGTTGTTTATGCTATATAAGTTTGAAGTCTTCTGCATCTGATTTTCACAGAATGTGTA 2940
Db 2921 TTGTTGTTTATGCTATATAAGTTTGAAGTCTTCTGCATCTGATTTTCACAGAATGTGTA 2980
Qy 2941 ACGAAACGGCTATATGATGCTGCTGAATGATGGAATTTGTATTTCTCTCTTTT 3000
Db 2981 ACGAAACGGCTATATGATGCTGCTGAATGATGGAATTTGTATTTCTCTCTTTT 3040
Qy 3001 TCAGTAAATCACTTCGACCAAAAAAAAA 3030
Db 3041 TCAGTAAATCACTTCGACCAAAAAAAAA 3070
```

## RESULT 3

```
ADW80563
ID ADW80563 standard; cDNA; 3070 BP.
XX
AC ADW80563;
XX
DT 21-APR-2005 (first entry)
XX
DE E. grandis caffeic acid O-methyltransferase cDNA SEQ ID NO:113.
XX
KW ss; wood; plant; transcription; caffeic acid O-methyltransferase;
XX transgenic plant.
XX
OS Eucalyptus grandis.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..1643
FT FT /*tag= a
FT promoter 1015..1676
FT FT /*tag= b
XX
PN US2005026162-A1.
XX
PD 03-FEB-2005.
XX
PF 06-NOV-2003; 2003US-00702319.
XX
PR 25-MAR-1999; 99US-00276599.
PR 30-JUL-1999; 99US-0146591P.
PR 24-FEB-2000; 2000WO-NZ000018.
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PR 20-JUN-2000; 2000US-00598401.
PR 28-NOV-2000; 2000US-00724624.
PR 09-NOV-2001; 2001US-0345397P.
PR 30-APR-2002; 2002US-00137036.
PR 08-NOV-2002; 2002US-00291447.
PR 08-NOV-2002; 2002US-0425087P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (RUBI-) RUBICON FORESTS HOLDINGS LTD.
XX
PI Perera R, Rice SJ, Eagleston CK;
XX WPI; 2005-131806/14.
XX
PT New isolated polynucleotide sequences comprising a functional vascular
PT tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase
PT promoter, useful for modifying gene expression.
XX
XX Claim 2; SEQ ID NO 113; 82pp; English.
XX
XX The invention relates to a novel isolated polynucleotide sequence
XX comprising a functional vascular tissue-specific Eucalyptus grandis
XX caffeic acid O-methyltransferase (cOMT) promoter (ADW80462 or ADW80563).
XX Also claimed is a genetic construct comprising the above polynucleotide
XX sequence or a sequence having 2096 base pairs fully defined in the
XX specification (ADW80510), a host cell comprising the above genetic
XX construct, a plant comprising the genetic construct, a method for
XX producing a plant with modified gene expression, and a method for
XX identifying a gene responsible for a desired function or phenotype. The
XX composition and methods are useful for modifying gene expression or for
XX modifying the transcription of endogenous and/or heterologous
XX polynucleotides involved in wood formation. The present sequence is used
XX in the exemplification of the invention.
SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 3030; DB 14; Length 3070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACCTGTTTCAGTTTGATTCCTCTTGAGATGACCTTACGTATAGCTTGTATGAATGAAGTGG 60
Db 41 CACCTGTTTCAGTTTGATTCCTCTTGAGATGACCTTACGTATAGCTTGTATGAATGAAGTGG 100
Qy 61 GATAATAGATTCCACGAGGGGATAAAGGTTAGGAGATAGGGGATCTCCCGTCTGATG 120
Db 101 GATAATAGATTCCACGAGGGGATAAAGGTTAGGAGATAGGGGATCTCCCGTCTGATG 160
Qy 121 CCTCGGTAGTTGAAAAATAAGCAAAAGTTTCGCCGTTGAATTTGACAGCAAAAAGACACC 180
Db 161 CCTCGGTAGTTGAAAAATAAGCAAAAGTTTCGCCGTTGAATTTGACAGCAAAAAGACACC 220
Qy 181 GTCGTTATGATTCATGATGATCCATTTGATCCATGATGAGGTGAATCTTAGAGTGAGAGA 240
Db 221 GTCGTTATGATTCATGATGATCCATTTGATCCATGATGAGGTGAATCTTAGAGTGAGAGA 280
Qy 241 TAGTCCTTTAGAAAGTCCCATTCACCCCTATCATAGGCTTCTCGCATATCATTTTAAAGA 300
Db 281 TAGTCCTTTAGAAAGTCCCATTCACCCCTATCATAGGCTTCTCGCATATCATTTTAAAGA 340
Qy 301 ACAGCCCGGAATTGACGCTACATTTTCTGACTTTAAATTAATGATAGAACCTCTTAGACT 360
Db 341 ACAGCCCGGAATTGACGCTACATTTTCTGACTTTAAATTAATGATAGAACCTCTTAGACT 400
Qy 361 ATTAAAAATATGTCCTGAATTTGACCTCACTGCAAAAAGCGCTTTGCTCTGGAATAATA 420
Db 401 ATTAAAAATATGTCCTGAATTTGACCTCACTGCAAAAAGCGCTTTGCTCTGGAATAATA 460
Qy 421 AGTACAGCGAGGTAGGGCTTAAGCGGATTTGGCATTCACCTTAGAATGATCTTATATGCG 480
Db 461 AGTACAGCGAGGTAGGGCTTAAGCGGATTTGGCATTCACCTTAGAATGATCTTATATGCG 520
Qy 481 TAATTACAAAGACTGATGGGCGGTATTGGTCTAATTGTTTCAGGATGTGGTACCTTGGGT 540
```

|||||  
521 TAATACAAAGACTGATGGGGCGGTATGTGCTAAATGTTTCAGAGTGTGTACTCTGGGT 580  
QY  
541 ATTAGGGCTATGATGGTTCGAATTGAGATTCGGTGGTATGATGCCAGAAATTAATAAAGTGC 600  
Db  
581 ATTAGGGCTATGATGGTTCGAATTGAGATTCGGTGGTATGATGCCAGAAATTAATAAAGTGC 640  
QY  
601 TGCACTGATGAGAAATAGTTCATCTCGAGTATATCCCAATGATGCTGTGTTAGAAAGTCCA 660  
Db  
641 TGCACTGATGAGAAATAGTTCATCTCGAGTATATCCCAATGATGCTGTGTTAGAAAGTCCA 700  
QY  
661 TTCAAGCCATCTGACCGGGGCTTGTAAAGTCCCAAGTTGGAAAGTAGCCTCTCTAACT 720  
Db  
701 TTCAAGCCATCTGACCGGGGCTTGTAAAGTCCCAAGTTGGAAAGTAGCCTCTCTAACT 760  
QY  
721 TCCTTTCTGGTAAACAGGAGCTATTAGGGACATATTCATCTCATTAGTAAACAACCTAAGGA 780  
Db  
761 TCCTTTCTGGTAAACAGGAGCTATTAGGGACATATTCATCTCATTAGTAAACAACCTAAGGA 820  
QY  
781 CACTGGTTCAGAAATAGGCAAGTAGTCTCGATGTCCTCACTGTCTGAAATAGATGTGAAG 840  
Db  
821 CACTGGTTCAGAAATAGGCAAGTAGTCTCGATGTCCTCACTGTCTGAAATAGATGTGAAG 880  
QY  
841 TAACTATCGTCATCATCTTCAAAATTTCAAGATCGCGCACCCCAAGCTTGATGTATCC 900  
Db  
881 TAACTATCGTCATCATCTTCAAAATTTCAAGATCGCGCACCCCAAGCTTGATGTATCC 940  
QY  
901 TGCAACATCACTAATCTTGTCTGTTGTCTTTGTATAGTGTGTGATGAAAAATTTA 960  
Db  
941 TGCAACATCACTAATCTTGTCTGTTGTCTTTGTATAGTGTGTGATGAAAAATTTA 1000  
QY  
961 GTATTTTGTCCCCACAGCTGAGCCATTAATTTGAGAGACATCGGCCAAATTTATCT 1020  
Db  
1001 GTATTTTGTCCCCACAGCTGAGCCATTAATTTGAGAGACATCGGCCAAATTTATCT 1060  
QY  
1021 TCTTGTGCCATCACTGTCGAATTTCTTTTAGTAAAGTAAACAATGATGCCCATGT 1080  
Db  
1061 TCTTGTGCCATCACTGTCGAATTTCTTTTAGTAAAGTAAACAATGATGCCCATGT 1120  
QY  
1081 TGCAAAAAGGCTGATTAGTATGATCTTTGGAGTTGTTGGTCCAAATTTGCAAGCTGACGA 1140  
Db  
1121 TGCAAAAAGGCTGATTAGTATGATCTTTGGAGTTGTTGGTCCAAATTTGCAAGCTGACGA 1180  
QY  
1141 TGGCCCCCTCAGGGAATTAAGCGCCAAACCCAGATTCGAAAGAGACAAAGAGCAACGACC 1200  
Db  
1181 TGGCCCCCTCAGGGAATTAAGCGCCAAACCCAGATTCGAAAGAGACAAAGAGCAACGACC 1240  
QY  
1201 CAACCTTTCTTAAACAAGATCATCACAGATCGGCCAGTAAAGGGTAAATTTAATTTAACA 1260  
Db  
1241 CAACCTTTCTTAAACAAGATCATCACAGATCGGCCAGTAAAGGGTAAATTTAATTTAACA 1300  
QY  
1261 AATAGCTCTTGTACCGGAACTCCGTATTTCTCTCACTTCATNAACCCCTGATTAATTT 1320  
Db  
1301 AATAGCTCTTGTACCGGAACTCCGTATTTCTCTCACTTCATNAACCCCTGATTAATTT 1360  
QY  
1321 GGTGGAAAGCAGACCCAAACCCAAAGGTTCAGATGTCATCCACAGAGAGAGAGAG 1380  
Db  
1361 GGTGGAAAGCAGACCCAAACCCAAAGGTTCAGATGTCATCCACAGAGAGAGAGAG 1420  
QY  
1381 AGAGAGAGAGAGAGAGAGTTTCTCTCTATATTTCTGTTTCAACCGTGTGGAGTCAATGGCA 1440  
Db  
1421 AGAGAGAGAGAGAGAGAGTTTCTCTCTATATTTCTGTTTCAACCGTGTGGAGTCAATGGCA 1480  
QY  
1441 TCGGTGACAAATGTCATATTCGGTGTAGGGTCCAAATATTTTCGGGGAGGGTGTGTAAACC 1500  
Db  
1481 TCGGTGACAAATGTCATATTTGGTGTAGGGTCCAAATATTTTCGGGGAGGGTGTGTAAACC 1540  
QY  
1501 GCAGAGTTCCTATATCGAACTCCACACCATACCTCACTTCAATCCCACTATTTAT 1560  
Db  
1541 GCAAGGTTCCTATATCGAACTCCACACCATACCTCACTTCAATCCCACTATTTAT 1600  
QY  
1561 CCGTTTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAG 1620

Db  
1601 CCGTTTTATTTCTCTGCTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAG 1660  
QY  
1621 AGGAGAGATGGGTTTCGACGGCTCCGAGACCCAGATGACCCCGACCCCAAGTCTCGGACG 1680  
Db  
1661 AGGAGAGATGGGTTTCGACGGCTCCGAGACCCAGATGACCCCGACCCCAAGTCTCGGACG 1720  
QY  
1681 AGGAGCGCAACCTTTCCGCAATGACAGTGGGAGCGCCTCCGTGCTCCCAATGGTCTTAA 1740  
Db  
1721 ACAGCGGCAACCTTTCCGCAATGACAGTGGGAGCGCCTCCGTGCTCCCAATGGTCTTAA 1780  
QY  
1741 AGGCGCCCATCGAGATGACAGCTTCCGCAATGATGGCCAAAGACGGGCGGGCGGTTC 1800  
Db  
1781 AGGCGCCCATCGAGATGACAGCTTCCGCAATGATGGCCAAAGACGGGCGGGCGGTTC 1840  
QY  
1801 TCTCCACGGGGGAAATCGCGGCACAGCTCCGACCCAGAACCCCGAGGCACCCGTCATCG 1860  
Db  
1841 TCTCCACGGGGGAAATCGCGGCACAGCTCCGACCCAGAACCCCGAGGCACCCGTCATCG 1900  
QY  
1861 TCGACCGGATCTTCCGGGCTGCTGGCCAGCTACTCCGTGCTCACTCGTGCACCCCTCCGAC 1920  
Db  
1901 TCGACCGGATCTTCCGGGCTGCTGGCCAGCTACTCCGTGCTCACTCGTGCACCCCTCCGAC 1960  
QY  
1921 TCCCGATGGCAAGGTTCGAGCGGCTCTACGGCTTAGCGCCGCTGTCAGAGTTCTTGGTCA 1980  
Db  
1961 TCCCGATGGCAAGGTTCGAGCGGCTCTACGGCTTAGCGCCGCTGTCAGAGTTCTTGGTCA 2020  
QY  
1981 AGAACGAGACGGGCTCCATCGCGCACTCAACTTGATGAACCAAGGACAAAATCCTCA 2040  
Db  
2021 AGAACGAGACGGGCTCCATCGCGCACTCAACTTGATGAACCAAGGACAAAATCCTCA 2080  
QY  
2041 TGGAAAGCTGCTATTAACCTGAAAGATGCGGTCTTTGAAGCGGGAATTCCTATCAACAAG 2100  
Db  
2081 TGGAAAGCTGCTATTAACCTGAAAGATGCGGTCTTTGAAGCGGGAATTCCTATCAACAAG 2140  
QY  
2101 CGTACGGGATGACCGGCTTCGAGTATATGCGCACCGACCGGATTCACACAGATCTTTA 2160  
Db  
2141 CGTACGGGATGACCGGCTTCGAGTATATGCGCACCGACCGGATTCACACAGATCTTTA 2200  
QY  
2161 ACCGGGGAATGCTGATCACTCCACCATTAATATGAAGAGATATCTGGAACACATACAAG 2220  
Db  
2201 ACCGGGGAATGCTGATCACTCCACCATTAATATGAAGAGATATCTGGAACACATACAAG 2260  
QY  
2221 GCTTCGAGGCGCTTCGAGACCGGTGCTGATGTCGAGCGGCGCATCTGGGCGGCTCGCA 2280  
Db  
2261 GCTTCGAGGCGCTTCGAGACCGGTGCTGATGTCGAGCGGCGCATCTGGGCGGCTCGCA 2320  
QY  
2281 TGATCGTTGCCAAATACCCATCAATGAAGGGATCAACTTCGACCGCCCCCAACGGATTGA 2340  
Db  
2321 TGATCGTTGCCAAATACCCATCAATGAAGGGATCAACTTCGACCGCCCCCAACGGATTGA 2380  
QY  
2341 AGACGCCCCACCCCTTCTGCTCAAGCACGTCGGAGGCGCATGTTCTGACGCGTTC 2400  
Db  
2381 AGACGCCCCACCCCTTCTGCTCAAGCACGTCGGAGGCGCATGTTCTGACGCGTTC 2440  
QY  
2401 AAAGGGAGATGCCATTTTCATGAAGTGGATATGCCATGACTGGAGTGAACACATTTGCGC 2460  
Db  
2441 AAAGGGAGATGCCATTTTCATGAAGTGGATATGCCATGACTGGAGTGAACACATTTGCGC 2500  
QY  
2461 GAAGTTCTCAAGAACCTGCTACGATCGCTTCCCAATGGAAGAGTGTATCGTTGCGA 2520  
Db  
2501 GAAGTTCTCAAGAACCTGCTACGATCGCTTCCCAATGGAAGAGTGTATCGTTGCGA 2560  
QY  
2521 GTGCTACTCTCTGTGTACCCAGACGAGCTTAGCGACCAAGAAATGTGTATCCACATCGA 2580  
Db  
2561 GTGCTACTCTCTGTGTATCCAGACGAGCTTAGCGACCAAGAAATGTGTATCCACATCGA 2620  
QY  
2581 CTGCATCATGTTGGCCCAAAACCCAGCGGGAAGAGAGGACACAGAGGATTCGAGGC 2640  
Db  
2621 CTGCATCATGTTGGCCCAAAACCCAGCGGGAAGAGAGGACACAGAGGATTCGAGGC 2680  
QY  
2641 ATTGGCCAAAGGGGCGGATTTTCAGGGCTTTCAGAGTCAATGCTGTGCTGCTTTTCGCACTCA 2700  
Db  
2681 ATTGGCCAAAGGGGCGGATTTTCAGGGCTTTCAGAGTCAATGCTGTGCTGCTTTTCGCACTCA 2740



RESULT 5  
ABK17075  
ID ABK17075 standard; cDNA; 2096 BP.  
. XX

|    |                                                                           |
|----|---------------------------------------------------------------------------|
| C  | ABK17075;                                                                 |
| X  | 26-MAR-2002 (first entry)                                                 |
| X  | Eucalyptus grandis promoter polynucleotide #31.                           |
| X  | Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;   |
| X  | temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;     |
| W  | PCR primer.                                                               |
| W  | Eucalyptus grandis.                                                       |
| W  | WO2001198485-A1.                                                          |
| XX | 27-DEC-2001.                                                              |
| XX | 20-JUN-2001; 2001WO-NZ000115.                                             |
| XX | 20-JUN-2000; 2000US-00598401.                                             |
| XX | 28-NOV-2000; 2000US-00724624.                                             |
| XX | (GENE-) GENESIS RES & DEV CORP LTD.                                       |
| XX | (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.                               |
| XX | Perera R, Rice S, Eagleston C, Lasham A;                                  |
| XX | WPI; 2002-114583/15.                                                      |
| XX | P-PSDB; AAU80760.                                                         |
| DR | Novel polynucleotide promoter sequences from Pine and Eucalyptus useful   |
| DR | for modifying expression of endogenous and/or heterologous                |
| DR | polynucleotides in transgenic plants.                                     |
| XX | Claim 1; Page 78; 121pp; English.                                         |
| XX | The invention relates to isolated promoter sequences from Pinus radiata   |
| XX | and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,   |
| XX | flower-, pollen-, bud-, meristem-specific promoters or temporally         |
| XX | regulated promoters such as xylogenesis-specific promoters. The promoter  |
| XX | polypeptides and their related polynucleotides are useful in the          |
| XX | production of genetic constructs, used for modifying gene expression in a |
| XX | target organism, in particular a plant. The method is useful for          |
| XX | modifying expression of a polynucleotide that comprises an intron         |
| XX | sequence, through removal of the intron sequence. The method is useful    |
| XX | for modifying growth and development of plants, and cellular responses to |
| XX | external stimulus, such as environmental factors and disease pathogens.   |
| XX | The sequences are useful in genome and physical mapping, in positional    |
| XX | cloning of genes, in various assays to determine biological activity, to  |
| XX | raise antibodies, to isolate corresponding interacting proteins and other |
| XX | compounds, and to quantitatively determine levels of interacting proteins |
| XX | or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata   |
| XX | and Eucalyptus grandis polynucleotides and PCR primers used in the method |
| XX | of the invention                                                          |
| XX | Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;               |
| SQ |                                                                           |
|    | Query Match 66.7%; Score 2020.4; DB 6; Length 2096;                       |
|    | Best Local Similarity 99.3%; Pred. No. 0;                                 |
|    | Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;            |
| QY | 979 CTGAGCCATTAAATTCGAGAGCACATGCCCAAATAATTATTTCTTGTGCGCATTAACCTGT 1038    |
| Db | 41 CTGAGCCATTAAATTCGAGAGCACATGCCCAAATAATTATTTCTTGTGCGCATTAACCTGT 100      |
| QY | 1039 CGAATTTCTCTTTTAGTAAATCAACCATGGCCATGTTGCACAAAAGGCTGATTA 1098          |
| Db | 101 CGAATTTCTCTTTTAGTAAATCAACCATGGCCATGTTGCACAAAAGGCTGATTA 160            |
| QY | 1099 GTATGATCTTTGGAGTTGTTGGTGCAAAATTTTCCAAGCTGACGATGCCCTCAGGGAATTT 1158   |
| Db | 161 GTATGATCTTTGGAGTTGTTGGTGCAAAATTTTCCAAGCTGACGATGCCCTCAGGGAATTT 220     |
| QY | 1159 AAGGCGCCAACCCAGATTGCAAAGAGCACAAAGAGCACGCCCAACCTTTCTCTTTAAACAAG 1218  |









QY 1815 ATGCGGCACAGCTCCCGACCCAGAACCCCGAGGACCCCGTCTATGCTCGACCGGATCTTC 1874  
Db |||||  
881 GTGCGGCGCAGCTCCCGACCCAGAACCCCGAGGACCCCGTCTATGCTCGACCGGATCTTC 940  
QY 1875 CGGTGCTGCGCAGCTACTCCGTGCTCATGTCACCGTTCGGACCTCCCGATGCGCAAG 1934  
Db |||||  
941 CGGTGCTGCGCAGCTACTCCGTGCTCATGTCACCGTTCGGACCTCCCGATGCGCAAG 1000  
QY 1935 GTCGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGCTCAAGAACGAGGACGGG 1994  
Db |||||  
1001 GTCGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGCTCAAGAACGAGGACGGG 1060  
QY 1995 GTCTCCATCGCGCAGCTCAACTTGATGAACAGGACAAAATCTCATGGAAGCTGGTAT 2054  
Db |||||  
1061 GTCTCCATCGCGCAGCTCAACTTGATGAACAGGACAAAATCTCATGGAAGCTGGTAT 1120  
QY 2055 TACTGAAAGATGCGGTCTTGAAGGCGGAATCCATTCAACAGGCTACGGGATGACC 2114  
Db |||||  
1121 TACTGAAAGATGCGGTCTTGAAGGCGGAATCCATTCAACAGGCTACGGGATGACC 1180  
QY 2115 GCGTTCGAGTATCATGGCACCGACCCCGATTCAACAGATCTTTAACCGGGGAATGTCT 2174  
Db |||||  
1181 GCGTTCGAGTATCATGGCACCGACCCCGATTCAACAGATCTTTAACCGGGGAATGTCT 1240  
QY 2175 GATCACTCCACATTAATGAAGAAGATCTGAAACATCAAGGGCTTCGAGGGCTC 2234  
Db |||||  
1241 GATCACTCCACATTAATGAAGAAGATCTGAAACATCAAGGGCTTCGAGGGCTC 1300  
QY 2235 GAGACCGTGTGATGTGCGAGGCGGCACTGGGCGGTGCTCAGCATGATCGTTGCCAAA 2294  
Db |||||  
1301 GAGACCGTGTGATGTGCGAGGCGGCACTGGGCGGTGCTCAGCATGATCGTTGCCAAA 1360  
QY 2295 TACCACATCAATGAAGGATCAACTTCGACCGCGCCCAACGGATTGAAGCGCCCAACCC 2354  
Db |||||  
1361 TACCACATCAATGAAGGATCAACTTCGACCGCGCCCAACGGATTGAAGCGCCCAACCC 1420  
QY 2355 TTCTCGGTGTCAAGCAGCTGGAGGCGCATGTTGCTCAGCGTTCGAAAGGGAGATGCCA 2414  
Db |||||  
1421 TTCTCGGTGTCAAGCAGCTGGAGGCGCATGTTGCTCAGCGTTCGAAAGGGAGATGCCA 1480  
QY 2415 TTTTCATGAAGTGGATGCCATGACTCGAGTGAAGCATTTGCGCGAAGTTCTCTCAAGA 2474  
Db |||||  
1481 TTTTCATGAAGTGGATGCCATGACTCGAGTGAAGCATTTGCGCGAAGTTCTCTCAAGA 1540  
QY 2475 ACTGCTACGATCGGTTCCTCAACAATGGAAGGATGATGTTGCAAGTGCATCTCCCTG 2534  
Db |||||  
1541 ACTGCTACGATCGGTTCCTCAACAATGGAAGGATGATGTTGCAAGTGCATCTCCCTG 1600  
QY 2535 TGTACCCAGACAGGACCTTAGCGACCAAGATGTGATCCACATCGACTGCATCATGTTGG 2594  
Db |||||  
1601 TGTACCCAGACAGGACCTTAGCGACCAAGATGTGATCCACATCGACTGCATCATGTTGG 1660  
QY 2595 CCCACAACCCAGCGGGAAGAGAGACACAGAAGGATTCGAGGCATTTGGCCAAAGGGG 2654  
Db |||||  
1661 CCCACAACCCAGCGGGAAGAGAGACACAGAAGGATTCGAGGCATTTGGCCAAAGGGG 1720  
QY 2655 CCGGATTTCAAGGCTTCCAAAGTCATGCTGCTCGCTTTGGCACTCACTCATGTCATGAGTTCC 2714  
Db |||||  
1721 CCGGATTTCAAGGCTTCCAAAGTCATGCTGCTCGCTTTGGCACTCACTCATGTCATGAGTTCC 1780  
QY 2715 TGAAGACCGTTGATCTGCTCTGCTGCTGATGTTCAAGTTCCTGATTTTGAAGTTC 2774  
Db |||||  
1781 TGAAGACCGTTGATCTGCTCTGCTGCTGATGTTCAAGTTCCTGATTTTGAAGTTC 1840  
QY 2775 GTCAAGGAGCGCTTTCTCACAGTTGGCTTCGGCATACCAAGTTCCTCTCATAAAGGAA 2834  
Db |||||  
1841 GTCAAGGAGCGCTTTCTCACAGTTGGCTTCGGCATACCAAGTTCCTCTCATAAAGGAA 1900  
QY 2835 ACAATAAGAGCGACTGTATGATGCGGCAAGTGGAAAGTTACAGATTTGTTGTTATGT 2894  
Db |||||  
1901 ACAATAAGAGCGACTGTATGATGCGGCAAGTGGAAAGTTACAGATTTGTTGTTATGT 1960  
QY 2895 CTATAAAGTTTTCAGTCTTCGCTATCTGATTTTCACAGAAATGTGTAACGAAACGGCGTAT 2954

Db 1961 CTATAAAGTTTTCAGTCTTCGCTATCTGATTTTCACAGAAATGTGTAACGAAACGGCGTAT 2020  
QY 2955 ATGATGTGCTCGATGATGAAATGTGATATTTCTCTCTTTTTCAGTAATCACTT 3014  
Db 2021 ATGATGTGCTCGATGATGAAATGTGATATTTCTCTCTTTTTCAGTAATCACTT 2080  
QY 3015 CGAACAAAAA 3030  
Db 2081 CGAACAAAAA 2096

RESULT 8  
AAA68014  
ID AAA68014 standard; DNA; 1630 BP.  
XX  
AC AAA68014;  
XX  
DT 24-OCT-2000 (first entry)  
XX  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:107.  
XX  
KW Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;  
KW Pinus radiata; Monterey pine; ds.  
XX  
OS Eucalyptus grandis.  
XX  
PN WO200022099-A1.  
XX  
PD 20-APR-2000.  
XX  
PF 06-OCT-1999; 99WO-NZ000168.  
XX  
PR 09-OCT-1998; 98US-00169789.  
PR 14-JUL-1999; 99US-0143811P.  
XX  
(GENE-) GENESIS RES & DEV CORP LTD.  
(FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
PI Bloksberg LN, Havukkala IJ;  
XX  
WPI; 2000-317962/27.  
XX  
Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and structure.  
XX  
Claim 1; Page 90-91; 213pp; English.  
XX  
The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL), coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, caffeic acid methyl transferase, caffeoyl CoA methyl transferase, coumarate CoA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavonoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lignin biosynthetic pathway, and for producing a plant having altered lignin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any organism and for PCR amplification. The lignin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the exemplification of the present invention  
XX  
Sequence 1630 BP; 394 A; 433 C; 439 G; 364 T; 0 U; 0 Other;





|    | CC                                                          | polypeptides and genetic constructs are useful for modulating lignin content, composition and structure of plants, or for producing a plant having altered lignin content, composition and structure. The polynucleotides are also useful in genome mapping, physical mapping, positional cloning of genes, or as non-disruptive tags for marking organisms, particularly plants. The present sequence represents a polynucleotide associated with the lignin biosynthetic pathway. | CC |
|----|-------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|
| XX | Sequence 1630 BP; 394 A; 433 C; 439 G; 364 T; 0 U; 0 Other; |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |    |
| QY | Query Match 47.2%; Score 1429.6; DB 10; Length 1630;        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |    |
| QY | Best Local Similarity 99.0%; Pred. No. 0;                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |    |
| QY | Matches 1449; Conservative                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |    |
| QY | 1561                                                        | CCGTTTTATTCTCTGCTTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAG 1620                                                                                                                                                                                                                                                                                                                                                                                                                          |    |
| DB | 1                                                           | CCGTTTTATTCTCTGCTTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAG 60                                                                                                                                                                                                                                                                                                                                                                                                                            |    |
| QY | 1621                                                        | AGAGAGATGGGTCGAGCCGGTCGAGACCCAGATACCCGACCCCAAGTCTCGAGC 1680                                                                                                                                                                                                                                                                                                                                                                                                                         |    |
| DB | 61                                                          | AGAGAGATGGGTCGAGCCGGTCGAGACCCAGATACCCGAGTACCCGAGTCTCGAGC 120                                                                                                                                                                                                                                                                                                                                                                                                                        |    |
| QY | 1681                                                        | ACGAGGCGAACTCTTCGCCATCAGCTCGAGCGCCTCCGTCCTCCCATGTCCTAA 1740                                                                                                                                                                                                                                                                                                                                                                                                                         |    |
| DB | 121                                                         | AGGAGGCGAACTCTTCGCCATCAGCTCGAGCGCCTCCGTCCTCCCATGTCCTCA 180                                                                                                                                                                                                                                                                                                                                                                                                                          |    |
| QY | 1741                                                        | AGGCCGCCATCGAGATCGACTCTCGAGATCATGCCAAGGACGGCGCGCGGTCC 1800                                                                                                                                                                                                                                                                                                                                                                                                                          |    |
| DB | 181                                                         | AGGCCGCCATCGAGATCGACTCTCGAGATCATGCCAAGGACGGCGCGCGGTCC 240                                                                                                                                                                                                                                                                                                                                                                                                                           |    |
| QY | 1801                                                        | TCTCCACGGGGAAATCCGGCAGCTCCCGACCCAGAACCCCGAGGACCCCGTCATGC 1860                                                                                                                                                                                                                                                                                                                                                                                                                       |    |
| DB | 241                                                         | TCTCCCGGGGAAGTCCGGCCAGCTCCCGACCCAGAACCCCGAGGACCCCGTCATGC 300                                                                                                                                                                                                                                                                                                                                                                                                                        |    |
| QY | 1861                                                        | TCGACCGGATCTTCGGGCTGTGGCAGCTACTCCGTCCTCAGCTGCACCTCCGCGACC 1920                                                                                                                                                                                                                                                                                                                                                                                                                      |    |
| DB | 301                                                         | TCGACCGGATCTTCGGGCTGTGGCAGCTACTCCGTCCTCAGCTGCACCTCCGCGACC 360                                                                                                                                                                                                                                                                                                                                                                                                                       |    |
| QY | 1921                                                        | TCCCGCATGGCAAGGTTCAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGCTCA 1980                                                                                                                                                                                                                                                                                                                                                                                                                     |    |
| DB | 361                                                         | TCCCGCATGGCAAGGTTCAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGCTCA 420                                                                                                                                                                                                                                                                                                                                                                                                                      |    |
| QY | 1981                                                        | AGAACGAGGACGGGTCTCCATCCCGGCACTCAACTTGATGAACGAGCAAAATCCTCA 2040                                                                                                                                                                                                                                                                                                                                                                                                                      |    |
| DB | 421                                                         | AGAACGAGGACGGGTCTCCATCCCGGCACTCAACTTGATGAACGAGCAAAATCCTCA 480                                                                                                                                                                                                                                                                                                                                                                                                                       |    |
| QY | 2041                                                        | TGGAAGCTGTATTACCTGAAAGATGGGTCTTGAAAGCGGAATCCCAATCAACAAGG 2100                                                                                                                                                                                                                                                                                                                                                                                                                       |    |
| DB | 481                                                         | TGGAAGCTGTATTACCTGAAAGATGGGTCTTGAAAGCGGAATCCCAATCAACAAGG 540                                                                                                                                                                                                                                                                                                                                                                                                                        |    |
| QY | 2101                                                        | CGTACGGGATGACCGGTTTCAGTATCATGGCAACCGCCGATTCACAAGATCTTTA 2160                                                                                                                                                                                                                                                                                                                                                                                                                        |    |
| DB | 541                                                         | CGTACGGGATGACCGGTTTCAGTATCATGGCAACCGCCGATTCACAAGATCTTTA 600                                                                                                                                                                                                                                                                                                                                                                                                                         |    |
| QY | 2161                                                        | ACCGGGGATGTCTCATCACTCCACCATTTATGAGGAAGATCTGGAACATACAAGG 2220                                                                                                                                                                                                                                                                                                                                                                                                                        |    |
| DB | 601                                                         | ACCGGGGATGTCTCATCACTCCACCATTTATGAGGAAGATCTGGAACATACAAGG 660                                                                                                                                                                                                                                                                                                                                                                                                                         |    |
| QY | 2221                                                        | GCTTCGAGGGCTTCGAGACCGTGTGTCATGTCGAGGCGGCACTGGGGCGTGTCAAGCA 2280                                                                                                                                                                                                                                                                                                                                                                                                                     |    |
| DB | 661                                                         | GCTTCGAGGGCTTCGAGACCGTGTGTCATGTCGAGGCGGCACTGGGGCGTGTCAAGCA 720                                                                                                                                                                                                                                                                                                                                                                                                                      |    |
| QY | 2281                                                        | TGATCGTTCGCAAAATACCATCAATGAAGGATCAACTTCGACC-GCCCCAAGCGATTG 2339                                                                                                                                                                                                                                                                                                                                                                                                                     |    |
| DB | 721                                                         | TGATCGTTCGCAAAATACCATCAATGAAGGATCAACTTCGACC-GCCCCAAGCGATTG 780                                                                                                                                                                                                                                                                                                                                                                                                                      |    |
| QY | 2340                                                        | AAGACGCCCAACCCCTCTCGTGTGTCAGCAAGTTCGAGGCGGACATGTCGAGCGTTC 2399                                                                                                                                                                                                                                                                                                                                                                                                                      |    |
| DB | 781                                                         | AAGACGCCCAACCCCTCTCGTGTGTCAGCAAGTTCGAGGCGGACATGTCGAGCGTTC 840                                                                                                                                                                                                                                                                                                                                                                                                                       |    |
| QY | 2400                                                        | CAAAGGGAGATGCCATTTTCATGAAGTGCATGATGCCATGAGTACGACCATTCGCG 2459                                                                                                                                                                                                                                                                                                                                                                                                                       |    |
| DB | 841                                                         | CAAAGGGAGATGCCATTTTCATGAAGTGCATGATGCCATGAGTACGACCATTCGCG 900                                                                                                                                                                                                                                                                                                                                                                                                                        |    |

|           |                                                                           |                                                                 |      |
|-----------|---------------------------------------------------------------------------|-----------------------------------------------------------------|------|
| QY        | 2460                                                                      | CGAAGTTCCTCAAGAACTGCTACGATGGCTTCCCAACAATGGAAAGTGATGCTGTGCAG     | 2519 |
| Db        | 901                                                                       | CGAAGTTCCTCAAGAACTGCTACGATGGCTTCCCAACAATGGAAAGTGATGCTGTGCAG     | 960  |
| QY        | 2520                                                                      | AGTGCCTACTCCCTGTGTGTTACCGACACGAGCCTAGCCAGCAAGTAATGTGATCCACATCG  | 2579 |
| Db        | 961                                                                       | AGTGCCTACTCCCTGTGTGTTACCGACACGAGCCTAGCCAGCAAGTAATGTGATCCACATCG  | 1020 |
| QY        | 2580                                                                      | ACTGCATCATGTTGGCCCAACAACCCAGGCGGAGAGAGAGACACAGAAAGGAGTTCGAGG    | 2639 |
| Db        | 1021                                                                      | ACTGCATCATGTTGGCCCAACAACCCAGGCGGAGAGAGAGAGACACAGAAAGGAGTTCGAGG  | 1080 |
| QY        | 2640                                                                      | CATTGGCCAAAGGGCGCGGATTTCAAGGCTTCCAAAGTCAATGTGCTCGCGCTTTCCGACATC | 2699 |
| Db        | 1081                                                                      | CATTGGCCAAAGGGCGCGGATTTCAAGGCTTCCAAAGTCAATGTGCTCGCGCTTTCCGACATC | 1140 |
| QY        | 2700                                                                      | ACGTCATGAGATTCCTGAAGACCGCTTGATCTGCTCTCTGCTGGTGATGTTTCATGTTCT    | 2759 |
| Db        | 1141                                                                      | ACGTCATGAGATTCCTGAAGACCGCTTGATCTGCTCTCTGCTGGTGATGTTTCATGTTCT    | 1200 |
| QY        | 2760                                                                      | TGGATTTGAAAGGTCGTGAAGGAGCCCTTTTCTCAGATTGCTTGGCATACCAAGTTC       | 2819 |
| Db        | 1201                                                                      | TGGATTTGAAAGGTCGTGAAGGAGCCCTTTTCTCAGATTGCTTGGCATACCAAGTTC       | 1260 |
| QY        | 2820                                                                      | TTCTCATAAAGGAAACAATAAGAGCGACTGTATGATGGCCCAAGTGAAGTTACAAGA       | 2879 |
| Db        | 1261                                                                      | TTCTCATAAAGGAAACAATAAGAGCGACTGTATGATGGCCCAAGTGAAGTTACAAGA       | 1320 |
| QY        | 2880                                                                      | TTTGTGTTTATGCTCTATAAAGTTTGGAGTCTCTGTCATCTGATTTTCACAGAAATGTGT    | 2939 |
| Db        | 1321                                                                      | TTTGTGTTTATGCTCTATAAAGTTTGGAGTCTCTGTCATCTGATTTTCACAGAAATGTGT    | 1380 |
| QY        | 2940                                                                      | AACGAAACGGCGTATATGATGTGCTTGAATGATGAAATGTGATATTCCTGCTCTTT        | 2999 |
| Db        | 1381                                                                      | AACGAAACGGCGTATATGATGTGCTTGAATGATGAAATGTGATATTCCTGCTCTTT        | 1440 |
| QY        | 3000                                                                      | TTCAGTAAATCACTTCGAACAAA                                         | 3023 |
| Db        | 1441                                                                      | TTCAGTAAATCACTTCGAACAAA                                         | 1464 |
| RESULT 10 |                                                                           |                                                                 |      |
| AAL60735  |                                                                           |                                                                 |      |
| ID        | AAL60735 standard; DNA; 1876 BP.                                          |                                                                 |      |
| AC        | AAL60735;                                                                 |                                                                 |      |
| DT        | 03-SEP-2003 (first entry)                                                 |                                                                 |      |
| DE        | Strawberry O-methyltransferase (STOMT) DNA.                               |                                                                 |      |
| KW        | Strawberry; O-methyltransferase; 2,5-dimethyl-4-hydroxy-3 (2H)-furanone;  |                                                                 |      |
| KW        | STOMT; DMHF; dithiothreitol; 2,5-dimethyl-4-methoxy-3 (2H)-furanone; DTT; |                                                                 |      |
| KW        | DMHF; enzyme; plant; gene; ds.                                            |                                                                 |      |
| OS        | Fragaria x ananassa.                                                      |                                                                 |      |
| Key       | Location/Qualifiers                                                       |                                                                 |      |
| FF        | 106..1203                                                                 |                                                                 |      |
| FT        | /*tag= a                                                                  |                                                                 |      |
| FT        | /product= "STOMT protein"                                                 |                                                                 |      |
| XX        | W02003046163-A2.                                                          |                                                                 |      |
| XX        | 05-JUN-2003.                                                              |                                                                 |      |
| XX        | 26-NOV-2002; 2002WO-EP013320.                                             |                                                                 |      |
| XX        | 26-NOV-2001; 2001US-0332534P.                                             |                                                                 |      |
| XX        | (UYBA-) UNIV BAYERISCHE JULIUS MAXIMILIANS WUERZ.                         |                                                                 |      |

PI Schwab W, Kaldehoff R, Wein M;  
XX WPI; 2003-532772/50.  
DR P-PSDB; AAO30114.  
DR  
XX Novel isolated strawberry O-methyltransferase polypeptide useful for  
PT methylating ortho-dihydroxy substituted ring system such as catechol,  
PT caffeic acid, protocatechuic aldehyde or pyrogallol.  
XX  
XX Claim 1; Page 75-76; 78pp; English.  
XX  
XX The invention relates to novel strawberry O-methyltransferase (STOMT)  
CC polypeptides capable of methylating an ortho-dihydroxy substituted ring  
CC system and nucleic acid molecules encoding such polypeptides. The  
CC invention is useful for methylating of an ortho-dihydroxy substituted  
CC ring system and/or its mimetics (such as 2,5-dimethyl-4-hydroxy-3(2H)-  
CC furanone (DMF) or dithiothreitol (DTT)). The invention is also useful  
CC for the synthesis of naturally occurring substances preferably aroma  
CC compounds such as 2-methoxyphenol, vanillin, ferulic acid, feruoyl-CoA or  
CC DMMP, for enhancing the function of naturally-occurring STOMT in plants  
CC or tissue cultured cells, or to enhance the production of flavour-  
CC enhancing substances such as vanillin or 2,5-dimethyl-4-methoxy-3(2H)-  
CC furanone (DMMP). The present sequence is *Fragaria x ananassa* (strawberry)  
CC O-methyltransferase DNA  
XX  
SQ Sequence 1876 BP; 432 A; 449 C; 429 G; 566 T; 0 U; 0 Other;  
  
Query Match 22.3%; Score 676; DB 9; Length 1876;  
Best Local Similarity 77.0%; Pred. No. 8.4e-176;  
Matches 850; Conservative 0; Mismatches 250; Indels 4; Gaps 2;  
  
QY 1626 AGAATGGGTTCCGACCGCTCCGAGACCCAGATGACCCGACCAAGTCTCGGACGACGAG 1685  
DB 103 AAAATGGGTTCCACGG---CGAGACTCAGATGACTCCGACCCATGTTCTCCGACGAGGA 159  
  
QY 1686 GCGAACCTCTTTCGACATGAGCTGCGAGCGCTCCGTCCTCCCATAGTCTTAAAGGCC 1745  
DB 160 GCCAACCTCTTTCGACATGAGCTGCGAGCGCTCCGTCCTCCCATAGTCTTAAAGGCC 219  
  
QY 1746 GCCATGAGATGACCTCTCGAGATGATGCGCAAGAGCGGCGCGGCTTCTCTCC 1805  
DB 220 GCCATGAGATGACCTCTCGAGATGATGCGCAAGAGCGGCGGCTTCTCTCTCC 279  
  
QY 1806 ACGGGGAAATCGGGACAGCTCCGACCCAGACCCCGAGGACCGCTCATGCTGAC 1865  
DB 280 CTTAGTATCTAGCTCTCAGCTTCCGACCAAGAACCCCGAGGCTCCGCTCATGCTGAC 339  
  
QY 1866 CGGATCTTCCGGCTGCTGGCAGCTACTCCGTCGCTCAGTGCACCCCTCCGCGACCTCC 1925  
DB 340 CGTATGCTTCCGCTTCCGCGAGCTACTCCATCTTAACCTGCTCATTTGCGTACGTTCCG 399  
  
QY 1926 GATGCAAGGTGCGAGCGGCTCTAGCGCTTAGCGCGGTGTCAGAGTTCTTGCTCAAGAAC 1985  
DB 400 GACGCAAGTTGAGAGGCTCTACTGTTTGGGACCTGTGTAAAGTTCTTGACCAAGAA 459  
  
QY 1986 GAGGACGGGTCTCCATCGCGCACTCAATTTGATGACCAAGGCAAAATCTCATGAA 2045  
DB 460 GAAGATGGGCTCTTAATGCTGCTCTGCTCTATGAACCAAGGCAAGGCTCTGTCGAG 519  
  
QY 2046 AGCTGGTATTACCTGAAAGATCGGCTCTTGAAGCGGAATCCCATTTCAACAGCGGTAC 2105  
DB 520 AGCTGGTATTACCTGAAAGATCGAGTCTTGTATGTTGGGATTCATTTAAGGCGCTAT 579  
  
QY 2106 GGGATGACCGGTTGAGATATCATGGCACCGACCGCGGATTCACCAAGATCTTTAACGG 2165  
DB 580 GGCATGATGCTGATTTGATTACCATGGAATGACCCCTAGATTCACCAAGGCTCTTCAACAAG 639  
  
QY 2166 GGAATGCTGATCTCACTCCACCATTAATGAGAGATGACTGGAACATCAAGGGCTTC 2225  
DB 640 GGAATGGCTGACCACTCCACCATTAATGAGAGATGACTGGAACATCAAGGGCTTC 699  
  
QY 2226 GAGGCGCTTCGAGACCGTGGTGTGATGTCGAGGCGGCACTGGGCGGCTCTCAGCATGATC 2285

DB 700 GAGGGCCTCAATTCATCGTTGATGTCGGTGGCGGCACCGAGCTGTGGTGAACATGATC 759  
QY 2286 GTTGCCAAATACCATCAATGAAGGATCAACTTCGAC-CGCCCAACCGATGAAGAC 2344  
DB 760 GTTTCGAAGTACCTTCGATCAAGGATCAACTTCGACTTGCTCATGTTATCGAAGAT 819  
QY 2345 GCGCCACCCCTTCTCGTGTCAAGCAGCTCGGAGCGACATGTTGTCAGCGTTCCAAAG 2404  
DB 820 GCTCTCATATATCTCGTGTTCACACGTTGGAGGGGACATGTTGTTAAGTGTACCAAG 879  
QY 2405 GGAGATGCCATTTTCATGAAGTGTGATGCTGAGTGCAGACCATTTGCGCGAAG 2464  
DB 880 GGAATGCAATTTTCATGAAGTGTGATGCTGAGTGCAGACCATTTGCAATAAA 939  
QY 2465 TTCTCTAAGAACTGCTACGATGCGCTTCCCAACAATGAAAGGTGATCGTTGCAGAGTGC 2524  
DB 940 TTCTTGAAGAACTGCTACGATGCGCTTCCAGACGATGCGCAAGTGTCTTGTGAGTGC 999  
QY 2525 GTACTCCTGTGTACCCAGACAGAGCTTAGCGACCAAGAAATGTGATCCACATCGACTGC 2584  
DB 1000 ATTCTTCTGTGTCACCAAGTGTGCTTCCCAAGGAGTGTGCTCATATGATGTG 1059  
QY 2585 ATCATGTTGCGCCCAACACCCAGCGGGAAGAGAGGACACAGAGGATTCGAGGCAATG 2644  
DB 1060 ATCATGTTGCGCACACACCTTGGCGGCAAGAGAGGACCGAGCGAGAAATTTGAAGCCCTG 1119  
QY 2645 GCCAAGGGGCGGATTTTCAGGCTTCCAAAGTGTGCTGCGCTTTTCGGCACTCAAGTC 2704  
DB 1120 GCTAAGGTTCTGATTTCCAAAGCATTCGCGTGTGCTGTGATGCTTTCAACACCTATGTC 1179  
QY 2705 ATGAGTTCCTGAAGCCGCTTGA 2728  
DB 1180 ATTGAGTTCTTAAGAAGATCTGA 1203  
  
RESULT 11  
AAC62762  
ID AAC62762 standard; DNA; 661 BP.  
XX  
AC AAC62762;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE O-methyl transferase promoter coding sequence #1.  
XX Promoter; eucalyptus; pine; gene transcription; ds.  
XX  
OS Eucalyptus grandis.  
XX OS  
XX WO200058474-A1.  
XX  
PD 05-OCT-2000.  
XX  
XX 24-FEB-2000; 2000WO-NZ000018.  
XX  
XX 25-MAR-1999; 99US-00276599.  
XX 30-JUL-1999; 99US-0146591P.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
XX Perera R, Rice SJ, Eagleston CK;  
XX  
XX WPI; 2000-647236/62.  
DR  
XX  
XX Novel promoter sequences useful for modulating transcription of plant DNA  
PT sequences of interest and production of polypeptides.  
PT  
XX  
XX Claim 1; Page 48; 93pp; English.  
XX  
XX The present invention relates to promoter sequences from eucalyptus and  
CC pine. The present sequence is one such promoter. This sequence is useful  
CC for modulating the transcription of DNA sequences of interest. The



Db 361 AACCACAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAG 420  
 Qy 1395 AGAGTTTCTCTCTATATCTGGTTACCGGTTGAGTCAATGCGATCGTGAGATGT 1454  
 Db 421 AGAGTTTCTCTCTATATCTGGTTACCGGTTGAGTCAATGCGATCGTGAGATGT 480  
 Qy 1455 ACATATTGGTGTAGGTCCTCAATATTTTGGGGAGGTTGGTGAACCGCAAAAGTTTCTTATA 1514  
 Db 481 ACATATTGGTGTAGGTCCTCAATATTTTGGGGAGGTTGGTGAACCGCAAAAGTTTCTTATA 540  
 Qy 1515 TATCGAACTCCACCAACCATCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCT 1574  
 Db 541 TATCGAACTCCACCAACCATCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCT 600  
 Qy 1575 CTGCTTTCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGATGGGT 1634  
 Db 601 CTGCTTTCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGATGGGT 660  
 Qy 1635 T 1635  
 Db 661 T 661

RESULT 13  
 ADH75428  
 ID ADH75428 standard; DNA; 661 BP.

XX ADH75428;

DT 22-APR-2004 (first entry)

DE Eucalyptus grandis superubiquitin related sequence #6.

ds; Monterey pine; superubiquitin; promoter; gene expression;

transgenic plant.

OS Eucalyptus grandis.

PN WO2003093475-A1.

PD 13-NOV-2003.

PF 30-APR-2003; 2003WO-NZ000076.

PR 30-APR-2002; 2002US-00137036.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI (RUBI-) RUBICON FORESTS HOLDINGS LTD.

PI Rice SJ, Wood M, Eagleton CK, Visser ES, Perera R;

DR WPI; 2003-903678/82.

PT New polynucleotide of the superubiquitin promoter from Pinus radiata,

PT useful in modifying gene expression in a target organism.

PS Disclosure; SEQ ID NO 12; 123pp; English.

XX The invention relates to a new isolated polynucleotide comprising the  
 CC Pinus radiata (Monterey pine) superubiquitin promoter sequence, its  
 CC complement, reverse complement, reverse sequence or inverted repeat or a  
 CC sequence having at least 40, 60, 75 or 90% identity with the promoter.  
 CC The polynucleotide is useful in modifying gene expression in a target  
 CC organism, especially in transgenic plants. This sequence corresponds to a  
 CC superubiquitin promoter related sequence.

SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 21.1%; Score 638.2; DB 10; Length 661;  
 Best Local Similarity 98.9%; Pred. No. 1.4e-165;  
 Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 979 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTTATTCTTCTGTCCTCAACTGT 1038  
 Db 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTTATTCTTCTGTCCTCAACTGT 60  
 Qy 1039 CGAATTTTCTTTTAGTAAAGTAAACCAATGATCGGCATATTTGACAAAAGGCTGATTA 1098  
 Db 61 CGAATTTTCTTTTAGTAAAGTAAACCAATGATCGGCATATTTGACAAAAGGCTGATTA 120  
 Qy 1099 GTATGATCTTGGAGTCTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGCGAAATTT 1158  
 Db 121 GTATGATCTTGGAGTCTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGCGAAATTT 180  
 Qy 1159 AAGCGCCCAACCCAGATTTGCAAGAGACACAAAGAGACGACCCAACTTTCTTTAAACAAG 1218  
 Db 181 AAGCGCCCAACCCAGATTTGCAAGAGACACAAAGAGACGATCCAACTTTCTTTAAACAAG 240  
 Qy 1219 ATCATACCCAGATCGGCAGTAAAGGTAATTAATTTTAAACAATAGCTCTTTGACCGGG 1278  
 Db 241 ATCATACCCAGATCGGCAGTAAAGGTAATTAATTTTAAACAATAGCTCTTTGACCGGG 300  
 Qy 1279 AACTCCGTATTTCTCTCACTTTCCATAAAACCCCTGATTAAATTTGGTGGAAAGCGACAGCC 1338  
 Db 301 AACTCCGTATTTCTCTCACTTTCCATAAAACCCCTGATTAAATTTGGTGGAAAGCGACAGCC 360  
 Qy 1339 AACCACAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1394  
 Db 361 AACCACAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 Qy 1395 AGAGTTTCTCTCTATATTTCTGGTTACCGGTTGAGTCAATGCGATCGTGAGATGT 1454  
 Db 421 AGAGTTTCTCTCTATATTTCTGGTTACCGGTTGAGTCAATGCGATCGTGAGATGT 480  
 Qy 1455 ACATATTGGTGTAGGTCCTCAATATTTTGGGGAGGTTGGTGAACCGCAAAAGTTTCTTATA 1514  
 Db 481 ACATATTGGTGTAGGTCCTCAATATTTTGGGGAGGTTGGTGAACCGCAAAAGTTTCTTATA 540  
 Qy 1515 TATCGAACTCCACCAACCATCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCT 1574  
 Db 541 TATCGAACTCCACCAACCATCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCT 600  
 Qy 1575 CTGCTTTCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGATGGGT 1634  
 Db 601 CTGCTTTCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGATGGGT 660  
 Qy 1635 T 1635  
 Db 661 T 661

RESULT 14

ADW80462  
 ID ADW80462 standard; cDNA; 661 BP.

XX AC

XX ADW80462;

DT 21-APR-2005 (first entry)

XX E. grandis caffeic acid O-methyltransferase promoter SEQ ID NO:12.

ss; wood; plant; transcription; caffeic acid O-methyltransferase;

transgenic plant.

OS Eucalyptus grandis.

XX Key Location/Qualifiers

FT TATA\_signal 537..543

FT /\*tag= a

XX US2005026162-A1.

XX 03-FEB-2005.

XX 06-NOV-2003; 2003US-00702319.

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XX PR 25-MAR-1999; 99US-00276599.
XX PR 30-JUL-1999; 99US-0146591P.
XX PR 24-FEB-2000; 2000WO-NZ000018.
XX PR 20-JUN-2000; 2000US-00598401.
XX PR 28-NOV-2000; 2000US-0072462A.
XX PR 09-NOV-2001; 2001US-0345397P.
XX PR 30-APR-2002; 2002US-00137036.
XX PR 08-NOV-2002; 2002US-00291447.
XX PR 08-NOV-2002; 2002US-0425087P.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PA (RUBI-) RUBICON FORESTS HOLDINGS LTD.
XX PI Perera R, Rice SJ, Eagleton CK;
XX DR WPI; 2005-131806/14.
XX XX
XX XX New isolated polynucleotide sequences comprising a functional vascular
XX PT tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase
XX PT promoter, useful for modifying gene expression.
XX PS Claim 2; SEQ ID NO 12; 82pp; English.
XX XX
XX CC The invention relates to a novel isolated polynucleotide sequence
XX CC comprising a functional vascular tissue-specific Eucalyptus grandis
XX CC caffeic acid O-methyltransferase (cOMT) promoter (ADW80462 or ADW80563).
XX CC Also claimed is a genetic construct comprising the above polynucleotide
XX CC sequence or a sequence having 20% base pairs fully defined in the
XX CC specification (ADW80510), a host cell comprising the above genetic
XX CC construct, a plant comprising the genetic construct, a method for
XX CC producing a plant with modified gene expression, and a method for
XX CC identifying a gene responsible for a desired function or phenotype. The
XX CC composition and methods are useful for modifying gene expression or for
XX CC modifying the transcription of endogenous and/or heterologous
XX CC polynucleotides involved in wood formation. The present sequence is used
XX CC in the exemplification of the invention.
XX SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;
Query Match 21.1%; Score 638.2; DB 14; Length 661;
Best Local Similarity 98.9%; Pred. No. 1.4e-165;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
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DB 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTTGTCGCATAACTGT 60
QY 1039 CGAATTTTCTCTTTAGTGAATGACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 1098
DB 61 CGAATTTTCTCTTTAGTGAATGACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 120
QY 1099 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCCCTCAGGGAAT 1158
DB 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCCCTCAGGGAAT 180
QY 1159 AAGGCGCCCAACCCAGATTGCAAGAGACAAAGACACAGCCACCTTCTTTAAACAAG 1218
DB 181 AAGGCGCCCAACCCAGATTGCAAGAGACAAAGACACAGCCACCTTCTTTAAACAAG 240
QY 1219 ATCATCACCAGATCGCCAGTAAGGTAATATTAATTTAAACAATAGCTCTTGACCGGG 1278
DB 241 ATCATCACCAGATCGCCAGTAAGGTAATATTAATTTAAACAATAGCTCTTGACCGGG 300
QY 1279 AACTCGGTATTTCTCTCACTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACGCC 1338
DB 301 AACTCGGTATTTCTCTCACTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACGCC 360
QY 1339 ACCCCACAAAGGTGATGATCTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1394
DB 361 AACCCCAAAAGGTGATGATCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 1395 AGAGTTTCTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCATGCGTGACGAATGT 1454
```

```
DB 421 AGAGTTTCTCTCTATATTTCTGTTCCACCGTTGGAGTCAATGGCATCGTGACGAATGT 480
QY 1455 ACATATTGGTGTAGGTTCCAATATTTTCGGGAGGTTGGTGAACCGCAAGTTCTTATA 1514
DB 481 ACATATTGGTGTAGGTTCCAATATTTTCGGGAGGTTGGTGAACCGCAAGTTCTTATA 540
QY 1515 TATCGAACCCTCCACCACCATACCTCACTTCAATCCCACTTTATTCGTTTATTTCT 1574
DB 541 TATCGAACCCTCCACCACCATACCTCACTTCAATCCCACTTTATTCGTTTATTTCT 600
QY 1575 CTGCTTTTCTTCTGCTCGAGTCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1634
DB 601 CTGCTTTTCTTCTGCTCGAGTCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 1635 T 1635
DB 661 T 661
RESULT 15
ABK48067
ID ABK48067 standard; cDNA; 1501 BP.
XX AC ABK48067;
XX DT 15-JUL-2002 (first entry)
XX DE cDNA encoding 5-hydroxyconiferaldehyde O-methyltransferase (AldOMT).
XX KW Plant; aspen; phenylpropanoid pathway; agronomic; lignin; paper;
XX KW 4-coumarate-CoA ligase; 4CL; coniferyl aldehyde 5-hydroxylase; CAlD5H;
XX KW S-adenosyl-L-methionine-dependent; SAM; AldOMT; transgenic; grass;
XX KW 5-hydroxyconiferaldehyde O-methyltransferase; cellulose; pulp;
XX KW coniferyl alcohol dehydrogenase; CAD; sinapyl alcohol dehydrogenase; SAD;
XX KW syringyl; guaiacyl; agriculture; gene; ss.
XX OS Populus tremuloides.
XX FH Key Location/Qualifiers
XX CDS 65..1162
XX FT /*tag= a
XX FT /product= "5-hydroxyconiferaldehyde O-methyltransferase
XX FT (AldOMT)"
XX XX
XX DN WO200220717-A2.
XX PD 14-MAR-2002.
XX XX
XX PF 05-SEP-2001; 2001WO-US027445.
XX XX
XX PR 05-SEP-2000; 2000US-0230086P.
XX XX
XX PA (UNMT) UNIV MICHIGAN TECHNOLOGICAL.
XX PI Chiang VLC, Li L;
XX XX
XX DR WPI; 2002-351773/38.
XX DR P-PSDB; AAU80015.
XX XX
XX PT Genetically transforming plant with multiple genes from phenylpropanoid
XX PT pathways, comprises incorporating number of genes into the genome of the
XX PT plant, to produce plants displaying altered agronomic traits.
XX PS Example 2; Fig 4A; 95pp; English.
XX XX
XX CC The invention relates to a method of genetically transforming a plant
XX CC simultaneously with multiple genes from the phenylpropanoid pathways,
XX CC comprising incorporating into the genome of the plant, a number of genes,
XX CC their substantially similar fragments or their combinations, to produce
XX CC plants displaying altered agronomic traits. The genes are selected from 4
XX CC -coumarate-CoA ligase (4CL), coniferyl aldehyde 5-hydroxylase (CAlD5H), S
XX CC -adenosyl-L-methionine (SAM)-dependent 5-hydroxyconiferaldehyde O-
```

CC methyltransferase (AldomT), coniferyl alcohol dehydrogenase (CAD) and  
CC sinapyl alcohol dehydrogenase (SAD). The method is useful for the  
CC transformation of plant tissue for the alteration of lignin monomer  
CC composition, increased syringyl/guaiacyl (S/G) lignin ratio and increased  
CC cellulose content and transgenic plants resulting from such  
CC transformations. This is an improved method to simultaneously control the  
CC lignin quantity, lignin compositions, and cellulose contents in plants,  
CC and is applicable to all plant species that are susceptible to the  
CC transfer of genetic information by Agrobacterium or other gene delivery  
CC system. The method is of particular value to paper and pulp industries,  
CC because lignin containing higher syringyl monomer content is more  
CC susceptible to chemical delignification. Woody plants transformed with  
CC DNA constructs offer a significant advantage in the delignification  
CC process over conventional paper feedstocks. Similarly, modification of  
CC the lignin composition in grasses by insertion and expression of  
CC heterologous SAD gene offers a unique method for increasing the  
CC digestibility of grasses and is of significant potential economic benefit  
CC to the farm and agricultural industries. The present sequence represents  
CC the coding sequence of 5-hydroxyconiferinaldehyde O-methyltransferase  
CC (AldomT) used in the method of the invention  
XX

SQ Sequence 1501 BP; 396 A; 344 C; 331 G; 430 T; -0 U; 0 Other;

Query Match 20.8%; Score 631; DB 6; Length 1501;

Best Local Similarity 74.5%; Pred. No. 2.1e-163;

Matches 807; Conservative 0; Mismatches 275; Indels 1; Gaps 1;

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| Db | 80   | GAATCTCAGATGACTCCAACTCAGGTATCAGATGAAGAGGCACACCTTTTGGCCATGCAA   | 139  |
| Qy | 1707 | CTGGCGAGCGCTCGTGTCTCCCATGCTCTAAAGCGCGCATCGAGATCGACTCTCTC       | 1766 |
| Db | 140  | CTAGCCATGCTTCTAGTTCTACCAATGATCTCTAAACAGCCATTTGAATCGACTCTTT     | 199  |
| Qy | 1767 | GAGATCATGGCCAAAGGACGGCGCGCGTTCCTCTCCACGGGGGAAATCGCGGCACAG      | 1826 |
| Db | 200  | GAATCATGGCTAAAGCTGGCCCTGGTGTCTTTCTTGTCACATCTGAGATAGTCTCTCAC    | 259  |
| Qy | 1827 | CTCCGACCCAGAACCCGAGGACCCCGTATGCTGACCGGATCTTCGGGCTGCTGGCC       | 1886 |
| Db | 260  | CTCCCTACCAAAAACCCCTGATGCGGCTGTATGTTAGACCGTATCTCGGCTCTCTGGCT    | 319  |
| Qy | 1887 | AGCTACTCGTGTCACTGACGACCTCGCGACCTCCCGGATGCGAGGTGAGGGGCTC        | 1946 |
| Db | 320  | AGCTACTCCATCTTACCTGTCTCTGAAAGATCTTCTGTATGGGAGGTTGAGAGACTG      | 379  |
| Qy | 1947 | TACGCTTAGCGCGGCTGTGCAAGTTCTTGGTCAAGAACGAGGACGGGCTCTCCATCGCC    | 2006 |
| Db | 380  | TATGGCTCGTCTCTGTTTGTAAATCTTGTACCAAGAACGAGGACGGTGTCTCTGTACG     | 439  |
| Qy | 2007 | GCATCTAACTTGATGAACACGAGCAAAATCTCATGGAAGCTGGTATTACTGAAAGAT      | 2066 |
| Db | 440  | CCTCTCTCTCATGAACAGGACAAAGGTCTCTATGGAAGCTGGTATTATTGAAAGAT       | 499  |
| Qy | 2067 | CGGTCTTTGAGGGGGAATCCCATTTCAAGGGGTACGGGATGACCGGTTTCGAGTAT       | 2126 |
| Db | 500  | GCAATTTCTTGTATGGAGGAATTCATTTTAAAGGCTATGGGATGACTGCAATTTGAAATAT  | 559  |
| Qy | 2127 | CATGGCACCGACCCCGGATTTCAAGAGATCTTTAAACCGGGGAATGTCTGTGACTCTCCACC | 2186 |
| Db | 560  | CATGGCACGGATCCAGATTTCAACAGGTCTTCAACAGGGANATGTCTGACCACTCTACC    | 619  |
| Qy | 2187 | ATTACTATGAAGAAGATATCTGGAACATACAGGGCTTCGAGGGCTTCGAGACCGTGGTC    | 2246 |
| Db | 620  | ATTACCATGAAGAAGATCTTTGAGACCTACAAAGGCTTTGAAGGCTCACGCTCTTGGTG    | 679  |
| Qy | 2247 | GATGTGAGAGGGGCACTGGGGCCGTGCTCAGCATGATCGTTGCAATATCCCATCAATG     | 2306 |
| Db | 680  | GATGTGTGTGGGACTGGAGCGGCTCGTTAAACCACTCGTCTCTTAAATACCCCTTCAATC   | 739  |
| Qy | 2307 | AAAGGGATCAACTTCGA-CCGCCCCCAACGGATTGAAGACGCCCCACCCCTTCTCTGGTGC  | 2365 |

Search completed: November 1, 2006, 00:21:24

Job time : 1285.86 secs

|    |      |                                                              |      |
|----|------|--------------------------------------------------------------|------|
| Db | 740  | AAGGGCAATTAACCTTCGATCTGCCACGTCATTTGAGGATGCCCATCTTATCCCGAGTG  | 799  |
| Qy | 2366 | AAGCAGCTCGAGGCGGACATGTTGTCAGCGTTTCCRAAGGGAGATGCCATTTTCATGAAG | 2425 |
| Db | 800  | GAGCATGTTGTCGCGACATGTTTGTAGTGTGCCCAAAGCAGATGCCGTTTTCATGAAG   | 859  |
| Qy | 2426 | TGGATATGCCATGATGAGGACGACCATTTGCGCGAAGTTCCTCAAGAACTGCTACGAT   | 2485 |
| Db | 860  | TGGATATGCCATGATGAGGACGACCATTTGCTTAAATTTCTTGAAGAATTGCTATGAC   | 919  |
| Qy | 2486 | GCGTTCCTCCCAACATGGAAGGTGATCGTTGCAGAGTGCCTACTCCTGTGTACCCAGAC  | 2545 |
| Db | 920  | GCGTTGCGGAAACCGCAAGGTGATCTTGTAGTGCATTTCTCCGTTGGCTCTCTGAC     | 979  |
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| Qy | 2726 | TGA 2728                                                     |      |
| Db | 1160 | TAA 1162                                                     |      |

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:29:19 ; Search time 9846.88 Seconds  
(without alignments)  
17207.024 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues..

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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| 2:  | gb_est3.* |
| 3:  | gb_est4.* |
| 4:  | gb_est5.* |
| 5:  | gb_est6.* |
| 6:  | gb_hic.*  |
| 7:  | gb_est2.* |
| 8:  | gb_est7.* |
| 9:  | gb_est8.* |
| 10: | gb_est9.* |
| 11: | gb_gss1.* |
| 12: | gb_gss2.* |
| 13: | gb_gss3.* |
| 14: | gb_gss4.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2          | 533   | 17.6        | 951    | 10 | DT546163    |
| 3          | 512   | 15.9        | 907    | 8  | CO072302    |
| 4          | 504.2 | 16.6        | 930    | 10 | DT566827    |
| 5          | 504   | 16.6        | 848    | 4  | CB975481    |
| 6          | 494.8 | 16.3        | 958    | 10 | DV465073    |
| 7          | 490.8 | 16.2        | 853    | 8  | CO071813    |
| 8          | 489.6 | 16.2        | 864    | 8  | CO082948    |
| 9          | 489.2 | 16.1        | 895    | 10 | DT558009    |
| 10         | 489   | 16.1        | 880    | 8  | CO087218    |
| 11         | 488.6 | 16.1        | 961    | 9  | CB975481    |
| 12         | 484.8 | 16.0        | 931    | 9  | CB975481    |
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| 14         | 479.8 | 15.8        | 917    | 9  | CB975481    |
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| 21 | 466.4 | 15.4 | 936 | 9  | CX665083 |
| 22 | 464.2 | 15.3 | 904 | 9  | CX664451 |
| 23 | 462.8 | 15.3 | 847 | 10 | DT571100 |
| 24 | 461.6 | 15.2 | 833 | 8  | CO080205 |
| 25 | 460.4 | 15.2 | 778 | 8  | CO113461 |
| 26 | 459.4 | 15.2 | 809 | 8  | CO094187 |
| 27 | 458.6 | 15.1 | 903 | 9  | CX664005 |
| 28 | 457   | 15.1 | 892 | 9  | CX664055 |
| 29 | 456   | 15.0 | 901 | 8  | CX053237 |
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| 45 | 429.2 | 14.2 | 758 | 9  | DN759581 |

## ALIGNMENTS

## RESULT 1

## CNS092RE

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

## FEATURES

CNS092RE 1315 bp mRNA linear HTC 06-FEB-2004  
Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
GSLTPGH15ZH04 of Hormone Treated Callus of strain coi-0 of  
Arabidopsis thaliana (thale cress).

Accession BX831565.1 GI:42456552

Version HTC; GSLT cDNA.

Keywords Arabidopsis thaliana (thale cress)

Source Arabidopsis thaliana

Organism Arabidopsis thaliana

Reference 1 (bases 1 to 1315)

Authors Castell, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.

Title Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

Journal Unpublished

Reference 2 (bases 1 to 1315)

Authors Direct Submission

Journal Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)

Comment - Web : www.genoscope.cns.fr

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castell V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full

length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

Location/Qualifiers

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RESULT 2
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LOCUS EST1056803 TMO Gossypium hirsutum cDNA, mRNA sequence.
DEFINITION DT546163
ACCESSION DT546163.1 GI:78325889
VERSION DT546163.1
KEYWORDS EST.
SOURCE Gossypium hirsutum (upland cotton)
ORGANISM Gossypium hirsutum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 951)
AUTHORS Yang,S.S., Cheung,F., Wei,N.E., Lee,J.J., Ha,M., Stelly,D.M.,
Thaxton,P., Sze,S.H., Triplett,B.A., Town,C.D. and Chen,Z.J.
TITLE ESTs from immature ovule (-3 to 3 DPA) of G. hirsutum TM-1
JOURNAL Unpublished (2005)
COMMENT Contact: Z. Jeffrey Chen
The Chen lab: A Home of Polyploidy (http://polyploidy.tamu.edu)
Texas A&M University
Department of Soil & Crop Sciences, MS2474, College Station, TX
77842-2474, USA
Tel: 979 862 2359
Fax: 979 845 0456
Email: zjchen@neo.tamu.edu
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Seq primer: CAG GAA ACA GCT ATG ACC.
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/clone_lib="TMO"
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G. hirsutum L. Texas Marker-1 (TM-1) plants were grown in
a greenhouse at the Texas A&M University and in the field
at the USDA-ARS, New Orleans. The bolls were tagged and
harvested at 3 days before anthesis (-3DPA), the day of
anthesis (0 DPA), and 3 days post anthesis (3DPA) from a
pool of ~20 plants. Total RNA was extracted from immature
ovules or fiber-bearing ovules. An equal amount of total
RNA from three samples was mixed and sent to Invitrogen
Corp. (Carlsbad, California) for full-length cDNA library
construction. Messenger RNA was isolated from the total
RNA using a filter syringe containing oligo (dT). The
first-strand cDNA was synthesized from 15 ug mRNA using
SuperscriptMIII reverse transcriptase, and the
second-strand cDNA was synthesized using E. coli RNase H,
DNA polymerase I, and DNA ligase. The double-stranded cDNA

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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                            |                                                                     |                 |          |                      |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-----------------|----------|----------------------|
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 269                                                                                                        | ACCGCATCTTGGCGCTCTCTGGCTACTTACTCCATCTCTCACTTGTCTCTTGGCACTCTTC       | 328             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1924                                                                                                       | CCGATGGCAAGTTCGAGCGCTCTACGGCTTAGCGCGGTGTCACAGTTCTTGGTCAAGA          | 1983            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 329                                                                                                        | CTGATGGCAAAAGTGGAGAGACTCTATGGTCTTGGCCCTGTCTGCAATTCGTGACCAAGA        | 388             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1984                                                                                                       | ACGAGGACGGGCTCTCCATCGCCCACTCAACTTGTATGAACACAGGCAAAATCCTCATGG        | 2043            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 389                                                                                                        | ATGAAGATGGCGGTCACTCTTCCGCCCTCAGTCTCATGATCAAGCAAGTCTTATGG            | 448             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2044                                                                                                       | AAAGCTGGTATTACCTGAAAGATCGGTCCTTTGAAGCGGAAATCCCATTCACAAAGCGT         | 2103            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 449                                                                                                        | AGAGCTGGTACTACTTTGAAGATCGCGTGTGGAGGTGGAATTCCTTCAACAAAGCCT           | 508             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2104                                                                                                       | ACGGGATGACCGCGTTCGAGTATCATGGCACCGACCGCGATTCACCAAGATCTTTAAAC         | 2163            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 509                                                                                                        | ATGGTATGACCGCAATTCGAGTACCATGCGACCGGATCCTAGATTCACCAAGGTTTCAACA       | 568             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2164                                                                                                       | GGGGATGTCTGATCACTCCACCATTAATGAAGAAGATCTGGAACATACAAAGGGCT            | 2223            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 569                                                                                                        | GGGGATGTCTGATCACTCTACCATTAATGAAGAAGATCTTGAAGACCTATGATGGCT           | 628             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2224                                                                                                       | TCGAGGGCTTCGAGACCGGTGTCATGTCGAGGCGGCACCTGGGGCGTCTCAGCATGA           | 2283            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 629                                                                                                        | TTGAGGGACTCAAAACACTGGTTCGATGTTGGCGCGTACTGGAGCTACGCTTAACATGA         | 688             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2284                                                                                                       | TGTTGCCAAATACCATCAATGAAGGATCACTTCGA-CCGCCCAACGGATTGAAG              | 2342            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 689                                                                                                        | TTGTCAACCAAGCACCTTCTATAAGGGCATCAACTTTGATTTGCCCTCATGTCATTGAGG        | 748             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2343                                                                                                       | ACGCCCAACCCCTTCTGCTGTGTCAGCAGCTCGGAGGCGACATGTTGTCAGCGTTCCAA         | 2402            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 749                                                                                                        | ATGCTCTCTTATCTGCTGTGGAGCATGTTGGTGGAGACATGTTTGAAGTGTTCCAA            | 808             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2403                                                                                                       | ACGGAGATGCCATTTTCATGAAGTGGATATGCCATGATGGAGTGACGACCATTTGCCGA         | 2462            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 809                                                                                                        | AAGGAGACGCATCTTTCATGAAGTGGATATGCCAGATTTGGAGTGGATGAGCACTGCTCCA       | 868             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2463                                                                                                       | AGTTCCTCAAGAACTGCTACGATGGCTTCCCAACA                                 | 2498            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 869                                                                                                        | AGTTTTGGAAGTGTCTACGAAGCTTTTGGCGGACA                                 | 904             |          |                      |
| RESULT 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | DT566827                                                                                                   | 930 bp                                                              | mRNA            | linear   | EST 31-OCT-2005      |
| LOCUS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | EST1077467                                                                                                 | TMO                                                                 | Gossypium       | hirsutum | cdna, mRNA sequence. |
| DEFINITION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | DT566827                                                                                                   |                                                                     |                 |          |                      |
| ACCESSION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | DT566827.1                                                                                                 | GI:78346553                                                         |                 |          |                      |
| VERSION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | EST.                                                                                                       |                                                                     |                 |          |                      |
| KEYWORDS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Gossypium                                                                                                  | hirsutum                                                            | (upland cotton) |          |                      |
| SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Gossypium                                                                                                  | hirsutum                                                            |                 |          |                      |
| ORGANISM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;                                         |                                                                     |                 |          |                      |
| REFERENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;                                         |                                                                     |                 |          |                      |
| AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.                                           |                                                                     |                 |          |                      |
| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 1 (bases 1 to 930)                                                                                         |                                                                     |                 |          |                      |
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Yang,S.S., Cheung,F., Wei,N.E., Lee,J.J., Ha,M., Stelly,D.M.,                                              |                                                                     |                 |          |                      |
| COMMENT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Thaxton,P., Sze,S.H., Triplett,B.A., Town,C.D. and Chen,Z.J.                                               |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ESTs from immature ovule (-3 to 3 DPA) of G. hirsutum TM-1                                                 |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Unpublished (2005)                                                                                         |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Contact: Z. Jeffrey Chen                                                                                   |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | The Chen lab: A Home of Polyploidy ( <a href="http://polyploidy.tamu.edu">http://polyploidy.tamu.edu</a> ) |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Texas A&M University                                                                                       |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Department of Soil & Crop Sciences, MS2474, College Station, TX                                            |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 77842-2474, USA                                                                                            |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Tel: 979 862 2359                                                                                          |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Fax: 979 845 0456                                                                                          |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Email: zjchen@neo.tamu.edu                                                                                 |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TIGR sequence name: G0AIE57TR                                                                              |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Seq primer: CAG GAA ACA GCT ATG ACC.                                                                       |                                                                     |                 |          |                      |
| FEATURES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Location/Qualifiers                                                                                        |                                                                     |                 |          |                      |
| source                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 1..930                                                                                                     |                                                                     |                 |          |                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | /organism="Gossypium hirsutum"                                                                             |                                                                     |                 |          |                      |
| /mol_type="mRNA"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                            |                                                                     |                 |          |                      |
| /cultivar="Texas Maker-1 (TM-1)"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                            |                                                                     |                 |          |                      |
| /db_xref="taxon:3635"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                            |                                                                     |                 |          |                      |
| /tissue_type="Immature ovules"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                            |                                                                     |                 |          |                      |
| /dev_stage="Immature ovules (-3 to 3 days post anthesis, DPA) with or without fibers"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                            |                                                                     |                 |          |                      |
| /clone_lib="TMO"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                            |                                                                     |                 |          |                      |
| /note="Vector: pCMV-SPORT6.1; Site 1: EcoRI; Site 2: NotI; G. hirsutum L. Texas Marker-1 (TM-1) plants were grown in a greenhouse at the Texas A&M University and in the field at the USDA-ARS, New Orleans. The bolls were tagged and harvested at 3 days before anthesis (-3DPA), the day of anthesis (0 DPA), and 3 days post anthesis (3DPA) from a pool of ~20 plants. Total RNA was extracted from immature ovules or fiber-bearing ovules. An equal amount of total RNA from three samples was mixed and sent to Invitrogen Corp. (Carlsbad, California) for full-length cDNA library construction. Messenger RNA was isolated from the total RNA using a filter syringe containing oligo (dT). The first-strand cDNA was synthesized from 15 ug mRNA using SuperScriptTMIII reverse transcriptase, and the second-strand cDNA was synthesized using E. coli RNase H, DNA polymerase I, and DNA ligase. The double-stranded cDNA was blunt-ended using T4 DNA polymerase, digested with NotI, size-selected using agarose gel electrophoresis, and directionally cloned into the NotI-EcoRV sites of the pCMV-SPORT6.1. The ligated products were transformed using ELECTROMAXYMDHI0BT1 cells. The library contained 4.2x10 <sup>6</sup> cfu with ~100% of colony growth rate. It is estimated that over 60% clones contained full-length cDNA inserts with an average insert size of 1.53-kb. A total of 51,072 colonies were arrayed in duplicate sets each with 133 384-well plates for sequencing and storage, respectively." |                                                                                                            |                                                                     |                 |          |                      |
| ORIGIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                            |                                                                     |                 |          |                      |
| Query Match 16.6%; Score 504.2; DB 10; Length 930;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                            |                                                                     |                 |          |                      |
| Best Local Similarity 74.5%; Pred. No. 5.5e-134;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                            |                                                                     |                 |          |                      |
| Matches 662; Conservative 0; Mismatches 223; Indels 4; Gaps 2;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                            |                                                                     |                 |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1647                                                                                                       | GAGACCCAGATGACCCCGACCCCAAGTCTCGGACGACGAGCGCAACCTCTTCGCCATGCGAG      | 1706            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 42                                                                                                         | GAAACTCAATGACACCCACCCCAAGTCTCAGATGATGAAGCCACTTATTCGCTATGCAA         | 101             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1707                                                                                                       | CTGCGGAGCGCCTCCGTGCTCCCATGGTCTCTAAAGCGCCCATCGAGATCGACCTCTCTC        | 1766            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 102                                                                                                        | CTTGCCAGTGCATCAGTCTCTCCCATGGTCTCTCAATCAGCCATTGAATCTGACTTGCTC        | 161             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1767                                                                                                       | GAGATCATGGCCAAAGACGGCGCGGCTTCTCTCTCCACGGGGGAAATCGCGGCACAG           | 1826            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 162                                                                                                        | GAGATCATGGCTAAAGCTGGTCCAGGTGCTTTTGTCTCCCAAAAGAGTGGCTTCCAAG          | 221             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1827                                                                                                       | CTCCCGACCCAGAACCCCGAGGCAACCGTCATGCTCGACGGATCTTCGGGCTCTGTGCC         | 1886            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 222                                                                                                        | CTCCCGACCCAGAACCCCTGATGACCCGTATCTTGGCTACCTTCCCTGGTGGCAAGTGGAAAGACTC | 281             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1887                                                                                                       | AGTACTCTCGTCTCAGCTGCACCTCCCGACCTCCCGATGCGAAGGTCGAGCGGCTC            | 1946            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 282                                                                                                        | AGCTACAAAGCTCTCACTTGTCTCTTGGCTACCTTCCCTGGTGGCAAGTGGAAAGACTC         | 341             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1947                                                                                                       | TACGGCTTAGCGCGGTGTGCAAGTCTTGTGTTCAAGAACGAGGACGCGGGTCTCCATCGCC       | 2006            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 342                                                                                                        | TATGGCTTAGCGCGCTGTGCAAAATCTTGACCAAGAACGAGATGGTGTCACTCTTTCC          | 401             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2007                                                                                                       | GCATCTCAACTTGTATGAACCCAGGACAAATCCTCATGGAAGCTGTGTTACTCTGAAGAT        | 2066            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 402                                                                                                        | GCCCTTAGTCTCATGAATCAAGACAAGTCTCTTATGAGAGCTGTGTACTTCTTGAAGAT         | 461             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2067                                                                                                       | GCGGTCTTTGAAGCGGGAATCCCAATTCAAAGGCGTACGGGATGACCGCGTTCAGATAT         | 2126            |          |                      |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 462                                                                                                        | GCTGTGCTGGATGGTGAATTCCAATTCACCAAGGCTTATGGTATGACTGCATTTGAGTAC        | 521             |          |                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 2127                                                                                                       | CATGGCACCGACCCGCGGATTCACCAAGATCTTTTAACCGGGGAATGTCTGATCATCTCCACC     | 2186            |          |                      |

Db 522 CATGCCACTGATCTCTAGATTCAACAGGTTTTTCAACAGGGGAATGTCTGATCACTTACC 581  
QY 2187 ATTACTATGAAGATAGTCTGAACATACAAAGGCTTCGAGGGCTCGAGACCTGTGC 2246  
Db 582 ATCACCATGAAGAAGATTCTCATATATGATGTTTCCAAAGGCTAAACATTTGGTC 641  
QY 2247 GATGTCGAGGGCGGCACTGGGGCCGTGCTCAGCATGATCGTTGCCCCAAATACCCATCAATG 2306  
Db 642 GATGTTGGCGGTGGTACCGGTGCCAGCTTAGCATGATGCTCTCTAAGTACCCACCATTA 701  
QY 2307 AAAGGATCACTTGA-CGGCCCCAACGGATTGAAGAGCGCCACCCCTTCT---GGT 2362  
Db 702 AAAGCATTAACCTTTGATTGCTCATGTCAATGAGGATGCTCTAGCTGCTCTAGTAGT 761  
QY 2363 GTCAAGCAGCTCGAGGGGACATGTTGTCAGCGTTTCCAAAGGGAGATGCCAATTTTCATG 2422  
Db 762 GTGGAGCATGTTGGTGAGACATGTTGTAAGTGATACCAAGGAGATGCCAATTTTCATG 821  
QY 2423 AAGTGGATATGCCATGACTGGAGTGACGACCAATTCGCGGAAGTTCTCTCAAGAACTGTAC 2482  
Db 822 AAGTGGATATGTCATGATTGGAGCGACGAACACTGGCCCAAGTTTGAAGAACTGCTAT 881  
QY 2483 GATGCGCTTCCAAACAATGGAAAGTGATCGTTGCGAGATGCGTACTCC 2531  
Db 882 GAAGCTTTGCCAGACAACGGGAAGTGATTGTTGCCGAATGCATTCTTC 930

RESULT 5  
CB975481  
LOCUS  
DEFINITION  
CB975481  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 848)  
Jones, K. and Cook, D.  
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'  
berries at various developmental stages  
Unpublished (2003)  
Contact: Douglas Cook, PhD  
CAES Genome Facility  
UC Davis, Plant Pathology  
One Shields Ave, Davis, CA 95616, USA  
Tel: 530 754 6561  
Fax: 530 754 6617  
Email: drcocook@ucdavis.edu  
Seq primer: ACGGTACCGACATATGCC.

FEATURES  
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1..848  
/organism="Vitis vinifera"  
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/clone="CB975481.1b\_Fa\_F02"  
/sex="Hermaphrodite"  
/dev\_stage="Berry stage I"  
/lab\_host="DH5alpha"  
/clone\_lib="Cabernet Sauvignon Berry Stage I - CAB3"  
/note="Organ: Berry; Vector: pBMR; Site 1: Sfil; Site 2:  
Sfil; CAB3 is a cDNA library of Vitis vinifera 'Cabernet  
Sauvignon' clones 8 berries. Samples were collected after  
berry set from field-grown vines during stage I of berry  
growth, 17 days after full bloom. The average berry size  
was 6 millimeters. Sampled vines were located at the  
University of California, Davis, Experimental Vineyard.  
cDNAs were made by oligo-dT priming and directionally

cloned. 5' and 3' adaptors were used in cloning as follows:  
5'-AAGCAGTGTATCAACGAGATGCGCATTAACGCGGG-3' and  
5'-ATTCTAGAGCGGAGCGGCGAGCATG-dt(30)NN-3'. Library was  
constructed using the Clontech Creator SMART kit and  
size-selected to contain the 0.5-3 kb size fraction."

ORIGIN  
Query Match 16.6%; Score 504; DB 4; Length 848;  
Best Local Similarity 75.6%; Pred. No. 6, 1e-134;  
Matches 638; Conservative 0; Mismatches 205; Indels 1; Gaps 1;  
QY 1786 GGC CGG CGC GTT CCT CTCTCAACGGGGGAAATCGCGGCACAGCTCCGACCCAGAACCCCG 1845  
Db 1 GGGCTGGGGCGTGTGTCTCCACTTCTGAGATTGCTGCTCAGCTCCCAACCCAGAACCCAG 60  
QY 1846 AGCACCCGTCATCTCGACCGGATCTTCCGGCTGTGGCCAGTACTCCCGTCTCAGT 1905  
Db 61 AAGCCCTGTCTATCTGGACGCTATCTTCCGCCCTTCTTGGCCACCTATGCTGTGGTCAAGT 120  
QY 1906 GCACCTCCGCGACTCTCCCGATGGCAAGTCGAGCGGCTCTAGCGCTTAGCGCGGTGT 1965  
Db 121 GCTCTCTTCGCAACTCTCCCTGATGGAGGGTTGAGAGGCTCTATGGGCTCGCCCTGTCT 180  
QY 1966 GCAAGTCTTCTGGTCAAGAACGAGGACGGGGTCTCCATGCGCGCACTCAACTTGTATGAA 2025  
Db 181 GCAAGTACTTGACTAGGAACGAAGATGGGGTGTCTGTAGCCCTCTTCTCTCATGAATC 240  
QY 2026 AGGACAAATCTCTATGGAAAGCTGGTATTACCTGAAAGATGCGGTCTTGAAGCGGAA 2085  
Db 241 AGGACAAAGTCTCTATGGAGAGCTGGTACTATTGAAAGATGCAAGTCTTCTGATGGTGA 300  
QY 2086 TCCCATTAACAACAGGCGTACGGGATGACCGGTTTCGAGTATCATGGGACCGACCCCGCAT 2145  
Db 301 TCCCTTTCAACAAAGCCTATGGAATGATCTGCTTTGAGTATCATGGACAGATCTTAGAT 360  
QY 2146 TCAACAAGATCTTTAACCGGGGAATGTCTGATCACTCCACCATTAATATGAAAGATAC 2205  
Db 361 TCAACAAGTGTTCACAAATGGAATGTCTGTCTATCCACCATTAACCATGAAGAAATTC 420  
QY 2206 TGGAAACATCAACAGGCTTTCGAGGCGCTCGAGACCGTGTGTCGATGTGGAGCGGCGCATG 2265  
Db 421 TTGAAGCCTCAACAGGGGTTTTGAGGGGCTCACTCAATTTGTTGATGTTGGTGGGACTG 480  
QY 2266 GGGCGGTGCTCAGCATGATCGTTCCCAAAATACCCTCAATGAAAGGATCACTTTCGAC- 2324  
Db 481 GAGCACCTTAAATGATCATATCCAAATACCCTCAATTTAAGGGCATTAATCTTGAAT 540  
QY 2325 CGCCCCAACGGAATTGAAGACGCCCCACCCCTTCTCTGGTGTCAAGCAGCTCGGAGCGGACA 2384  
Db 541 TGCCTCATGTTATTGATGATGTCCTTATCTGTTGGAGAAATGTTTGGGGGAGACA 600  
QY 2385 TGTTCGTGAGGTTCCAAAGGGAGATGCCATTTTCATGATGAGTATGCCATGATGGA 2444  
Db 601 TGTGTTGAGTGTCCCAAGGGAGATGCCATCTTTTCATGAAGTGTGATATGTCATATTGGA 660  
QY 2445 GTGACGACCATGTCGCGAAGTTCTCAAGAACTCTAGATGCGCTTCCCAACCAATGAA 2504  
Db 661 GTGATGCTCATGTTGTAAGTTCCTTGAAGAACTCTATCAGGCACTTCCAGACAAATGGA 720  
QY 2505 AGGTGATCGTTTGCAGAGTGGGTACTCCCTGTGTGTACCCAGACACGAGCGCTAGCCACCA 2564  
Db 721 AGGTAAATGTTGTGTAATGCATCTTCTGTGGGCCCCAGACACCCAGCTAGCCCAAGG 780  
QY 2565 ATGTGATCCATCATGCACTGCAATCATGTTGGGCCCAACACCCAGGCGGGAAGAGAGACAC 2624  
Db 781 ATGTGTCCTCATATCGAGCTTATCATGTTAGTCTATAACCCCTGTGTGAAAAAATAAAAA 840  
QY 2625 AGAA 2628  
Db 841 AAAA 844

RESULT 6

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|
| <p>DV465073</p> <p>LOCUS</p> <p>DEFINITION</p> <p>MTUNUL1.P34.F07 NUL Populus fremontii x Populus angustifolia cDNA, mRNA sequence.</p> <p>ACCESSION</p> <p>DV465073</p> <p>VERSION</p> <p>DV465073.1</p> <p>KEYWORDS</p> <p>EST.</p> <p>SOURCE</p> <p>ORGANISM</p> <p>Populus fremontii x Populus angustifolia</p> <p>Populus fremontii x Populus angustifolia</p> <p>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eusoids I; Malpighiales; Salicaceae; Populus.</p> <p>REFERENCE</p> <p>AUTHORS</p> <p>TITLE</p> <p>1 (bases 1 to 958)</p> <p>Harding,S.A., Elliott,S.G., Montag,J.D. and Tsai,C.-J.</p> <p>Expressed sequence tags from Populus fremontii x Populus angustifolia</p> <p>UNPUBLISHED</p> <p>Contact: Chung-Jui Tsai</p> <p>Biotech Research Center</p> <p>Michigan Technological University, School of Forest Resources &amp; Environmental Science</p> <p>1400 Townsend Drive, Houghton, MI 49931-1295, USA</p> <p>Tel: 906 487 2914</p> <p>Fax: 906 487 2915</p> <p>Email: chtsai@mtu.edu.</p> | <p>958 bp</p> <p>mRNA</p> <p>linear</p> <p>EST 20-OCT-2005</p> |
| <p>FEATURES</p> <p>source</p> <p>1..958</p> <p>/organism="Populus fremontii x Populus angustifolia"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:352374"</p> <p>/dev_stage="2-month-old hydroponic plants"</p> <p>/lab_host="E. coli DH10B, T1 phage resistant"</p> <p>/clone_lib="NUL"</p> <p>/note="Vector: pCEM-52f(+); Site 1: StuI (custom-generated at Sall 1; Site2: NotI,3'-end of cDNA; Clone: NUL. Leaves and stems (LPI 1-5) harvested from control plants at different diurnal points (noon or midnight), and systemic leaves (LPI 1-5) harvested 48-hr after SA treatment were used for mRNA isolation. mRNA from these sources were pooled for cDNA library construction and normalization according to Gruber et al. (1993) Focus 15: 59-65."</p>                                                                                                                                                                                                                                                                                                                                                  |                                                                |
| <p>ORIGIN</p> <p>Query Match</p> <p>Best Local Similarity</p> <p>Matches 656; Conservative</p> <p>16.3%; Score 494.8; DB 10; Length 958;</p> <p>73.7%; Pred. No. 3e-131;</p> <p>0; Mismatches 232; Indels 2; Gaps 2;</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                |
| <p>QY</p> <p>1647</p> <p>GAGACCCAGATGACCCGACCAAGTCTCGGACGACGAGGCGAACCTCTTCGCCATCGCAG</p> <p>1706</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                |
| <p>Db</p> <p>69</p> <p>GAAACTCAGATGACTCCAACTCAGGTATCAGATGAAGAGGCACACCTCTTTGCCATGC</p> <p>128</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                |
| <p>QY</p> <p>1707</p> <p>CTGGCGAGCGCCTCCGTGCTCCCATGGTCTCTAAAGCCGCGCATFCGAGATCGACCTCTC</p> <p>1766</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                |
| <p>Db</p> <p>129</p> <p>CTAGCCAGTGCTTCAGTTCTACCAATGATCTCTCAAAACAGGCCATTGAACTCGACCTTCT</p> <p>188</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                |
| <p>QY</p> <p>1767</p> <p>GAGATCATGGCCAAGACGGCGCGGCG -CGTTCTCTCCACGGGGGAATCGCGCACA</p> <p>1825</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                |
| <p>Db</p> <p>189</p> <p>GAAATCATGGCTAAAGCTGGCCCTGGTGCCTTCTTGTCACATCTCAGATAGTCTTCTCA</p> <p>248</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                |
| <p>QY</p> <p>1826</p> <p>GCTCCGACCCAGAACCCCGAGGACCCGTGATGCTCGACCGGATCTTCGGGCTGCTGGC</p> <p>1885</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                |
| <p>Db</p> <p>249</p> <p>CCTCCCTACCAAAAACCCCTGATCGCCCTGTCTAGTTAGACCGTATCTTGGCCCTCCTGGC</p> <p>308</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                |
| <p>QY</p> <p>1886</p> <p>CAGCTACTCCGTGCTCACGTGACCCCTCGGACCTCCCGATGGCAAGTTCGACGGCT</p> <p>1945</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                |
| <p>Db</p> <p>309</p> <p>TAGCTACTCAATCTTTACTTTGCTCTCTGAAAGATCTTCTGATGGGAAGTTGAGAGACT</p> <p>368</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                |
| <p>QY</p> <p>1946</p> <p>CTAGCGCTTAGCCCGGTGTGCAAGTTCTTGCTCAAGAACGAGGACGGGTCTCCATCGC</p> <p>2005</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                |
| <p>Db</p> <p>369</p> <p>GTATGGCCCTTGCTCCCTGTGTGAAATTTCTTGACCAAGAACGAGACGCTGTCTCTGTG</p> <p>428</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                |
| <p>QY</p> <p>2006</p> <p>CGCACTCAACTTGATGAACGAGGACAAAATCCTCTCATGAAAGCTGGTATTACCTGAAAGA</p> <p>2065</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                |

EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

## ORIGIN

Query Match 16.2%; Score 490.8; DB 8; Length 853;  
Best Local Similarity 74.4%; Pred. No. 4.2e-130;  
Matches 632; Conservative 0; Mismatches 217; Indels 1

|      |    |                                                                 |      |
|------|----|-----------------------------------------------------------------|------|
| 1662 | Qy | CCGACCCCAAGTCTCGGACGACGAGGCGAACCCTCTTCGCCCATGACGTGGCGAGGCGCTCC  | 1721 |
| 4    | Db | CCCACCCCAAGTCTCAGATGAGGAGCCCACTTATTGCTATGCAACTTGGCAGTGCATCA     | 63   |
| 1722 | Qy | GTGCTCCCAATGGTCTTAAAGGCGCCATCGAGATCGACCTCTCCAGATCATGGCCCAAG     | 1781 |
| 64   | Db | GTCTCTCCCAATGGTCTCAAATCAGCCATTTGAACCTTGCTTGGAGATCATGGCCCAA      | 123  |
| 1782 | Qy | GACGGGCGGGCGGGTTCCTCTCCACGGGGGAAATCGCGGCACAGCTCCCGACCCAGAAC     | 1841 |
| 124  | Db | GCTGGTCCAGTGCTTCTTGTCCTCCCAAGAAGTGGCTTCCAAGCTCTCCCAACCAAC       | 183  |
| 1842 | Qy | CCGAGGCAACCCGTATGCTCGACCGGATCTTCGGGTGCTGGCGACGTACTACGTGCTC      | 1901 |
| 184  | Db | CCTGATGCACCCCGTCATGCTGACCGGTATCTTGGCTCTCCGTAGCTACAACGCTCTC      | 243  |
| 1902 | Qy | ACGTGCACCTTCGGCAGCTCCCCGATGGCAAGGTGAGCGGCTCTACGGCTTAGCGCG       | 1961 |
| 244  | Db | ACTTGTCTCTGGGTACCTCTCTGATGGCAAGTGGAAAGACTATATGGCCCTTGGCCCT      | 303  |
| 1962 | Qy | GTGTGCAAGTCTTTGGTCAAGAACGAGACGGGGTCTCCATCGCGGACCTCAACTTGATG     | 2021 |
| 304  | Db | GTCTGCMAATCTTGACCAAGACGAAGATGGTGTCACTCTTTCGGCCCTTAGTCTCATG      | 363  |
| 2022 | Qy | AACGAGGACAAATCTCTATGGAAGCTGGTATTAACCTGAAGATCGGTCTCTGAAGGC       | 2081 |
| 364  | Db | AATCAAGACAAGTCTCTTATGGAGAGCTGGTACTACTTTGAAAGATGCTGTGCTGGATGGT   | 423  |
| 2082 | Qy | GGAATCCCATTTCAACAGGGCTACGGGATGACCGGTTTCGAGTATCATGCGACCGACCG     | 2141 |
| 424  | Db | GGAATTCATTTCAACAAGGCTATGGTATGACTGCAATTTGAGTACCATGCGACTGATCT     | 483  |
| 2142 | Qy | CGATTTCAACAAGATCTTTAACCGGGGAATGCTGTGATCACCTCCACCTACTATGAAGAAG   | 2201 |
| 484  | Db | AGATTTCAACAAGGTTTTCAACAAGGGAATGCTGTATCACTCTACCATCCATGAAGAAG     | 543  |
| 2202 | Qy | ATACTGAAACATACAAGGGCTTCGAGGGCTCGAGACCGTGGTCGATGTCGAGGCGCGC      | 2261 |
| 544  | Db | ATTCTCGATACATATGATGGTTTCCAAGGACTAANAACATTTGTCGATGTTGGCGGTGGT    | 603  |
| 2262 | Qy | ACTGGGCGGTGCTCAGCATGATGTTTGGCAAAATACCCATCAATGAAGGATCAACTTC      | 2321 |
| 604  | Db | ACCGGTGCCACGCTTAGCATGATCGTCTCTAAGTACCCCACTAAAAGCAATTAACCTT      | 663  |
| 2322 | Qy | GA-CCGCCCCAACGGATTGAAGAGGCCCAACCCCTCTCGTGTCAAGCAGCTCGGAGGC      | 2380 |
| 664  | Db | GATTTGCCCTCATGTCAATTGAGSAGTGTCTCTAGCTGTCCCGGTGGAGCATGTTGGTGA    | 723  |
| 2381 | Qy | GACATGTTCTGTCAGCGGTTCCAAAGGGAGATGCCATTTTCAATGAAGTGGATATGCCATGAC | 2440 |
| 724  | Db | GACATGTTTGTAGTGTACCAAAGGAGATGCCATTTTCAATGAAGTGGATATGTCATGAT     | 783  |
| 2441 | Qy | TGGAGTGACGACCATTCGCGCAAGTTCCTCAAGAACCTGCTACGATGCGCTTCCCAACAAT   | 2500 |
| 784  | Db | TGGAGCGAGAACACTGCGCCAAAGTTTTTGAAGAACTGCTATGAAGCTTTTGGCCAGACAAC  | 843  |
| 2501 | Qy | GGAAAGGTGA                                                      | 2510 |
| 844  | Db | GGGAAAGTGA                                                      | 853  |

RESULT 8  
CO082948  
LOCUS

|            |                                                                                                                                                                                                                                                       |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| DEFINITION | GR_Ea47M18.r GR_Ea Gossypium raimondii cDNA clone GR_Ea47M18 3', mRNA sequence.                                                                                                                                                                       |
| ACCESSION  | CO082948                                                                                                                                                                                                                                              |
| VERSION    | CO082948.1                                                                                                                                                                                                                                            |
| KEYWORDS   | GI:48752429                                                                                                                                                                                                                                           |
| SOURCE     | EST.                                                                                                                                                                                                                                                  |
| ORGANISM   | Gossypium raimondii<br>Gossypium raimondii<br>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eucotsids II; Malvales; Malvaceae; Malvoideae; Gossypium. |
| REFERENCE  | 1 (bases 1 to 864)                                                                                                                                                                                                                                    |
| AUTHORS    | Kim H., Yu,Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and Wing, R.A.                                                                                                       |
| TITLE      | Global assembly of Cotton ESTs                                                                                                                                                                                                                        |
| JOURNAL    | Unpublished (2004)                                                                                                                                                                                                                                    |
| COMMENT    | Contact: Rod A. Wing<br>Arizona Genomics Institute<br>The University of Arizona<br>Forbes Building Room 303, Tucson, AZ, 85721-0036, USA<br>Tel: 520 626 9595<br>Fax: 520 621 1259<br>Email: rwing@genome.arizona.edu                                 |

|      | FEATURES | SOURCE |
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| 94.  | ...      | ...    |
| 95.  | ...      | ...    |
| 96.  | ...      | ...    |
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## ORIGIN

| Query Match           | 16.2%;          | Score 489.6;                                                       | DB 8;     | Length 864; |
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| Best Local Similarity | 75.9%;          | Pred. No. 9.3e-130;                                                |           |             |
| Matches 617;          | Conservative 0; | Mismatches 195;                                                    | Indels 1; | Gaps 1;     |
| QY                    | 1647            | GAGACCCAGATGACCCCGACCCAAAGTCTCGGACGACGAGCGCAACCTCTTCGCCATATGCAG    | 1706      |             |
| DB                    | 52              | GAACCCCAATGACTCCACCCCAAGTCTCGGATGAGGAAGCCAACTATTTCGCCATGCAA        | 111       |             |
| QY                    | 1707            | CTGGCGAGGCGCTTCCTGTCTCCCATGTGTCCTTAAAGGCGCGCCATCGAGATCGACTTCCTC    | 1766      |             |
| DB                    | 112             | CTCACCAAGTGCCTCAGTCTCTTCCATATGGTCTCTCAAGTCGGGCCATAGAACTTGACCTTGCTG | 171       |             |
| QY                    | 1767            | GAGATCATGCGCAAGACGCGGCGGCGTCTCTCTCCACGGGGGAAATCGCGGCACAG           | 1826      |             |
| DB                    | 172             | GAGATCATGCGCCAAAGCTGGCCAGTGTCTTCTCTCCCAAAAGAAATTTGGCTTCCAG         | 231       |             |
| QY                    | 1827            | CTCCGACCCAGAACCCCGAGGACCCGTCTATGTCGACCGGATCTTCGGCTGTCTGGCC         | 1886      |             |
| DB                    | 232             | CTCCCAACACAGCAACCCCGATGACCTGTCTATGCTAGACCGCATCTTTGGCCCTCTCTGGCT    | 291       |             |
| QY                    | 1887            | AGCTACTCCGTCGTCAAGTGCACCTCTCCGACCTCTCCCGATGGCAAGTTCGAGCGGCTC       | 1946      |             |
| DB                    | 292             | ACCTACTCCATCTCACTTGTCTCTTGGCACTCTTCTTGATGGCAAGTTGGAGAGACTC         | 351       |             |
| QY                    | 1947            | TACGGCTTAGCGCCGCTGTGCAAGTTCTTTGGTCAAGAACGAGGACGGGGTCTCCATCGCC      | 2006      |             |
| DB                    | 352             | TATGGTCTTTGGCCCTCTCTGCAAAATTCGTGACCAAGAAATGAAGATGGCGGTCACTCTTTCC   | 411       |             |
| QY                    | 2007            | GCACCTCAACTTGATGAACAGGACAAATCTCTCATGGAAGCTGTGATTACCTGAAGAAT        | 2066      |             |
| DB                    | 412             | GCCTCTCAGTCTCATGAATCAAGACAAGGTCTCTTATGGAGAGCTGTGTACTACTTTGAAGAT    | 471       |             |
| QY                    | 2067            | GCGGTCTCTTGAAGGGCGAAATCCCATTTCAACAAGGGCGTACGGGATGACCGGGTTTCGAGTAT  | 2126      |             |







||||| 62 GAGCATGTTGGTGAGACATGTTTGAAGTGTAACAAAGGAGATGCCATTTTCATGAAG 821  
||||| 2426 TGGATATGCCATGACT-GGATGAGACCATGTCGGCGAAGTTCCTCAAGAACTGTACGA 2484  
||||| 82 TGGATATGTCATGATTTGGGAGCGACGAACACTGGCCCAAGTTTTTGAAGAACTGCTATGA 881  
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DEFINITION GR\_Ea05J07.f GR\_Ea Gossypium raimondii cDNA clone GR\_Ea05J07 5',  
mRNA sequence.  
ACCESSION CO087218  
VERSION CO087218.1 GI:48777852  
KEYWORDS EST.  
SOURCE Gossypium raimondii  
ORGANISM Gossypium raimondii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 880)  
REFERENCE Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,  
AUTHORS Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and  
Wing,R.A.  
TITLE Global assembly of Cotton ESTs  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
Plate: 05 row: J column: 07.  
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Wendle lab. Directional cloned into NotI-EV. Colonies  
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ORIGIN  
Query Match 16.1%; Score 489; DB 8; Length 880;  
Best Local Similarity 75.5%; Pred. No. 1.4e-129;  
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QY 1684 AGCGAACTCTTCCCATGACGTGGGAGCGCTCCGTGCTCCCATGTCCTTAAGG 1743  
||||| 103 AAGCAACTTATTCGCAATGCAACTCACAGTGCTCAGTCTTCCCATGCTCTCAAGT 162  
|||||  
QY 1744 CGGCATCGATCGACTCTCTCGAGATCATGGCCAGGACGGCGCGCGCTTCCTCT 1803  
||||| 163 CGGCATGAAGACTTGACTCTGTGGAGATCATGGCCAAAGCTGGCCAGGTGCTTCTCT 222  
||||| 1804 CCACGGGGGAATCGCGCACAGTCTCCGACCCAGACCCGAGGACCCCGTCATGCTCG 1863  
|||||

Db 223 CCCCCAAGAATTTGGCTTCCAGCTCCCCACCAGCAACCCCGATGCACCTGTCTATGCTAG 282  
QY 1864 ACCGATCTCCGGCTGCTGSCCAGCTACTCCGTGCTCAAGTGCACCTCCGCGACCTCC 1923  
||||| 283 ACCGATCTTGGGCTCTCTGGCTACCTACTCCATCTCACTTGTCTCTTGGCACTCTTC 342  
||||| 1924 CCGATGGCAAGGTTCGAGCGGCTTACCGCTTAGCGCGGTGTGCAAGTCTTGTGTCAGA 1983  
||||| 343 CTGATGGCAAGTTCGAGAGACTCTTATGCTTGGCCCTGTCTGCAAAATTCGTGACCAAGA 402  
QY 1984 ACAGAGACGGGTCTCCATCGCCGACCTCAACTGTATGTAACACAGGACAAATTCCTCATGG 2043  
||||| 403 ATGAAGATGGCGTCACTCTTTCCGCGCTCAGTCTCATGAATCAAGACAAAGGTCCTTATGG 462  
QY 2044 AAAGCTGTATTTACCTGAAGATCGGTCTTGAAGCGGAATCCCATTTCAACAAGGGCT 2103  
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||||| 523 ATGATGACCGCATTCGAGTACCATGCGCGGATCTAGATTCAACAAGGTTTCAACA 582  
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Db 583 GGGAAATGTCGATCACTTACCAATTAAGTAAAGAGATTAAGTAAACATACAGGCT 642  
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QY 2403 AGGAGATGCGATTTTCATGAAGTGGATATGCCATGCTGAGTGAGCAGCATTCGCGC 2460  
Db 823 AAGGAGCGCCATCTTCATGAAGTGGATATTCACGATTGGAGTGATGAGCAGCTGCTC 880  
  
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LOCUS CX664219  
DEFINITION UCRCP01\_008\_G04\_T7 Swingle citrumele nematode-challenged root cDNA  
library - UCRCP01 Citrus x paradisi x Poncirus trifoliata cDNA  
clone UCRCP01\_008\_T7\_G04, mRNA sequence.  
ACCESSION CX664219  
VERSION CX664219.1 GI:57922195  
KEYWORDS EST.  
SOURCE Citrus x paradisi x Poncirus trifoliata  
ORGANISM Citrus x paradisi x Poncirus trifoliata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Sapindales; Rutaceae; Citrus x Poncirus.  
1 (bases 1 to 961)  
REFERENCE Close,T.J., Roese,M.L., Becker,O., Darso,J., Federici,C.F.,  
AUTHORS Fenton,R.D., Wanmaker,S., Choi,Y.G and Kingan,T.  
TITLE Development of EST Resources and New Genetic Markers for California  
JOURNAL Citrus - Swingle citrumele nematode-challenged roots - UCRCP01  
COMMENT Unpublished (2005)  
Contact: Timothy J. Close  
Department of Botany & Plant Sciences  
University of California  
Riverside, CA 92521-0124, USA  
Tel: 909-787-3318  
Fax: 909-787-4437  
Email: timothy.close@ucr.edu  
Seq primer: T7.  
Location/Qualifiers  
1..961  
source



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/clone="UCRCP01_037_T7_E09"
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/dev_stage="seedling"
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cDNA library - UCRCP01"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Twelve seedlings were
transplanted from cones to 4 inch pots of sand mix, then
grown in greenhouses (Darsow, Becker lab). Citrus
nematodes (Tylenchulus semipenetrans) were extracted from
contaminated soil from the UC Riverside Citrus Research
Center then suspended in water and added to pots (Darsow).
Growing roots were collected by clipping them away from
the old root ball 24 hr and 4 days after inoculation
(Federici). Total RNA was extracted using Concert Plant
RNA Reagent (Invitrogen) followed by RNeasy (Qiagen), an
equal amount of RNA was pooled from each of the two
collection times, poly(A) RNA was purified using Oligotex
(Qiagen), a cDNA library was made using a cDNA synthesis
kit (Stratagene), then 0.45 million primary lambda cDNA
clones were in vivo excised to give a population of
pBluescript SK(-) phagemids (Fenton, Close lab). Phagemids
were plated, plasmid DNA purified, cDNA clones archived,
and DNA sequences determined bi-directionally using an
ABI3730 at the University of California Riverside
Institute of Integrative Genome Biology Genomics Core
Instrumentation Facility, (Choi, Kingan). Chromatogram
files were downloaded by FTP by Close, then processed by
Wanamaker (Close lab) using the Harvest pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a phred 17
region of at least 100 bases were assembled, then chimeras
were removed following manual inspection of assemblies
(Close, Roose, Wanamaker). Sequences that survived all
removal steps were submitted to GenBank."
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Db 444 AAGGTTCTCATGAGAGCTGGTACTACTTAAAGATGCAGTGTGAAGGTGGCATTCGA 503

Qy 2091 TTCAACAGGCGGTACGGGATGACCGGTTTCAGATATCATGCGACCGACCCGCGATTCAAC 2150

Db 504 TTTAACAAGGCGGTATGGGATGAATGCATTCCATTACCAATGGCAAGATCTAAGATTCAAC 563

Qy 2151 AAGATCTTTTAAACCGGGGAATCTGTGATCATCTCCACCAATTACTATGAAGAAGATCTGAA 2210

Db 564 AAGATTTTCAACAATGGAATGCTCTCTCATTTCTACCATTTACCATGAAGAAAATTTCTTGA 623

Qy 2211 ACATACAAGGCGTTCGAGGCGCTCGAGACCGTGTGATGTCGAGGCGGCGCACTGGGGCC 2270

Db 624 AATTACAAGGCGTTGAAGGCGCTCAATCAGTGTGCGACGTTGGTGGTGGAAATTTGAGGCC 683

Qy 2271 GTGCTCAGCATGATGCTGTGGCCAAATACCCATCAATGAAAGGATCAACTTCGA -CCGCCC 2329

Db 684 ACATTAAATGATTAATCTCCAGTATCCATGATTAAGGCAATCACTTTGATTGGCA 743

Qy 2330 CAACGGATTGAAGACGCCGCCCTTCTCGTGTCAAGCACGTCGGAGGCGACATGTTTC 2389

Db 744 CATGTTATTAGGATGCTCCAGCTTTTCTCGTGTGCGAGCATGTTGGGGGAGACATGTTT 803

Qy 2390 GTCAGGCTTCAAAAGGAGATGCCATTTTCATGAAGTGATATGCCATGACTGAGTGAC 2449

Db 804 GTTAGTGTTCAAAAGGAGATGCCATTTTATCAAGTGATATGTCATGATTTGGAGTGAT 863

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Qy 2510 ATCGTTGC 2517

Db 924 ATTGTTGC 931

RESULT 13

LOCUS CX664056/c 964 bp mRNA linear EST 19-JAN-2005

DEFINITION UCRCP01\_007\_F10\_T7 Swingle citrusmelo nematode-challenged root cDNA library - UCRCP01 Citrus x paradisi x Poncirus trifoliata cDNA clone UCRCP01\_007\_T7\_F10, mRNA sequence.

ACCESSION CX664056

VERSION CX664056.1 GI:57922014

KEYWORDS EST.

SOURCE Citrus x paradisi x Poncirus trifoliata

ORGANISM Citrus x paradisi x Poncirus trifoliata

REFERENCE 1 (bases 1 to 964)

AUTHORS Close,T.J., Roose,M.L., Becker,O., Darsow,J., Federici,C.F., Fenton,R.D., Wanamaker,S., Choi,Y.G and Kingan,T.

TITLE Development of EST Resources and New Genetic Markers for California Citrus - Swingle citrusmelo nematode-challenged roots - UCRCP01 Unpublished (2005)

JOURNAL Contact: Timothy J. Close

COMMENT Department of Botany & Plant Sciences University of California Riverside, CA 92521-0124, USA Tel: 909-787-3318 Fax: 909-787-4437 Email: timothy.close@ucr.edu

Seq primer: T7.

Location/Qualifiers

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FEATURES

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Query Match 16.0%; Score 484.8; DB 9; Length 931;

Best Local Similarity 71.6%; Pred. No. 2.4e-128;

Matches 650; Conservative 0; Mismatches 257; Indels 1; Gaps 1;

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Db 84 GGCTCGGATGAAGAGGCAACCTTTCGCGATGCGAATTAACAGTGCCTCAGTCTTGCT 143

Qy 1731 ATGTCCTAAAGCGCCGATCGAGATGCGACCTTCCTCGAGATCATGGCAAGACGGGCG 1790

Db 144 ATGTTCTCAATACGACCATTCAGCTTGATCTTTTAGAGATCATCGCTAAAGCTGGGCC 203

Qy 1791 GCGCGTTCTCTCCACGGGGAATTCGGGACAGCTCCGACCCAGACCCCGAGGCA 1850

Db 204 GATGCTTTTCATGCTCTCCAAAGACATAGCTTCTCAGCTGCCCAAAAGAACCCAGATCC 263

Qy 1851 CCGCTCATGCTCGACCGGATCTTCGGGCTGTGGCGAGCTACTCCGTGTCTACGTGACCC 1910

Db 264 CATATCGTGTGATCGTATATGGCCCTCTGGCGAGCTATTAGTCTTAAATGCTCT 323

Qy 1911 CTCGCGACCTCCCGATGGCAAGGTTCGAGCGGCTTACGGCTTAGCGCGGTGTGCAAG 1970

Db 324 TTGCGCAATCTCCCGACGGCAAGGTTCGAGAGCTTTATGGCTTTGCGCCCGCTTTGTAA 383

Qy 1971 TTCTTGGTCNAGACGAGACGGGCTCTCCATCGCGGCACTCACTTGTAGTGAACGAGAC 2030

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/note="vector: Lambda Uni-ZAP XR, excised phagemid;  
Site 1: EcoRI; Site 2: XhoI; Twelve seedlings were  
transplanted from cones to 4 inch pots of sand mix, then  
grown in greenhouses (Darsow, Becker lab). Citrus  
nematodes (Tylenchulus semipenitrans) were extracted from  
contaminated soil from the UC Riverside Citrus Research  
Center then suspended in water and added to pots (Darsow).  
Growing roots were collected by clipping them away from  
the old root ball 24 hr and 4 days after inoculation  
(Federici). Total RNA was extracted using Concert Plant  
RNA Reagent (Invitrogen) followed by RNeasy (Qiagen), an  
equal amount of RNA was pooled from each of the two  
collection times, poly(A) RNA was purified using Oligotex  
(Qiagen), a cDNA library was made using a cDNA synthesis  
kit (Stratagene), then 0.45 million primary lambda cDNA  
clones were in vivo excised to give a population of  
pBluescript SK(-) phagemids (Fenton, Close lab). Phagemids  
were plated, plasmid DNA purified, cDNA clones archived,  
and DNA sequences determined bi-directionally using an  
ABI3730 at the University of California Riverside  
Institute of Integrative Genome Biology Genomics Core  
Instrumentation Facility, (Choi, Kingan). Chromatogram  
files were downloaded by FTP by Close, then processed by  
Wanmaker (Close lab) using the HarvEST pipeline  
(http://harvest.ucr.edu) to remove vector and cloning  
oligo sequences and various contaminants, and to trim to a  
high quality region. Sequences that retained a phred 17  
region of at least 100 bases were assembled, then chimeras  
were removed following manual inspection of assemblies  
(Close, Roose, Wanmaker). Sequences that survived all  
removal steps were submitted to GenBank."

## ORIGIN

Query Match 15.9%; Score 480.6; DB 9; Length 964;  
Best Local Similarity 72.6%; Pred. No. 3.9e-127;  
Matches 635; Conservative 0; Mismatches 239; Indels 1; Gaps 1;  
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DB 903 GCAATCTCCCGACGGCAAGTTGAGAGGCTTTATGGCTTTGCCCGCTTTGTAATTC 844  
QY 1975 TGGTCAAGAACGAGGACGGGTCTCCATCGCGCACTCACTTGATGAACAGACAAAA 2034  
DB 843 TCACATAAATGAAGATGGTGTACACTTTCGATCTTTGTCTCATGAACCAAGCAAGG 784  
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## RESULT 14

CX663706

LOCUS

DEFINITION

CX663706

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CX663706 917 bp mRNA linear EST 19-JAN-2005  
UCRCP01\_005\_E01\_T3 Swingle citrumelo nematode-challenged root cDNA  
library - UCRCP01 Citrus x paradisi x Poncirus trifoliata cDNA  
clone UCRCP01\_005\_T3\_E01, mRNA sequence.  
CX663706 GI:57921620  
EST.  
Citrus x paradisi x Poncirus trifoliata  
Citrus x paradisi x Poncirus trifoliata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Sapindales; Rutaceae; Citrus x Poncirus.  
1 (bases 1 to 917)  
Close, T.J., Roose, M.L., Becker, O., Darsow, J., Federici, C.F.,  
Fenton, R.D., Wanmaker, S., Choi, Y.G and Kingan, T.  
Development of EST Resources and New Genetic Markers for California  
Citrus - Swingle citrumelo nematode-challenged roots - UCRCP01  
Unpublished (2005)  
Contact: Timothy J. Close  
Department of Botany & Plant Sciences  
University of California  
Riverside, CA 92521-0124, USA  
Tel: 909-787-3318  
Fax: 909-787-4437  
Email: timothy.close@ucr.edu  
Seq primer: T3.  
Location/Qualifiers  
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cDNA library - UCRCP01"  
/note="vector: Lambda Uni-ZAP XR, excised phagemid;  
Site 1: EcoRI; Site 2: XhoI; Twelve seedlings were  
transplanted from cones to 4 inch pots of sand mix, then  
grown in greenhouses (Darsow, Becker lab). Citrus  
nematodes (Tylenchulus semipenitrans) were extracted from  
contaminated soil from the UC Riverside Citrus Research

| Query Match           | 15.8%          | Score 479.8                                                      | DB 9     | Length 917 |
|-----------------------|----------------|------------------------------------------------------------------|----------|------------|
| Best Local Similarity | 71.7%          | Pred. No. 6.6e-127                                               |          |            |
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| QY                    | 1720           | CGGTGTCCTCCGATGGTCTTAAAGCCGCCATCGAGATCGACCTCTCGAGATCATGGCCA      | 1779     |            |
| Db                    | 139            | CAGTCTTGGCTATGGTTCTCAAAATCAGCCATTCAGCTTGTATCTTTTAGAGATCATAGCTA   | 198      |            |
| QY                    | 1780           | AGGACGGGCGGGCGGTCTCTCTCCACGGGGGAAATCGCGGCACACCTCCCGACCCAGA       | 1839     |            |
| Db                    | 199            | AGCTGGGCCGATGCTTTTATGTCTCAAAAGACATAGTCTTCTCAGTGCCTCCACAAGA       | 258      |            |
| QY                    | 1840           | ACCCGAGGCACCCGTCATGCTCGACCGGATCTTCGGGCTGCTGGCCAGCTACTCCGTGC      | 1899     |            |
| Db                    | 259            | ACCAGATGCCATATCGTGTGGATCGTATATTTGGCCCTCTGGCGAGCTATTCAGTCC        | 318      |            |
| QY                    | 1900           | TCAGGTGACCCCTCCGGACCTCCCCCATGGCAAGTTCGAGCGGCTCTACGGCTTAGCGC      | 1959     |            |
| Db                    | 319            | TTAATGTCTCTTTGCGCAATCTCCCCACGGCAAGTTGAGAGGCTTTATGGGCTTGCCC       | 378      |            |
| QY                    | 1960           | CGGTGTCAAGTCTTGGTCAAGAAACGAGACGGGGTCTCCATCGCGCACTCAACTTGA        | 2019     |            |
| Db                    | 379            | CCGTTTGTAATTCCTCACTTAAATCGAAGTGTGTTCACATTCGATCTTTGTCTCA          | 438      |            |
| QY                    | 2020           | TGAACCAAGCAAAATCCTCATGAAAGCTGGTATTACCTGAAAGATGCGGTCTTGAAG        | 2079     |            |
| Db                    | 439            | TGAACCAAGCAAGGTTCTCATGGAGAGCTGGTACTACTTTAAAAGATGCAAGTGTGAAG      | 498      |            |
| QY                    | 2080           | GCGGAATCCATTCACAAAGCGCTACGGGATGACCGGGTTCGAGTATCATGGCACCGGACC     | 2139     |            |
| Db                    | 499            | GTGGCATTCATTTAAACAAGGCCCTATGGGATGAAATGCAATTCGATTCACACGGCAAGATC   | 558      |            |
| QY                    | 2140           | CGCGATTCAACAAGATCTTTAAACGGGGAAATGCTGATCACTCCACCACTTACTATGAAGA    | 2199     |            |
| Db                    | 559            | TAAGATTCAACAGAGATTTTCAACATGGAAATGCTTCTCATTTCTACCATTCACATGAAGA    | 618      |            |
| QY                    | 2200           | AGATPACTGGAAACATAACAAGGGCTTCGAGGGCCTTCGAGACCGGTGGTGCATGTGCGAGCGC | 2259     |            |

| ORIGIN                    |      | propagation."                                                    |      |  |  |
|---------------------------|------|------------------------------------------------------------------|------|--|--|
| Query Match               |      | 15.6%; Score 473; DB 10; Length 911;                             |      |  |  |
| Best Local Similarity     |      | 74.7%; Pred. No. 6.2e-125;                                       |      |  |  |
| Matches 607; Conservative |      | 0; Mismatches 205; Indels 1; Gaps 1;                             |      |  |  |
| Qy                        | 1647 | GAGACCCAGATGACCCCGACCCAAAGTCTCGGACGACGAGGGGAACCTCTTCGCCCATGCGAG  | 1706 |  |  |
| Db                        | 99   | GAAACTCAGATGACTCCAACTCAGGTATCAGATGAGAGGACACACCTCTTTGGCCATGCAA    | 158  |  |  |
| Qy                        | 1707 | CTGGGAGCGCTCCGTCCTCCCATGGTCTAAAGGCCGCCATCGAGATCGACCTCCTC         | 1766 |  |  |
| Db                        | 159  | CTAGCCAGTGTCTCAGTTCTACCAATGATCTCAAAACAGCCATTGAACCTCGACCTTCTT     | 218  |  |  |
| Qy                        | 1767 | GAGATCATGGCCAAAGGACGGGCCGGCGCTTCCTCTCCACGGGGGAAATCGCGGCACAG      | 1826 |  |  |
| Db                        | 219  | GAATCATGGCTAAGCTGGCCCTGGTGTCTTCTGTCCACATCTGAGATAGCTTCTCAC        | 278  |  |  |
| Qy                        | 1827 | CTCCCGACCCAGAACCCCGAGGACCCCGTCATGCTCGACCGGATCTTCGGGCTGCTGGCC     | 1886 |  |  |
| Db                        | 279  | CTCCCTACCAAAAACCCCTGATGCGCTGTCTATGTTAGACCGTATCTTGGCGCTCCTGGCT    | 338  |  |  |
| Qy                        | 1887 | AGCTACTCCGTCCTCAGCTGACCCCTCGCGACCTCCCGCATGCCGATGCAAGCTCGAGCGGCTC | 1946 |  |  |
| Db                        | 339  | AGTACTCCATCTTACTTCTCTCTGAAAGATCTTCTGTGGGAAAGTTGAGAGACTG          | 398  |  |  |
| Qy                        | 1947 | TACGGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGGACGGGGTCTCCATCGCC      | 2006 |  |  |
| Db                        | 399  | TATGGCCTTGCTCTGTTTGCATATCTTGACCAAGAACGAGGATGGTGTCTCTGTGAGC       | 458  |  |  |
| Qy                        | 2007 | GCATCAACTTGATGAACACAGGACAAAATCCTCATGTGGAAGCTGGTATTACCTGAAAGAT    | 2066 |  |  |
| Db                        | 459  | CCTCTCTCTCATGAACAGGACAAAGTCTCTCATGGAAGCTGGTATTATTGAAAGAT         | 518  |  |  |
| Qy                        | 2067 | CGGTCTTTGAGGGGGAATCCATTCAACAAAGGCTACGGGATGACCGGCTTCGAGTAT        | 2126 |  |  |
| Db                        | 519  | GCAATCTTGATGGAGGAATTCATTTAACAAAGGCTATGGGATGACTGCAATTTGAATAT      | 578  |  |  |
| Qy                        | 2127 | CATGGCACCGACCCCGGATTCAACAAGATCTTTAACCGGGGAATGTCTGATCACTCCACC     | 2186 |  |  |
| Db                        | 579  | CATGGCACGGATCCAAGATTCAACAAGGTGTTCAATAAGGGAAATGCTGACCACCTCTACC    | 638  |  |  |
| Qy                        | 2187 | ATTACTATGAAGAATGATCTGGAACACATACAGGGCTTCGAGGGCTCGAGACCGTGGTC      | 2246 |  |  |
| Db                        | 639  | ATTAACATGAGAGAGCTTCTTGAGACCTACAAAGGCTTTGAAGGCTTCACATCCTTGGTG     | 698  |  |  |
| Qy                        | 2247 | GATGTGGAGCGGCGCACTGGGCGCTGCTCAGCATGATCGTTGCCAAATACCCATCAATG      | 2306 |  |  |
| Db                        | 699  | GATGTGGTGGGACTGGAGCTGCTCGTTAACACCATCGTCTCTAAATACCCITCAATT        | 758  |  |  |
| Qy                        | 2307 | AAAGGGATCAACTTCGA - CCGCCCCAACGGATTGAAGACGCCGCCACCCCTTCCTGGTCTC  | 2365 |  |  |
| Db                        | 759  | AGGGCATTAATTTTGATCTGCCACCGTCATTGAGGATGCCCATCTTATCCCGGTGTG        | 818  |  |  |
| Qy                        | 2366 | AAGCAGCTCGAGGGGACATGTTGCTCAGCGTTCCAAAGGGAGATGCCATTTTCATGAAG      | 2425 |  |  |
| Db                        | 819  | GAGCATGTTGGTGGGACATGTTTGTAGTGTGCCCAAGCAGATGCCGTTTTCATGAAG        | 878  |  |  |
| Qy                        | 2426 | TGGATATGCCATGACTGGAGTGACACCATTCG                                 | 2458 |  |  |
| Db                        | 879  | TGGATATGCCATGATTGGAGCGACGACACTGC                                 | 911  |  |  |

Search completed: November 1, 2006, 07:01:24  
Job time : 9848.88 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:41:44 ; Search time 563.148 Seconds  
(without alignments)  
10067.438 Million cell updates/sec

Title: US-10-702-319A-113\_COPY\_41\_3070

Perfect score: 3030

Sequence: 1 cacctgttcagttgattcc.....acttcgaacaaaaaaa 3030

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 3030   | 100.0       | 3070   | 3  | US-09-598-401C-113 |
| 2          | 2020.4 | 66.7        | 2096   | 3  | US-09-598-401C-60  |
| 3          | 1429.6 | 47.2        | 1630   | 3  | US-09-615-192A-107 |
| 4          | 1429.6 | 47.2        | 1630   | 3  | US-09-169-789-107  |
| 5          | 638.2  | 21.1        | 661    | 3  | US-09-276-599-12   |
| 6          | 638.2  | 21.1        | 661    | 3  | US-09-598-401C-12  |
| 7          | 631    | 20.8        | 1503   | 3  | US-09-947-027-5    |
| 8          | 629.4  | 20.8        | 1503   | 2  | US-08-715-325-1    |
| 9          | 618.2  | 20.4        | 1368   | 2  | US-08-204-288-1    |
| 10         | 603.8  | 19.9        | 1370   | 3  | US-09-500-569-3    |
| 11         | 603.8  | 19.9        | 1370   | 3  | US-09-971-823B-3   |
| 12         | 589    | 19.4        | 1380   | 3  | US-08-991-677-5    |
| 13         | 556.6  | 18.4        | 1314   | 3  | US-09-500-569-17   |
| 14         | 556.6  | 18.4        | 1314   | 3  | US-09-971-823B-17  |
| 15         | 523    | 17.3        | 1507   | 3  | US-09-453-323-1    |
| 16         | 509.4  | 16.8        | 1430   | 2  | US-08-204-288-4    |
| 17         | 478.8  | 15.8        | 1244   | 2  | US-08-204-288-3    |
| 18         | 467.6  | 15.4        | 1314   | 3  | US-09-500-569-5    |
| 19         | 467.6  | 15.4        | 1314   | 3  | US-09-971-823B-5   |
| 20         | 397.4  | 13.1        | 1308   | 3  | US-09-500-569-13   |
| 21         | 397.4  | 13.1        | 1308   | 3  | US-09-971-823B-13  |
| 22         | 391.4  | 12.9        | 421    | 2  | US-08-975-316-24   |
| 23         | 391.4  | 12.9        | 421    | 3  | US-09-615-192A-24  |

24 391.4 12.9 421 3 US-09-169-789-24 Sequence 24, Appl  
25 391 12.9 407 3 US-09-615-192A-106 Sequence 106, App  
26 391 12.9 407 3 US-09-169-789-106 Sequence 106, App  
27 353.8 11.7 1494 3 US-09-235-153-5 Sequence 5, Appli  
28 353.8 11.7 1525 2 US-08-186-833-3 Sequence 3, Appli  
29 343.4 11.3 1195 3 US-09-500-569-11 Sequence 11, Appl  
30 343.4 11.3 1195 3 US-09-971-823B-11 Sequence 11, Appl  
31 319.2 10.5 1008 3 US-09-500-569-1 Sequence 1, Appli  
32 319.2 10.5 1008 3 US-09-971-823B-1 Sequence 1, Appli  
33 300.8 9.9 1471 2 US-08-204-288-6 Sequence 6, Appli  
34 300.2 9.9 926 3 US-09-500-569-19 Sequence 19, Appl  
35 300.2 9.9 926 3 US-09-971-823B-19 Sequence 19, Appl  
36 259.4 8.6 744 2 US-08-975-316-51 Sequence 51, Appl  
37 259.4 8.6 744 3 US-09-615-192A-51 Sequence 51, Appl  
38 259.4 8.6 744 3 US-09-169-789-51 Sequence 51, Appl  
39 254 8.4 661 3 US-09-615-192A-127 Sequence 127, App  
40 254 8.4 661 3 US-09-169-789-127 Sequence 127, App  
41 250 8.3 1458 3 US-09-500-569-15 Sequence 15, Appl  
42 250 8.3 1458 3 US-09-971-823B-15 Sequence 15, Appl  
43 230.2 7.6 1036 3 US-09-615-192A-191 Sequence 191, App  
44 229.2 7.6 1342 3 US-09-500-569-9 Sequence 9, Appli  
45 229.2 7.6 1342 3 US-09-971-823B-9 Sequence 9, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-598-401C-113  
; Sequence 113, Application US/09598401C  
; Patent No. 6596925  
; GENERAL INFORMATION:  
; APPLICANT: Petera, J. Ranjan  
; APPLICANT: Eggleston, Clare  
; APPLICANT: Rice, Stephen J.  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1036C2  
; CURRENT APPLICATION NUMBER: US/09/598.401C  
; CURRENT FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 113  
; LENGTH: 3070  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis

Query Match 100.0%; Score 3030; DB 3; Length 3070;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CACCTGTTTCAGTTTGGATTCCTTGGAGATGACCTACAGTATAGCTTGTGATGAATAGATGG 60  
Db 41 CACCTGTTTCAGTTTGGATTCCTTGGAGATGACCTACAGTATAGCTTGTGATGAATAGATGG 100  
Qy 61 GATTAATGATTCACACGAGGATAAAGGTAGGAGATAGGGATCTCCCGCTCTGATG 120  
Db 101 GATTAATGATTCACACGAGGATAAAGGTAGGAGATAGGGATCTCCCGCTCTGATG 160  
Qy 121 CCTCGGTAGTTGAAAATAAGCAAAAGTTTCGCCGTTGAAATTTGACAGCAAAAGACACC 180  
Db 161 CCTCGGTAGTTGAAAATAAGCAAAAGTTTCGCCGTTGAAATTTGACAGCAAAAGACACC 220  
Qy 181 GTCGTTATGATTCATGATGATCCATGTGACCATGATGAGGTGAATCTCTAGAGTGAGAGA 240  
Db 221 GTCGTTATGATTCATGATGATCCATGTGACCATGATGAGGTGAATCTCTAGAGTGAGAGA 280



[illegible]







|    |      |                                                                  |      |
|----|------|------------------------------------------------------------------|------|
| Db | 661  | CGTTTCGAGGGCCTCGAGACCGTGTGTCATGTTCGAGAGGGGCACTGGGGCGGTGCTCAGCA   | 720  |
| Qy | 2281 | TGATCGTTGGCAAAATACCCATCAATGAAGGGATCAACTTCGACC-GCCCCAACGGAATTG    | 2339 |
| Db | 721  | TGATCGTTGGCAAAATACCCATCGATGAAGGGATCACTTCGACCTGCCCTCACGTGATTG     | 780  |
| Qy | 2340 | AAGACGCCCAACCCCTTCCTGGTGTCAAGCACGTCGGAGGCGACATGTTTGGTCAGCGTTC    | 2399 |
| Db | 781  | AAGACGCTCCACCCCTTCCTGGTGTCAAGCACGTCGGAGGCGACATGTTTGGTCAGCGTTC    | 840  |
| Qy | 2400 | CAAAAGGGAGATGCCATTTTTCATGAAGTGGATATGCCATGACTGAGAGTGAAGCAATTCGCG  | 2459 |
| Db | 841  | CAAAAGGGAGATGCCATTTTTCATGAAGTGGATATGCCATGACTGAGAGTGAAGCAATTCGCG  | 900  |
| Qy | 2460 | CGAAGTTTCCTCAAGAACTGCTACGATCGCTTCCCAACAAATGGAAGAGGTGATCGTTCGAG   | 2519 |
| Db | 901  | CGAAGTTTCCTCAAGAACTGCTACGATCGCTTCCCAACAAATGGAAGAGGTGATCGTTCGAG   | 960  |
| Qy | 2520 | AGTGCCTACTCCCTGTGTACCCAGACACGAGCCTTAGCGACCAAGAAATGTGATCCACATCG   | 2579 |
| Db | 961  | AGTGCCTACTCCCTGTGTGTACCCAGACACGAGCCTTAGCGACCAAGAAATGTGATCCACATCG | 1020 |
| Qy | 2580 | ACTGCATCATGTTTGGCCCCACAACCCAGCGCGGAAAGAGAGGACACAGAAAGGAGTTCGAGG  | 2639 |
| Db | 1021 | ACTGCATCATGTTTGGCCCCACAACCCAGCGCGGAAAGAGAGGACACAGAAAGGAGTTCGAGG  | 1080 |
| Qy | 2640 | CATTGGCCAAAGGGGCGGATTTTCAGGGCTTCCAAGTTCATGTGCTGCGCTTTCGGCACTC    | 2699 |
| Db | 1081 | CATTGGCCAAAGGGGCGGATTTTCAGGGCTTCCAAGTTCATGTGCTGCGCTTTCGGCACTC    | 1140 |
| Qy | 2700 | ACGTATGGAGTTCCTGAAGACCGCTTGATCTGCTCCTCTGTGGTGAATGTTCATGTTCT      | 2759 |
| Db | 1141 | ACGTATGGAGTTCCTGAAGACCGCTTGATCTGCTCCTCTGTGGTGAATGTTCATGTTCT      | 1200 |
| Qy | 2760 | TGGATTTGAAGGTCGTGAAGGAGCCCTTTCTCACAGTTGGCTTCGGCATACCAAGTTC       | 2819 |
| Db | 1201 | TGGATTTGAAGGTCGTGAAGGAGCCCTTTCTCACAGTTGGCTTCGGCATACCAAGTTC       | 1260 |
| Qy | 2820 | TTCTCATAAAGGAAACAAATAAGAAAGCGACTGTATGATGGCGCAAGTGGAAAGTTACAAGA   | 2879 |
| Db | 1261 | TTCTCATAAAGGAAACAAATAAGAAAGCGACTGTATGATGGCGCAAGTGGAAAGTTACAAGA   | 1320 |
| Qy | 2880 | TTTGTGTTTTTATGCTATAAAGTTTTGAGTCTTTCGCATACACTGATTTACAGAAATGTT     | 2939 |
| Db | 1321 | TTTGTGTTTTTATGCTATAAAGTTTTTGAAGTCTTTCGCATACACTGATTTACAGAAATGTT   | 1380 |
| Qy | 2940 | AACGAAACGGCGTATATGGATGTGCTGAAATGATGGAAATTTGTGATATTTCTGTCTCTTT    | 2999 |
| Db | 1381 | AACGAAACGGCGTATATGGATGTGCTGAAATGATGGAAATTTGTGATATTTCTGTCTCTTT    | 1440 |
| Qy | 3000 | TTCTAGTAAATCATCTCGAACAAAA 3023                                   |      |
| Db | 1441 | TTCTAGTAAATCATCTCGAACAAAA 1464                                   |      |

## RESULT 4

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US-09-169-789-107
; Sequence 107, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: US 08/713,000
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSEQ for Windows Version 3.0

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QY 2520 AGTCGGTACTCCCTGTGTATCCACAGACAGAGCCCTAGCGACCAAGAAATGTGATCCACATCG 2579  
DB 961 AGTCGGTACTCCCTGTGTATCCACAGACAGAGCCCTAGCGACCAAGAAATGTGATCCACATCG 1020  
QY 2580 ACTGCATCATGTTGGCCCAACACCCAGCGGGAAGAGAGACACAGAAGAGTTTCAGAG 2639  
DB 1021 ACTGCATCATGTTGGCCCAACACCCAGCGGGAAGAGAGACACAGAAGAGTTTCAGAG 1080  
QY 2640 CATTGGCCAAAGGGGCGCGAATTTTCAGGGCTTCCAAAGTCATGTGCTGCGCTTTGGCACTC 2699  
DB 1081 CATTGGCCAAAGGGGCGCGAATTTTCAGGGCTTCCAAAGTCATGTGCTGCGCTTTGGCACTC 1140  
QY 2700 ACCTCATGGAGTTCTCTGAAGACCCCTTGATCTGCTCTCTCTGCTGATGTTTCATGGTTCT 2759  
DB 1141 ACCTCATGGAGTTCTCTGAAGACCCCTTTGATCTGCTCTCTCTGCTGATGTTTCATGGTTCT 1200  
QY 2760 TGGATTTGAAAGTCTGTGAAGGAGCCCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTC 2819  
DB 1201 TGGATTTGAAAGTCTGTGAAGGAGCCCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTC 1260  
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DB 1261 TTCTCATAAAAGGAAACCAATAAGAGCGACTGTATGATGGCGCAAGTGAAGTTTACAAGA 1320  
QY 2880 TTTGTTGTTTATGTTCTATAAAGTTTGGAGTCTTCTGCTACTGATTTTCACAGNATGTGT 2939  
DB 1321 TTTGTTGTTTATGTTCTATAAAGTTTGGAGTCTTCTGCTACTGATTTTCACAGNATGTGT 1380  
QY 2940 AACGAAACGGCGTATATGATGTCCTGAATGATGGAAATTTGATATTTCTGCTCTCTTT 2999  
DB 1381 AACGAAACGGCGTATATGATGTCCTGAATGATGGAAATTTGATATTTCTGCTCTCTTT 1440  
QY 3000 TTCAGTAATCACTTCGAAACAAA 3023  
DB 1441 TTCAGTAATCACTTCGAAACAAA 1464

RESULT 5

US-09-276-599-12  
; Sequence 12, Application US/09276599  
; Patent No. 6380459  
; GENERAL INFORMATION:  
; APPLICANT: Perera, J. Ranjan  
; APPLICANT: Rice, Stephen J.  
; TITLE OF INVENTION: Composition and methods for the  
; FILE REFERENCE: 11000.1036  
; CURRENT APPLICATION NUMBER: US/09/276,599  
; CURRENT FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 661  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)...(654)  
; NAME/KEY: TATA signal  
; LOCATION: (537)...(543)  
; NAME/KEY: CAAT signal  
; LOCATION: (499)...(502)  
US-09-276-599-12

Query Match 21.1%; Score 638.2; DB 3; Length 661;

Best Local Similarity 98.9%; Pred. No. 6e-162;  
Matches 654; Conservative, 0; Mismatches 3; Indels 4; Gaps 1;

QY 979 CTGAGCCATTTAATTCGAGAGCACATCGCCCAAAATTTCTTCTGCTGCCATACTGT 1038  
DB 1 CTGAGCCATTTAATTCGAGAGCACATCGCCCAAAATTTCTTCTGCTGCCATACTGT 60

QY 1039 CGAATTTTCTCTTTAGGTAAAGTAACCAATGATCGCCATTTGACAAAAGGCTGATTA 1098  
DB 61 CGAATTTTCTCTTTAGGTAAAGTAACCAATGATGATCATGTTGACAAAAGGCTGATTA 120  
QY 1099 GATGATCTTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 1158  
DB 121 GATGATCTTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 180  
QY 1159 AAGGCCCAACCCAGATTTGCAAGAGACACAAAGAGACACCAACCTTTCTTACCAAG 1218  
DB 181 AAGGCCCAACCCAGATTTGCAAGAGACACAAAGAGACACCAACCTTTCTTACCAAG 240  
QY 1219 ATCATCACCAGATCGGCCAGTAAGGTAATATTAATTTAAACAATAGCTCTTGTACCGGG 1278  
DB 241 ATCATCACCAGATCGGCCAGTAAGGTAATATTAATTTAAACAATAGCTCTTGTACCGGG 300  
QY 1279 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGCC 1338  
DB 301 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGCC 360  
QY 1339 AACCCCAAAAGTCAAGTGTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1394  
DB 361 AACCCCAAAAGTCAAGTGTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 1395 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGGCATGCTGACGAATGT 1454  
DB 421 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGGCATGCTGACGAATGT 480  
QY 1455 ACATATTTGGTGTAGGTTCCAATATTTTGGGGAGGTTGGTGAACCGCAAAAGTTCTCTATA 1514  
DB 481 ACATATTTGGTGTAGGTTCCAATATTTTGGGGAGGTTGGTGAACCGCAAAAGTTCTCTATA 540  
QY 1515 TATCGAACCTCCACACCATACCTCACTCAATCCCAACCATTTATCCGTTTATTTTCCT 1574  
DB 541 TATCGAACCTCCACACCATACCTCACTCAATCCCAACCATTTATCCGTTTATTTTCCT 600  
QY 1575 CTGCTTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1634  
DB 601 CTGCTTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
QY 1635 T 1635  
DB 661 T 661

RESULT 6

US-09-598-401C-12  
; Sequence 12, Application US/09598401C  
; Patent No. 6596925  
; GENERAL INFORMATION:  
; APPLICANT: Perera, J. Ranjan  
; APPLICANT: Eagleton, Clare  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1036c2  
; CURRENT APPLICATION NUMBER: US/09/598,401C  
; CURRENT FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 661  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-598-401C-12

Query Match 21.1%; Score 638.2; DB 3; Length 661;

Best Local Similarity 98.9%; Pred. No. 6e-162;  
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;  
QY 979 CTGAGCCATTTAATTCGAGAGACATCGCCCAAAATTTCTTCTGTCGCCATAACTGT 1038  
Db 1 CTGAGCCATTTAATTCGAGAGACATCGCCCAAAATTTCTTCTGTCGCCATAACTGT 60  
QY 1039 CGAATTTTCTCTTTTAGGTAAAGTAAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA 1098  
Db 61 CGAATTTTCTCTTTTAGGTAAAGTAAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA 120  
QY 1099 GTATGATCTTGAGTGTGTGTCAAAATTGCAAGCTGACGATGCCCTCAGGGAATTT 1158  
Db 121 GTATGATCTTGAGTGTGTGTCAAAATTGCAAGCTGACGATGCCCTCAGGGAATTT 180  
QY 1159 AAGCGCCCAACCCAGATTCGAAGAGCAACAAGAGCAGACCCACCTTCTTAAACAAG 1218  
Db 181 AAGCGCCCAACCCAGATTCGAAGAGCAACAAGAGCAGACCCACCTTCTTAAACAAG 240  
QY 1219 ATCATCACAGATCGGCCAGTAAGGTAATATTAATTTAAACAATAGCTTTGTACCGGG 1278  
Db 241 ATCATCACAGATCGGCCAGTAAGGTAATATTAATTTAAACAATAGCTTTGTACCGGG 300  
QY 1279 AACTCCGATTTCTCTCACTTCCATAAACCCTGATTAATTTGGTGGAAAAGCGACGCC 1338  
Db 301 AACTCCGATTTCTCTCACTTCCATAAACCCTGATTAATTTGGTGGAAAAGCGACGCC 360  
QY 1339 AACCACAAAAGGTGAGTGTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1394  
Db 361 AACCACAAAAGGTGAGTGTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 1395 AGAGTTTCTCTATATTTCTGTTTACCGTTGAGTCAATGGCATCGGTGACGAATGT 1454  
Db 421 AGAGTTTCTCTATATTTCTGTTTACCGTTGAGTCAATGGCATCGGTGACGAATGT 480  
QY 1455 ACATATTTGGTGTAGGTTCCAAATATTTTCGGGAGGTTGGTGAACCCGAAAAGTTCTTATA 1514  
Db 481 ACATATTTGGTGTAGGTTCCAAATATTTTCGGGAGGTTGGTGAACCCGAAAAGTTCTTATA 540  
QY 1515 TATCGAACTCGACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTT 1574  
Db 541 TATCGAACTCGACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTT 600  
QY 1575 CTGCTTTCTTTTGTCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1634  
Db 601 CTGCTTTCTTTTGTCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
QY 1635 T 1635  
Db 661 T 661  
RESULT 7  
US-09-947-027-5  
; Sequence 5, Application US/09947027  
; Patent No. 685864  
; GENERAL INFORMATION:  
; APPLICANT: Chiang, Vincent Lee C.  
; APPLICANT: Li, Laigeng  
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIO  
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS  
; FILE REFERENCE: 066040-9718  
; CURRENT APPLICATION NUMBER: US/09/947,027  
; PRIORITY FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: 60/230,086  
; PRIORITY FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 1503  
; TYPE: DNA  
; ORGANISM: aspen populus tremuloides  
; FEATURE:

; NAME/KEY: misc feature  
; OTHER INFORMATION: AldomT; GenBank accession number: X62096  
US-09-947-027-5  
Query Match 20.8%; Score 631; DB 3; Length 1503;  
Best Local Similarity 74.5%; Pred. No. 7.9e-160;  
Matches 807; Conservative 0; Mismatches 275; Indels 1; Gaps 1;  
QY 1647 GAGACCCAGATGACCCCGACCCCAAGTCTCGACGACGAGGGAACCTCTTCGCCCATGCGAG 1706  
Db 80 GAAACTCAGATGATCTCAACTCAGGTATCAGATGAAGAGGACACCTCTTTGGCCATGCAA 139  
QY 1707 CTGCGAGCGCTCCGTCCTCCCATGCTTCTTAAAGCCGCGCATFCGAGATCGACCTCCTC 1766  
Db 140 CTAGCCAGTGTCTCAGTTCTACCAATGATCTCTAAAACAGCAATTGAATCGACCTCTT 199  
QY 1767 GAGATCATGCGCAAGGACGGCGCGGCTCTCTCTCCACGGGGGAATCGCGGCACAG 1826  
Db 200 GAAATCATGCTAAAGCTGGCCCTGTCTTGTCTCCACATCTGAGTAGCTTCTTCAC 259  
QY 1827 CTCCCGACCCAGAACCCCGAGGACCCGTCATGCTCGACCGGATCTTCCGCTCTCTGSCC 1886  
Db 260 CTCCCTACCAAAAACCCCTGATGCGCTGTCAAGTTAGACGATATCTCGGCTCTCTGCT 319  
QY 1887 AGCTACTCCGTCGTCACTGTCACCCCTCCGAGACCTCCCGATGGAAGGTGAGCGGCTC 1946  
Db 320 AGCTACTCCATCTTACTCTCTCTGAAAAGATCTTCTGATGGAAAGTTGAGAGACTG 379  
QY 1947 TAGGCTTTAGCGCGGTGTGCAAGTTCTTGTCTCAAGAACGAGGACGGGTCTTCATCGCC 2006  
Db 380 TATGGCTCGCTCCTGTTTGTAAATTTTGACCAAGAACGAGGACGGTGTCTCTGTGCGC 439  
QY 2007 GCATCTCAATCTGTATGAACACGAGCAAAATCTCTCATGAAAGCTGTATTAACCTCAAGAT 2066  
Db 440 CCTCTCTGTCTCATGAACACGAGCAAGGTCTCATGAAAGCTGTATTAATTTGAAAGAT 499  
QY 2067 GCGTCTCTTGAAGCGGGAATCCCATTTCAACAAGCGGTACGGGATGACCGGTTTCGAGTAT 2126  
Db 500 GCAATCTTGTATGGAGGAATTCATTTTAAACAGGCTATGGGATGACTGCAATTTGAATAT 559  
QY 2127 CATGGACACGACCGCGCATTTCAACAAGATCTTTTAAACCGGGGAATGTCTGATCACTCAAC 2186  
Db 560 CATGGACCGGATCCAAGATTTCAACAAGGTCTTCAACAAGGGAATGTCTGACCACTCTACC 619  
QY 2187 ATTTACTATGAGAGATACCTGGAACATACAAGGCTTCGAGGCTTCGAGACCGTGTGTC 2246  
Db 620 ATTACCATTAAGAGATTTCTTTGAGACCTTCAAAAGGCTTTGAAGGCTTCACGCTCTGTG 679  
QY 2247 GATGTCGAGGCGGCACTGGGCGCGTGTCTCAGCATGATCGTTGCAAAATACCCATCAATG 2306  
Db 680 GATGTTGTTGGTGGACTGGAGCGTGTAAACACCATCGTCTCTAATATCCCTTCAATC 739  
QY 2307 AAAGGATCAACTTTGCA-CCGCCCCAACCGGATTTGAAGACGCGCCCAACCCCTTCTGTGTGTC 2365  
Db 740 AAGGCAATTAATTCGATCTGCGCCACGTCAATGAGGATGCCCATCTTATTCGCGGAGTG 799  
QY 2366 AAGCAGCTCGAGGCGACATGTTGTCAGCGTTTCCAAAGGAGATGCAATTTTTCATGAAG 2425  
Db 800 GAGCATGTTGGTGGCGACATGTTTGTAGTGTGTCGCAAGAGAGATGCCGTTTTTCATGAAG 859  
QY 2426 TGGATATGCTATGACTGAGTGAAGACCATTTGGCGGAAGTTTCTTCAAGAACTGCTACGAT 2485  
Db 860 TGGATATGCTATGTTGAGGCGACGCCCATCTGCTTAAATTTCTTGAAGAAATGCTATGAC 919  
QY 2486 GCGCTTCCCAACAATGGAAGAGGTGATCGTTGCAAGTGTGCGTATCTCTCTGTGTATCCAGAC 2545  
Db 920 GCGTTGCCGGAACCGCAAGGTGATCTTGTGAGTGCAATCTTCCCGTGGCTCTCTGAC 979  
QY 2546 ACAGGCTTAGGACCAAGATGTATCCATCGACTGCAATGTTGGCCCAACCAACCA 2605  
Db 980 ACAAGCTTCCACCAAGGAGTGTGACGCTTGTATGTCATGCTGTGGGCGACCAACCCC 1039  
QY 2606 GCGGGGAAGAGAGGACACAGAGAGTTCGAGGCAATTGGCCAAAGGGGCGGATTTTCAG 2665

Db 1040 GGTGGGAAAGAGAGCCGAGAGGAATTTGAGGGCTTAGCTAAGGAGCTGGCTTCCAA 1099  
Qy 2666 GGCTTCCAAGTCAATGCTGCTGCTTTTCGGCACTCACGTCATGAGATTCTTGAAGACCGCT 2725  
Db 1100 GGTTTGAGTAAATGCTGCTGCAATTCACACATGTCATTGAATTCGCAAGAGGCC 1159  
Qy 2726 TGA 2728  
Db 1160 TAA 1162

RESULT 8  
US-08-715-325-1  
; Sequence 1, Application US/08715325  
; Patent No. 5886243  
; GENERAL INFORMATION:  
; APPLICANT: Chiang, Vincent L  
; APPLICANT: Tsai, Chung-Jui  
; APPLICANT: Podila, Gopi  
; TITLE OF INVENTION: Genetic Engineering of Wood Color  
; TITLE OF INVENTION: in Plants  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Michael, Best & Friedrich  
; STREET: 100 E. Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: United States of America  
; ZIP: 53202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; . COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS DOS 6.22  
; SOFTWARE: WordPerfect for Windows 5.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/715,325  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US60/007727  
; FILING DATE: 30 NOV 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gemignani, Joseph A  
; REGISTRATION NUMBER: 19,482  
; REFERENCE/DOCKET NUMBER: 66040/9627  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 271-6560  
; TELEFAX: (414) 277-0656  
; TELEX: 262057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1503 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; ORIGINAL SOURCE:  
; ORGANISM: Populus Tremuloides  
; DEVELOPMENTAL STAGE: four year old sapling  
; DEVELOPMENTAL STAGE: undergoing lignification in summer  
; TISSUE TYPE: secondary xylem  
; IMMEDIATE SOURCE:  
; LIBRARY: cDNA to total mRNA  
; CLONE: pTOWT1

US-08-715-325-1  
Query Match 20.8%; Score 629.4; DB 2; Length 1503;  
Best Local Similarity 74.4%; Pred. No. 2.1e-159;  
Matches 806; Conservative 0; Mismatches 276; Indels 1; Gaps 1;

Qy 1647 GAGACCCAGATGACCCCGACCCAAAGTCTCGGACGACGAGGCGAACTCTTCGCCATGCG 1706  
Db 80 GAAACTCAGATGACTCCCAACTCAGTATCAGATGAGAGGCACACCTCTCTTTGCCATGCAA 139  
Qy 1707 TTGGGAGCGGCTCCGCTGCTCCCAATGCTCTTAAGGCGGCCATCGAGATCGACCTCTC 1766  
Db 140 CTAGCCAGTGCTTCAGTTCTACCAATGATCTCTCAAAAACAGCCATTGAATCGACCTCTT 199  
Qy 1767 GAGATCATGGCCAAAGGACGGGCGCGGCTCTCTCCACGGGGGAAATCGCGCACAG 1826  
Db 200 GAAATCATGGCTAAAGCTGGGCCCTGGTCTTTCTTGTCCACATCTGAGATAGTCTCTCAC 259  
Qy 1827 CTCCGACCCAGAACCCCGAGGCACCCGTCATGCTCGACCCGATCTTCGGGTGTGGCC 1886  
Db 260 CTCCCTACCAAAAACCTGATGCGCTCTGTCATGTTAGACCGTATCTCGCGCTCTGGCT 319  
Qy 1887 AGCTACTCGTGTCTCAGTGTGACCCCTCCGCGACCTCCCGATGGCAAGGTGAGCGGCTC 1946  
Db 320 AGCTACTCCATTCTTACCTGTCTCTGAAAGATCTCTCTGATGGGAGGTTCGAGAGACTG 379  
Qy 1947 TAGGGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGGACGGGTCTCCATCGCC 2006  
Db 380 TATGGCTCGCTCCCTGTTTGTAAATTTCTTGACCAAGAACGAGACGGTGTCTCTGTGACG 439  
Qy 2007 GCACTCAACTTGATGAACCCAGGACAAAATCTCTATGGAAGCTGGTATTACCTGAAAGAT 2066  
Db 440 CCTCTCTGTCTCATGAACCCAGGACCAAGGTCTCTCATGGAAGCTGGTATTATTGAAAGAT 499  
Qy 2067 GCGGTCTTTGAAGGCGGAATCCANTTCAACAGGGGTACGGGATGACCCGGTTCGAGTAT 2126  
Db 500 GCAATTTCTTGATGGAGGAATTCATTTTAAACAAGGCTTGAAGGCTCTACGCTCTTGGTG 559  
Qy 2127 CATGGCACCGACCCGCGATTCAACAAGATCTTTAACCGGGGAATGCTCTCATCACTCCACC 2186  
Db 560 CATGGCACCGATCCAAAGATTCACAAAGGTCTTCAACAAGGGAATGCTCGACCACTACC 619  
Qy 2187 ATTACTATGAAGAAGATACTTGAACAATACAAGGGCTTCAGGGCTTCGAGACCGGTGGTC 2246  
Db 620 ATTACCATGAAGAAGATTCTTGAGACCTACAAGGCTTGAAGGCTCTACGCTCTTGGTG 679  
Qy 2247 GATGTCGAGGCGGCACTGGGGCGGTGCTCAGCATGATCGTTGCCAAATACCCATCAATG 2306  
Db 680 GATGTTGGTGGGACTGGACCCGCTGTTAAACACCATCGTCTTAAATACCCCTTCAATC 739  
Qy 2307 AAAGGATCAACTTCGA-CCGCCCAACGGAATGAAGACGCCCAACCCCTCTCTGTGTGTC 2365  
Db 740 AAGGCAATTAACTTCGATCTGCCCAAGTCAATTGAGATGCCCAATCTTATCCCGAGTG 799  
Qy 2366 AAGCACGTGCGAGGCGACATGTTGTCAGGTTTCAAAGGAGATGCCATTTTCATGAAG 2425  
Db 800 GAGCATGTTGGTGGGACATGTTGTTAGTGTGCCCCCAAAAGCAGATCCGTTTTTCATGAAG 859  
Qy 2426 TGGATATGCCATGACTGGAGTGACGACCATGCGCGAAGTTCTCAAGAACTGCTACGAT 2485  
Db 860 TGGATATGCCATGATTGGAGCGACGCCCACTGCTTAAATTTCTTGAAGAAATGCTATGAC 919  
Qy 2486 GCGCTTCCCAACAATGGAAGGTGATCGTTGTCAGAGTGGGTACTCCCTGTGTATCCCGAGAC 2545  
Db 920 GCGTTGCCGGAACCGCAAGGTGATCTGTTGAGTGCATCTTCCCGTGGCTCTCTGAC 979  
Qy 2546 ACAGGCTTAGCGACCAAGAAATGATCCACATCGATGTCATGTTGGCCCAACACCCA 2605  
Db 980 ACAAGCTTCCCAACCAAGGAGTCTGTCAGGATTCGAGGCATTCGCAAGGGCGGATTTTCAG 2665  
Qy 2606 GCGGGAAGAGAGGACACAGAAGGAGTTTCGAGGCATTCGCAAGGGCGGATTTTCAG 2665  
Db 1040 GGTGGAAAGAGAGACCCGAGAAAGAAATTTGAGGGCTTAGCTAAGGAGCTGGCTTCCAA 1099  
Qy 2666 GGCTTCCAAGTCAATGCTGCTGCTTTTCGGCACTCAAGTATGAGTTCCTGTAAGACCGCT 2725  
Db 1100 GGTTCGAGTAAATGCTGCTGTCATTCACACACATGTCATTCGAAATTCGCAAGAGGCC 1159  
Qy 2726 TGA 2728

|    |               |      |                                                               |      |
|----|---------------|------|---------------------------------------------------------------|------|
| Db | 1160 TAA 1162 | 1827 | CTCCGACCCAGAACCCGAGGCAACCGTCTCATGCTCGACCGGATCTTCCGGCTGCTGGCC  | 1886 |
|    |               | 244  | CTCCCTACCAAAACCCCTGATGCGCTGTCTGATGAGCCGTAATCTTGGCGCTCTCTGGCT  | 303  |
| Qy |               | 1887 | AGTACTCCGTGCTCAGTGTGACCCCTCCGGGACCTCCCGATGCGAAGGTGAGGGGCTC    | 1946 |
| Db |               | 304  | AGTACTCCATCTGCTGCTCTCTGAAAGATCATCTGATGGGAAAGTTGAGAGACTG       | 363  |
| Qy |               | 1947 | TACGGCTTAGCGCGGTGTCAGGTTCTTGTCTCAAGAACGAGGACGGGTCTCCATCGCC    | 2006 |
| Db |               | 364  | TATGGCTTGTCTCTGTTTGTCAAAATCTTGACCAAGAACGAGGAGGTCTCTGTGACG     | 423  |
| Qy |               | 2007 | GCACTCAACTTGATGAACACGAGCAAAAATCCTCATGGAAGCTGCTATTAATCTGAAAGAT | 2066 |
| Db |               | 424  | CCTCTCTGCTCATGACACGAGCAAGGCTCTCATGGAAGCTGCTATTAATCTGAAAGAT    | 483  |
| Qy |               | 2067 | GGGTCTTGAAGCGGGAATCCCAATCAAGCGGTACGGGATGACCGGTTTGAAGTAT       | 2126 |
| Db |               | 484  | GCAATTTCTGATGGAGGAATTCATTTAAACAGGCTATGGGATGACTGCAATTTGAATAT   | 543  |
| Qy |               | 2127 | CATGGCACCGACCCGCGATTCACCAAGATCTTTAACCGGGGAATGTCTGATCACTCCACC  | 2186 |
| Db |               | 544  | CATGGCACCGATCCAAGATTCACCAAGGCTCTTCAATAAGGGAATGTCTGACCACTCTACC | 603  |
| Qy |               | 2187 | ATTACTATGAAGAAGATACTTGGAAACATACAAAGGCTTCGAGGGCTTCGAGACCGTGGTC | 2246 |
| Db |               | 604  | ATTACTATGAAGAAGATCTTGAAGCTTCGAGACCTCAAAAGGCTTCGAGACCGTGGTC    | 663  |
| Qy |               | 2247 | GATGTCGGAGCGGCACCTGGGGCGTGTCTCAGCATGATGCTTGGCAATACCCATCAATG   | 2306 |
| Db |               | 664  | GATGTCGGTGGGACCTGGAGCTGTCTTAAACACCATGCTCTTAAATACCTTCAAT       | 723  |
| Qy |               | 2307 | AAAGGATCAACTTCGA-CCGCCCCAACGGATTCGAAGCGCCCAACCCCTCTCTGGTGTG   | 2365 |
| Db |               | 724  | AAAGGATCAACTTCGA-CCGCCCCAACGGATTCGAAGCGCCCAACCCCTCTCTGGTGTG   | 783  |
| Qy |               | 2366 | AAGCAGCTCGAGGCGGACATGCTTCGTCAGCGCTTCGAGGGGATGCGATTTTCATGAAG   | 2425 |
| Db |               | 784  | GAGCATGTTGGTGGGACATGTTTGTAGTGTGCGCCAAAGCAGATGCGGTTTTCATGAAG   | 843  |
| Qy |               | 2426 | TGGATATGCCATGATGAGGACGACCATTTGCGCGAAGTTTCTCAAGAACTGCTACGAT    | 2485 |
| Db |               | 844  | TGGATATGCCATGATGAGGACGACCATTTGCGCGAAGTTTCTCAAGAACTGCTACGAT    | 903  |
| Qy |               | 2486 | GGCTTCCCAACAATGGAAGGTGATGTTGTCAGATGCGTACTTCCCTGTGTACCCAGAC    | 2545 |
| Db |               | 904  | GGCTTCCCAACAATGGAAGGTGATGTTGTCAGATGCGTACTTCCCTGTGTACCCAGAC    | 963  |
| Qy |               | 2546 | ACGAGCCTAGCGACCAAGAAATGTCATCCATCGACTGTCATGTTGGGCCCAACAACCA    | 2605 |
| Db |               | 964  | ACGAGCCTAGCGACCAAGAAATGTCATCCATCGACTGTCATGTTGGGCCCAACAACCA    | 1023 |
| Qy |               | 2606 | GGCGGAAAGAGAGGACACAGAGGATTCGAGGATTCGAGGATTCGAGGAGGCGGATTCAG   | 2665 |
| Db |               | 1024 | GGTGGAAAGAGAGGACACAGAGGATTCGAGGATTCGAGGATTCGAGGAGGCGGATTCAG   | 1083 |
| Qy |               | 2666 | GGCTTCCCAAGTCAATGCTGCGCTTTTGGGACTCAAGTCAAGTCAAGTCAAGTCAAG     | 2725 |
| Db |               | 1084 | GGTTCGAGTCAATGCTGCGCTTTTGGGACTCAAGTCAAGTCAAGTCAAGTCAAG        | 1143 |
| Qy |               | 2726 | TGATCTGCTCC 2736                                              |      |
| Db |               | 1144 | GGCTCAAGTCC 1154                                              |      |

RESULT 10  
 US-09-500-569-3  
 ; Sequence 3, Application US/09500569  
 ; Patent No. 6329204  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cahoon, Rebecca E.  
 ; APPLICANT: Rafalski, Antoni

Db 1160 TAA 1162

RESULT 9  
 US-08-204-288-1  
 ; Sequence 1, Application US/08204288  
 ; Patent No. 5959178  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN DOORSELAERE, Jan  
 ; APPLICANT: FRITIG, Bernard J.M.  
 ; APPLICANT: INZE, Dirk G.  
 ; APPLICANT: JOUANIN, Lise  
 ; APPLICANT: KNIGHT, Mary E.  
 ; APPLICANT: VAN MONTAGU, Marc  
 ; APPLICANT: LEGRAND, Michel  
 ; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN  
 ; TITLE OF INVENTION: PLANTS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: D. C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005-3518  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/204,288  
 ; FILING DATE: 10-MAR-1994  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9119279.9  
 ; FILING DATE: 10-SEP-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB92/01460  
 ; FILING DATE: 09-SEP-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KOKULIS, Paul N.  
 ; REGISTRATION NUMBER: 16,773  
 ; REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 861-3000  
 ; TELEFAX: (202) 822-0944  
 ; TELEX: 6714627 CUSH  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1368 base pairs  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-204-288-1

Query Match 20.4%; Score 618.2; DB 2; Length 1368;  
 Best Local Similarity 73.5%; Pred. No. 2.2e-156;  
 Matches 802; Conservative 0; Mismatches 288; Indels 1; Gaps 1;

|    |      |                                                              |      |
|----|------|--------------------------------------------------------------|------|
| Qy | 1647 | GAGACCCAGATGACCCCGACCCAAAGTCTCGGACGACGAGGGAACTCTTCGCCATGACG  | 1706 |
| Db | 64   | GAATCTCAGATGACTCCAACTCAGGTATCAGATGAAGAGGCACACTCTTTGCCATGCAA  | 123  |
| Qy | 1707 | CTGGCGAGCGCTCGCTCCCTCCATGCTCTTAAGGGCGGCATCGAGATCGACCTCTC     | 1766 |
| Db | 124  | CTAGCCAGTGTCTTCAAGTCTTCAACAAATGATCTTCAAAACAGGCAATGAACTGACCTT | 183  |
| Qy | 1767 | GAGATCATGGCCCAAGGACGGCGGGCGGTTCCTCTCCACGGGGAAATCGCGGCACAG    | 1826 |
| Db | 184  | GAATCATGGCTTAAGCTGGCGCTGCTTCTTGTGTCCACATCTGAGATAGCTTCTCAC    | 243  |



APPLICANT: Shen, Jennie  
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs  
; FILE REFERENCE: BB1327 US NA  
; CURRENT APPLICATION NUMBER: US/09/500,569  
; CURRENT FILING DATE: 2000-02-09  
; EARLIER APPLICATION NUMBER: 60/119,587  
; EARLIER FILING DATE: 1999-February-10  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 3  
; LENGTH: 1370  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-500-569-3

Query Match 19.9%; Score 603.8; DB 3; Length 1370;  
Best Local Similarity 71.9%; Pred. No. 1.7e-152;  
Matches 802; Conservative 0; Mismatches 312; Indels 1; Gaps 1;

Qy 1647 GAGACCCAGATGACCCCGACCCCAAGTCTCGACACGAGGCGAACCTCTTCGCCATCGAG 1706  
Db 94 GAGACTCAGATTACCCCAACCCACGATCTGATGAAGAAGCAAAACCTTTTCGCCATCGAA 153

Qy 1707 CTGCGAGCGCTCGTGTCTCCCATGCTCTAAAGCGCGCATCGAGATCGACTCTCTC 1766  
Db 154 CTAGCGAGTGTCTGTCTCTCCATGATCTCAATCAGCACTTGAGCTTGATCTGTG 213

Qy 1767 GAGATCATGCGCAAGGACCGGCGCGTCTCTCCACGCGGGAATAACGCGGCAAG 1826  
Db 214 GAAATCATAGCAAGGCTGCTCTCTCCCACTCTCTCCCACTGACATTTCTTCTCAG 273

Qy 1827 CTCCGACCCAGAACCCCGAGCCCGTCACTCGACCGGATCTTCGGCTCTCGGCC 1886  
Db 274 CTCCCAACACAGAACCCCTGATGACCGCGTATGTTGACCGGTATTTTCGCCCTATTGGCT 333

Qy 1887 AGCTACTCGTGTCTCAGCTGACCTCGCGACCTCTCCGATGGCAAGGTTCGACGGGCTC 1946  
Db 334 TGCTACAATATCTCTCTCTCTCTCGACTCTCTCTGATGCGAAGGTTCGAGGCTC 393

Qy 1947 TACGCTTAGCGCGGTTGCAAGTCTTGTCTCAAGACGAGGACGCGGTTCTCCATCGCC 2006  
Db 394 TATGCTCTCGCCCGCTTTCGCAAGTCTTGTGTTGAAGACGAAGTGTGTCTCCATTGCT 453

Qy 2007 GCATCAACTTATGACACGAGCAAAATCTCTGGAAGCTGTATTAATCTCAAGAT 2066  
Db 454 CGCTCAACCTCATGAAACGAGCAAAAGTCTCTGGAAGCTGTATTAATCTCAAGAT 513

Qy 2067 CGGCTCTTGAAGCGGGAATCCCATTTCAACAGGCTGACGCGGATCGCGCTTCGAGTAT 2126  
Db 514 GCAGTCTTGAAGGAGGCAATTCATTTAAAGGCTTATGGAATGACAGCCTTTGAGTAC 573

Qy 2127 CATGCAACGACCCCGGATTCGAAGATCTTTAAACGCGGGAATGTCTGATCACTCCACC 2186  
Db 574 CATGGAACAGATCCCAAGGTTTAAACAGGTTTTCACAAAGGGAATGGCTGATCACTTACC 633

Qy 2187 ATTACTATGAGAAGTACTGGAACATACAGGCTTCGAGGCTTCGAGACGCTGTCTC 2246  
Db 634 ATCAACAATGAAGAAATCTTGAGACCTACACAGGTTTGAAGTCTTAAATCTCTGGTT 693

Qy 2247 GATGTCGAGGCGGCACTGGGCGCTGTCTGACGATGATCGTTGCGCAAAATACCCATCAATG 2306  
Db 694 GATGTTGGTGGGACTGGAGCTGTAATCAACATGATGTCTCAAGCATCCCACTATT 753

Qy 2307 AAAGGATCAACTTCGA-CCGCCCCAAGGATGGAAGACGCGCCACCCCTCTCTGGTGTCTC 2365  
Db 754 AAGGCAATTAATTTGATTTGCTCATGTCTATTGAAGATGCCCCATCTATTCTCTGGAGTG 813

Qy 2366 AAGCAGCTCGAGGCGACATGTTCTGACGCTTCCAAAGGAGATGCGATTTTCATGAAG 2425  
Db 814 GAGCATGTAGGTGGAGATGATGTTGCGAGTGTTCGAAAGCTGATGCTATTTTATGAAG 873

Qy 2426 TGGATATGCGATGACTGGAGTGACACCATTTGCGCGAAAGTTCTCTCAAGACTGTACGAT 2485

Db 874 TGGATTTGCCACGATTTGGAGTGATGAGCACTGCTTTGAAGTTTTTGAAGAACTGCTACGAG 933

Qy 2486 GCGCTTCCCAACAATCGAAAGGTGATCGTTGAGAGTGTACTCCCTGTGTACCCAGAC 2545

Db 934 GCATACACAGCAATGGGAAGGTGATTGGGAGAAATGATCTTCCAGTGGCTCCAGAC 993

Qy 2546 ACAGAGCTAGCGACCAAGAATGTGATCCACATCGACTGATCATGTGTGCCACAAACCCA 2605

Db 994 TCTAGCTTGCCCAACAAAGGTGTGGTTTCATCGATGTGATCATGTGCAATATCCA 1053

Qy 2606 GCGGGAAAGAGAGACACAGAAAGGTTCGAGGCAATGGCCAAAGGGGCGGATTCAG 2665

Db 1054 CGTGGAAAGAGAGAAACAGAAAGAGTTTGAGGCTCTGCGCCAAAGGGTCTGGATTCCAA 1113

Qy 2666 GCGTTCCAAGTCAATGCTGCGCTTTCGGCACTCACTGATCATGGAGTTCCTGAAGACCGCT 2725

Db 1114 GGTTCGAGTGTGTTGCTGTGCTTCAATCAACATCATGGAATTTCTCAAAAGATT 1173

Qy 2726 TGATCTGCTCTCTGTGTGATGTTTCATGTTCTT 2760

Db 1174 TAAAGTTTGGCATGGATTCAATGTCAGCTGCAT 1208

RESULT 11  
US-09-971-823B-3  
; Sequence 3, Application US/09971823B  
; Patent No. 6610521  
; GENERAL INFORMATION:  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs  
; FILE REFERENCE: BB1327 US NA  
; CURRENT APPLICATION NUMBER: US/09/971,823B  
; CURRENT FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/119,587  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 3  
; LENGTH: 1370  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-971-823B-3

Query Match 19.9%; Score 603.8; DB 3; Length 1370;  
Best Local Similarity 71.9%; Pred. No. 1.7e-152;  
Matches 802; Conservative 0; Mismatches 312; Indels 1; Gaps 1;

Qy 1647 GAGACCCAGATGACCCCGACCCCAAGTCTCGGACGAGGCGAACCTCTTCGCCATCGAG 1706  
Db 94 GAGACTCAGATTACCCCAACCCACGATCTGATGAAGAAGCAAAACCTTTTCGCCATCGAA 153

Qy 1707 CTGCGAGCGCTCGTGTCTCCCATGCTCTAAAGCGCGCATCGAGATCGACTCTCTC 1766  
Db 154 CTAGCGAGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 213

Qy 1767 GAGATCATGCGCAAGGACCGGCGCGTCTCTCCACGCGGGAATAACGCGGCAAG 1826  
Db 214 GAAATCATAGCAAGGCTGCTCTCTCCCACTCTCTCCCACTGACATTTCTTCTCAG 273

Qy 1827 CTCCGACCCAGAACCCCGAGGCAACCGTCACTGACCGGATCTTCGGCTCTCGGCC 1886  
Db 274 CTCCCAACACAGAACCCCTGATGACCGCGTATGTTGACCGGTATTTTCGCCCTATTGGCT 333

Qy 1887 AGCTACTCGTGTCTCAGCTGACCTCGCGACCTCTCCGATGGCAAGGTTCGACGGGCTC 1946  
Db 334 TGCTACAATATCTCTCTCTCTCTCGACTCTCTCTGATGCGAAGGTTCGAGGCTC 393

Qy 1947 TACGCTTAGCGCGGTTGCAAGTCTTGTCTCAAGACGAGGACGCGGTTCTCCATCGCC 2006  
Db 394 TATGCTCTCGCCCGCTTTCGCAAGTCTTGTGTTGAAGACGAAGTGTGTCTCCATTGCT 453

Qy 2007 GCATCAACTTATGACACGAGCAAAATCTCTGGAAGCTGTATTAATCTCAAGAT 2066



Db 454 GCGCTCAACCTCATGAACAGGACAAAGTCTCTCATGGAAGCTGGTACTATTTGAAAGAT 513  
Qy |||||  
Db 2067 GCGGTCTTTGAAGCGGAATCCATTCAACAGGCGTACGGGATGACCGCGTTGAGAT 2126  
Qy |||||  
Db 514 GCAGTCTTTGAAGGAGGCAATTCATTAAACAGGCTTATGAATGACAGCTTTGAGTAC 573  
Qy |||||  
Db 2127 CATGCAACCGACCCCGGATTTCAACAAGATCTTTAAACCGGGAATGTCTGATCACTCCACC 2186  
Qy |||||  
Db 574 CATGNAACAGATCCAAAGGTTTAAACAGGTTTCAACAGGGAATGGCTGATCACTCTACC 633  
Qy |||||  
Db 2187 ATTACTATGAAGAGATACCTGAAACATACAAAGGCTTCGAGGCTCGAGACCGTGTGTC 2246  
Qy |||||  
Db 634 ATCAATATGAAGAAATTTCTTGAGACCTACACAGGTTTGAAGTCTTAAATCTCTGGTT 693  
Qy |||||  
Db 2247 GATGTCGAGCGGCACCTGGGCGGTGTCTGACATGATCGTTGCGCAATATCCCATCATG 2306  
Qy |||||  
Db 694 GATGTTGGTGGGACTGGAGCTGTAAATCAACATGATGTCTMAAGCATCCCACTATT 753  
Qy |||||  
Db 2307 AAAGGATCAACTTCGA - CCGCCCCAACCGGATTTGAAGACGCCCCACCCCTTCTGTGTGTC 2365  
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Db 754 AAGGCATTAAATTTGATTTGCTTCATGTCTATTGAAGATGCCCATCTTATCTCGAGTG 813  
Qy |||||  
Db 2366 AAGCAGCTCGAGGCGACATGTTGTGAGCTGTCCAAAGGAGATGCCATTTTCAATGAAG 2425  
Qy |||||  
Db 814 GAGCATGTAGGTGGAGATATGTTGCGAGTGTTCGAAAGCTGATGCTATTTTATGAAG 873  
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Db 2426 TGGATATCCCATGCTGAGTGACACCATTCGCGGAGTTTCTCAAGAACTGCTACGAT 2485  
Qy |||||  
Db 874 TGGATTTCCACGATTTGGAGTGATGAGCACTGCTTGAAGTTTGAAGCACTGTACGAG 933  
Qy |||||  
Db 2486 GCGCTTCCAAATGGAAGGTGATCTGTCAGAGTGCCTGCTCTCTGTGTACCCAGAC 2545  
Qy |||||  
Db 934 GCATCTACAGACATGGAAGGTGATGTCGACAGATGATCTTCCAGTGGCTCCAGAC 993  
Qy |||||  
Db 2546 ACAGGCTTAGGACCAAGAAATGTGATCCATGCACTGATGCTGCTGCTGCTGCTGCTGCT 2605  
Qy |||||  
Db 994 TCTAGTTGGCCACAAAAGGTGTGTTTCAATCGATGATGATGATGATGATGATGATGAT 1053  
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Db 2606 GCGGGAAGAGGACACAGAGGTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2665  
Qy |||||  
Db 1054 CGTGGGAAGAGAGAACAGAGAGTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1113  
Qy |||||  
Db 2666 GCTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2725  
Qy |||||  
Db 1114 GCTTCCAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173  
Qy |||||  
Db 2726 TGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
Qy |||||  
Db 1174 TAAGTTCTTGGCATGGATTCTGTCAGCTGATGTCAGCTGAT 1208

## RESULT 12

US-08-991-677-5  
; Sequence 5, Application US/08991677A  
; Patent No. 6252135  
; GENERAL INFORMATION:  
; APPLICANT: Chiang, Vincent L  
; APPLICANT: Carraway, Daniel T  
; APPLICANT: Smeltzer, Richard H  
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms  
; FILE REFERENCE: 50617  
; CURRENT APPLICATION NUMBER: US/08/991,677A  
; CURRENT FILING DATE: 1997-12-16  
; EARLIER APPLICATION NUMBER: US 60/033,381  
; EARLIER FILING DATE: 1996-12-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1380  
; TYPE: DNA  
; ORGANISM: Liquidambar styraciflua  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (67)..(1170)  
US-08-991-677-5  
Query Match 19.4%; Score 589; DB 3; Length 1380;  
Best Local Similarity 72.8%; Pred. No. 1.7e-148;  
Matches 787; Conservative 0; Mismatches 290; Indels 4; Gaps 2;  
Qy 1670 AGTCTCGAGACACGAGCGAACTCTTCGCGCATGCGAGCGCGCTCCGCTGCTCCC 1729  
Db |||||  
Qy 1730 CATGGTCTTAAAGCCCGCATCGAGATCGACTCTCTCGAGATCATGCGCAAGGACGGCC 1789  
Db |||||  
Qy 171 CATGGTCTTAAATCAGCCATAGAGCTCGAGCTTTAGAAATCATGGCTAAAGCTGGTCC 230  
Qy 1790 GGGCGGCTTCTCTCCACGCGGGAATCGGGCACAGTCCCGACCCAGAAACCCGAGGC 1849  
Db |||||  
Qy 231 AGGTGGGACATATCCACATCTGACATAGCCTTAAAGCTGCCCAAAAGAAATCAGATGC 290  
Qy 1850 ACCGCTCATGCTGACCGGATCTTCGCGCTGCTGGCAGCTACTCCGCTGCTCAGGTGAC 1909  
Db |||||  
Qy 291 AGCGCTCATGCTTGAACGCTATGCTCCGCTCTTGGCTAGCTACTCTGTTCTAAAGTGTG 350  
Qy 1910 CCTCGGACCTCCCGATGCGAGGCTCGAGCGCTCTACGCTTAGCGCGCTGCTGCAA 1969  
Db |||||  
Qy 351 TCTCGCACCTCTCTGACGGAAGATCGAGAGCTTTACGCGCTTGACCCGCTTGTAA 410  
Qy 1970 GTTCTTGTCTAAGAAACGAGGACGGGTCTCCATCGCGCACTCAACTTTGATGAACCCAGA 2029  
Db |||||  
Qy 411 ATCTTGAACAGAAACATGATGAGGTCTCCATAGCGCTCTGCTCTCATGAATCAAGA 470  
Qy 2030 CAAATCTCTATGAAAGCTGGTATTACCTGAAAGATCGGTCTTGAAGCGGAAATCCC 2089  
Db |||||  
Qy 471 CAAGTCTCATGAGAGCTGTTACCACTTGACCGAGGAGTCTTGAAGGTGGAATTC 530  
Qy 2090 ATTCAAAGCGTACGCGGATGACCGGCTTGAAGTATCATGGAACCGACCCGCGATCAA 2149  
Db |||||  
Qy 531 ATTTAAACAGGCTTATGGAATGACGATTTGAGTACCATGGCACCGCATCCGATTC 590  
Qy 2150 CAAATCTTTAAACCGGGAATGCTGATCACTCCACCATTTACTATGAAGAGATCTGGA 2209  
Db |||||  
Qy 591 CACAGTTTCAACAAATGGAATGTCCAAATTCATTCACCAATTAACCAAGAAATTCCTTGA 650  
Qy 2210 AACATACAGGCTTTCAGGCGCTCGAGACGCTGCTGATGTCGAGGCGGCACTGGGCG 2269  
Db |||||  
Qy 651 GACTTACAGGCTTTCAGGAGCTTGGATCTGCTGCTGATGTTGTTGGTGGCATGGTGC 710  
Qy 2270 CGTCTCAGCATGATCGTTGCCAAATACCCATCAATGAAAGGATCACTTCGAC - CGCC 2328  
Db |||||  
Qy 711 CCACCTTAAACATGATTATCGCTAAATACCCCATGATCAAGGGCATTAACCTTCGACTTCC 770  
Qy 2329 CCAAGGATTTGAACACGCCCAACCCCTTCTGGTGTCAAGCAGCTCGGAGCGCATGTT 2388  
Db |||||  
Qy 771 TCATGTTATTGAGGAGCTCCCTCTATCTCTGCTGGAGCATGTTGGTGGAGATATGTT 830  
Qy 2389 CGTCAGGCTTCCAAAGGAGATGCTATTTTTCATGAAGTGGATATGCCATGCTGAGTGA 2448  
Db |||||  
Qy 831 TGTGATGTTCCAAAGAGAGATGCTATTTTCATGAAGTGGATATGTCATGATTGGAGCGA 890  
Qy 2449 CGACCATTTGCGGAAGTTCCTCAAGAACTGCTACGATGCGCTTCCCAACAATGGAAGGT 2508  
Db |||||  
Qy 891 TGAACACTGCTTGAAGTTTGAAGAAATGTTATGAAGCACTTCCAAACCAATGGAAGGT 950  
Qy 2509 GATGTTGAGAGTGGTACTCTCTCTGTTGTTCCACAGACAGGCTTAGGACCAAGATGT 2568  
Db |||||  
Qy 951 GATCCTTGTGAAATGCTATCTCTCCCGTGGCGCCAGACGCAAGCTTCCCACTAAGGCGAGT 1010  
Qy 2569 GATCCAGATGACTGCTCATGTTGGCCCAACCCAGGCGGGAAGAGAGACACAGAA 2628  
Db |||||  
Qy 1011 GGTCCATATTGATGCTCATGTTGGCTCATAAACCCAGGTGGGAAGAGAACTGAGAA 1070  
Qy 2629 GGAGTTCCAGGCAATTGGCCAAAGGGCGGATTTTCAGGGCTTCCAAAGTCAT ---GTGCTG 2685  
Db |||||

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Db 1071 GGAGTTTGGCCCTTGGCCAAAGGGGCTGGATTGGAAGTTTCCGAGTAGTAGCCCTCGTG 1130
Qy 2686 CGCTTTCCGCACTCACCTCATGAGATTCCTGGAAGACCGCTTGATCTGCTCTCTGTTGGTG 2745
Db 1131 CGCTTACAATACATGATCATCGAATTTTGAAGAGATTTGAGTCCCTACTCGGCTTTG 1190
Qy 2746 A 2746
Db 1191 A 1191

RESULT 13
US-09-500-569-17
; Sequence 17, Application US/09500569
; Patent No. 6329204
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BB1327 US NA
; CURRENT APPLICATION NUMBER: US/09/500,569
; EARLIER FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,587
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (472)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1156)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1180)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1262)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1302)
; US-09-500-569-17

Query Match 18.4%; Score 556.6; DB 3; Length 1314;
Best Local Similarity 72.2%; Pred. No. 9.2e-140;
Matches 765; Conservative 0; Mismatches 290; Indels 5; Gaps 3;

Qy 1647 GAGACCCAGATGACCCGACCCAAAGTCTCGACGACGAGGCGAACTCTTCGCCATGCGAG 1706
Db 87 GAGACTCAGATTACTCCAAACCATGTATCTGATGAAGAGGCAAACTTTTCGCCATGCAA 146
Qy 1707 CTGGGAGCGCTCGTCTGCTCCCATGCTCTTAAGGCGCCATCGAGATCGACTCTC 1766
Db 147 CTAGCCAGTGGCTCAGTACTCCCTATGTTCTCAAAATCAGCTCTGTGACCTGTGTTG 206
Qy 1767 GAGATCATGGCAAGGACGGGCGGGCGGCTTCTCTCCAGGGGGAATCGCGGCACAG 1826
Db 207 GAAATCATGACCAAGGCTGGCCCTGTTGTTTCACTTTTCCCTCCGACATTTCTCGG 266
Qy 1827 CTCGCCACCCAGAACCCCGAGGACCCGTCATGCTCGACCGGATCTTCGGCTGCTGCC 1886
Db 267 CTCGCCAACACACAAACCTCGATGACCCCGTTATGTTGGACCGTATATTGCGCTCTTG 326
Qy 1887 AGCTACTCGGTCTCAGCTGACCCCTCGCGACCTTCCCGATGGCAAGGTCGAGGGCTC 1946
Db 327 TGCTACAATATCCTCTCTTTTCTCTCGACTCTTCTCTATGGCAAGGTTGAGGGCTC 386
Qy 1947 TACGCGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGGACGGGGTCTCCATGCC 2006
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Db 387 TATGGTCTCGCCCTTGGTAACTTGGTTCAGGAACGAAGATGGTCTCTCCATTTGCT 446
Qy 2007 GCACCTCAACTTATGAACACGAGCAAAATCCTCATGGAAGCTGTTATACCTGAAAGAT 2066
Db 447 GCTCTCAACTCATGAACACGAGCANAATCCTCATGGAAGCTGTTATTTGAAAGAT 506
Qy 2067 GCGGTCTCTTGAAGCGGAATCCATTCAACAGGCGTACGGGATGACCCGCTTCGAGTAT 2126
Db 507 GCAGTCTTTGAAGGGGTATTCATTTAACAAGCATATGGAATGACAGCCTTTGAATAC 566
Qy 2127 CATGGCACCGACCCCGCATTTCAACAGATCTTTAAACCGGGGAATGCTGATCACTCCACC 2186
Db 567 CATGGAACGATCCCAAGGTTTAAACAAGGTTTCAACAAGGGATGGCTGATCACTCTACC 626
Qy 2187 ATTACTATGAAGAAGATACTGGAACATACAAGGGCTTCGAGGGCTCGAGACCGTGGTC 2246
Db 627 ATTACAAATGAAGAAAATTTCTTGAGACCTACACAGGCTTTTGAAGGACCTTAAATCCCTGGTT 686
Qy 2247 GATGTCGAGGCGGCACTGGGCGGTCTCAGCATGATCGTTGCCAAATACCCATCAATG 2306
Db 687 GATGTTGGTGGAGAACTGAGAGCTGTAGTCAACATGATTTGTCTCAAAGTATCCCACTATT 746
Qy 2307 AAAGGATCAACTTCGA-CCGCCCCAAACGGAATTGAAGACGCCCCACCCCTTCTCTGTGTGTC 2365
Db 747 AAGGGCATTAATTTTGATTTGCCCATGTCAITGAAGATGCCCATCTTTATCCAGGAGTG 806
Qy 2366 AAGCAGCTCGAGGCGACATGTTCTGACGGTTCCAAAGGGAGATGCCATTTTTCATGAAG 2425
Db 807 GAACATGTTGGTGGAGATATGTTGTGAGTTCCTTCAAAAGCTGATCTATTTTATGAAG 866
Qy 2426 TGATATGCTGACCTGAGTGAACGACCATTTGCGCAAGTTCTCAGAACTGCTACGAT 2485
Db 867 TGGATTTGCCACGATTTGGAGTGTAGTGAAGTCTGCTGAAGTTTGAAGAACTGCTATGAG 926
Qy 2486 GCGCTTCCCAACAAATGGAAGGTGATCGTTGACAGTGGTGTCTCCTGTGTACCCAGAC 2545
Db 927 GCATACAGATAATGGGAAGTGAATTGTGGCGGAATGCAATCTTCCGGTGGCTCCAGAC 986
Qy 2546 ACGAGCTAGCGACCAAGATGTGATCCACATCGCTGATCATGTTGGCCCAACACCCA 2605
Db 987 TCTAGCTTGGCCACAAAGGGTGTGTTTCAATCGATGTGATCATGTTGGCTCAATCCA 1046
Qy 2606 GCGCGG---AAAGAGAGGACACAGAAAGGAGTTTCGAGGCATTTGGCCAAAGGGCGGATTT 2662
Db 1047 GGTGGGGAAGAGAGAGAAAGAGTTTGAGGCTCTGGGCCAAAGGCTCTGGATTTC 1106
Qy 2663 CAGGCTTCCAACT-CATGTGCTGCGCTTTCGGCACTCAC 2701
Db 1107 CAAGGTTTCCAACTCCCTGTGCTGTGCTTTCAATACCTAC 1146

RESULT 14
US-09-971-823B-17
; Sequence 17, Application US/09971823B
; Patent No. 6610521
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BB1327 US NA
; CURRENT APPLICATION NUMBER: US/09/971,823B
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/119,587
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (472)
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OTHER INFORMATION: n = A, C, G or T  
NAME/KEY: unsure  
LOCATION: (1156)  
OTHER INFORMATION: n = A, C, G or T  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1180)  
OTHER INFORMATION: n = A, C, G or T  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1262)  
OTHER INFORMATION: n = A, C, G or T  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1302)  
OTHER INFORMATION: n = A, C, G or T  
US-09-971-823B-17

Query Match 18.4%; Score 556.6; DB 3; Length 1314;  
Best Local Similarity 72.2%; Pred. No. 9.2e-140;  
Matches 765; Conservative 0; Mismatches 290; Indels 5; Gaps 3;

Qy 1647 GAGACCCAGATGACCCCGGACCCAAAGTCTCGGACGACGAGGCGAACTCTTCGCCATGCGAG 1706  
Db 87 GAGACTCAGATTACTCCAAACCCATGTATCTGATGAGAGGCGAAACCTTTTCGCCATGCAA 146

Qy 1707 CTGGGAGCGCTCGTGTCTCCCATGTCTCTAAAGCGCGCCATCGAGATCGACTCTCTC 1766  
Db 147 CTAGCCAGTGTCTCAGTACTCTCCATGTCTCTCAATCAGCTCTTGAGCTTGTATCTGTTG 206

Qy 1767 GAGATATGGCAAGGAGCGGCGGCGTCTCTCCAGGGGAAATCGCGGCACAG 1826  
Db 207 GAATATCATAGCAAGGCTGGCCCTGTGTTCACCTTTCCCTCGCAATGTCTTCGG 266

Qy 1827 CTCCCGACCCAGAAACCCGAGGACCCGTATGTCTCGACCGGATCTTCGGCTCTCGCC 1886  
Db 267 CTCCCAACACACAAACCCCTGATGACCCCGTATGTGGACCGTATATTGGCGCTCTTGCT 326

Qy 1887 AGCTACTCCGTGTCTACGTGACCGCTCGGACCTCCCGATGGCAAGGTGCGGGGTC 1946  
Db 327 TGCTACAATATCTCTCTTTCTCTTCGCACTCTCCCTCATGGCAAGGTTGAGAGGCTC 386

Qy 1947 TACGGCTTAGCGCGGTGTGCAAGTCTTGTCTCAAGACGAGGACGGGTCTCCATCGCC 2006  
Db 387 TATGGTCTCGCCCTGTGTCTAAGTACTTGTCTAGAACGAAAGATGGTGTCTCCATGTCT 446

Qy 2007 GCATCTCACTTGTATGAACACGAGCAAAATCTCTATGAAAGCTGTATTAATCTGAAAGAT 2066  
Db 447 GCTCTCAACCTCATGACACGAGACANAATCTCTATGGNAAGCTGTACTATTGNAAGAT 506

Qy 2067 GCGTCTCTTGAAGCGGGAATCCCATTTCAAGGCTGACGCGATGACGCGGTTGAGTAT 2126  
Db 507 GCAGTCTCTGAAGGGGTATTCATTTAAAGGATATGGAATGACAGCGCTTTGAAATAC 566

Qy 2127 CATGGCCCGACCGCGATTCACAGATCTTTAAACCGGGAATGTCTGATCACTCCACC 2186  
Db 567 CATGGAACGGAATCAAGGTTTAAAGGTTTCAACAAAGGGGATGGCTGATCACTTACC 626

Qy 2187 ATTAATGAAAGAGATACTGGAACACATACAAGGCTTCGAGGGCTTCGAGACCGTGTCTC 2246  
Db 627 ATTACATGAGAAATTTCTTGAGACCTACACAGCTTTGAGGAACTTAATCTCGTT 686

Qy 2247 GATTCGAGCGGCACTGGGCGGTGTCTAGCATGATGTTGTCGAAATACCCATCAATG 2306  
Db 687 GATGTGTGGAGGAACTGGAGCTGTAGTCAACATGATTGTCTCAAAGTATCCCATATT 746

Qy 2307 AAAGGATCACTTTCGA-CCGCCCCACGGAATGAGACGCCCCACCCCTTCCTGTTGTC 2355  
Db 747 AAGGCAATTAATTTGATTTGCCCCCATGTGATTGAAGATGCCCATCTTATTCAGGAGTG 806

Qy 2366 AAGCACGTGCGAGGCGACATGTTGCTCAGCGTTCCAAAGGGAGATGCCATTTTCATGAAG 2425

Db 807 GAACATGTTGGTGAGATATGTTTGTCAAGTTCACAAAAGCTGATGCTATTTTATGAAG 866

Qy 2426 TGGATATGCCATGACTCGAGTGACGACATTTGGCGAAGTTTCCTCAAGAACTGCTACGAT 2485

Db 867 TGGATTTGCCACGATTGGAGTGATGACACTGCTTGAAGTTTTTGAAGAACTGCTATGAG 926

Qy 2486 GCGCTTCCCAACATGGAAGGTGATCGTTGCAGAGTGCGTACTCCCTGTGTATCCCAAGAC 2545

Db 927 GCATCCACAGATAATGGAAAGTATTGTGGCGAATGCAATCTTCCGGTGGCTCCAGAC 986

Qy 2546 ACAGACCTAGGACCAAGAATGTATCCATGACATGCGATCATGTTGGGCCCAACAACCA 2605

Db 987 TCTAGCTTGGCCACAAAGGGTGTGTTTCAATCGATGATCATGTTGGCTCACAATCCA 1046

Qy 2606 GCGGG--AAAGAGAGGACACAGAAGGATTTCGAGGCAATTTGGCAAGGGGCGGATTT 2662

Db 1047 GTGGGGAAAGAGAGAAACAAGAGAGATTGAGGCTCTGGGCCAAAGGCTCTGGATTC 1106

Qy 2663 CAGGGCTTCCAAGT-CATGTGCTGCGCTTTTCGGCACTCAC 2701

Db 1107 CAAGTTTCCAAGTCCCTGTGCTGCTTTCAATACCTAC 1146

RESULT 15  
US-09-453-323-1  
; Sequence 1, Application US/09453323  
; Patent No. 6441272  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Zheng-Hua  
; TITLE OF INVENTION: MODIFICATION OF LIGNIN CONTENT AND COMPOSITION IN  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 235.00090101  
; CURRENT APPLICATION NUMBER: US/09/453,323  
; CURRENT FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: 60/110,676  
; PRIOR FILING DATE: 1998-12-02  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1507  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
US-09-453-323-1

Query Match 17.3%; Score 523; DB 3; Length 1507;  
Best Local Similarity 59.1%; Pred. No. 1.2e-130;  
Matches 743; Conservative 0; Mismatches 330; Indels 2; Gaps 2;

Qy 1646 CGAGACCCAGATGACCCCGGACCCAAAGTCTCGGACGAGGCGGAACTCTTCGCCATGCA 1705  
Db 20 CGAGAGCCAGATGAACAGTCTCACTCACAGAGAGCAAGCTTTCTATTTCGATGCA 79

Qy 1706 GCTGGGAGCGCTCTCGTGTCTCCCATGTCCTAAAGCGCGCCATCGAGATCGACCTCT 1765

Db 80 ATTGTGTAGTGTCTCTGATCTCTCTATGTCCTTAAATCAGCGGTAGAACCTTGACCTCT 139

Qy 1766 CGAGATCATGCCCAAGACGCGGCGGCTCTCTCCACGGGGGAAATCGGGGACA 1825

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Qy 1826 GCTCCCGACCCAGAACCCCGAGGACCCGCTCATGCTCGACGGATCTTCGGGCTGCTGGC 1885

Db 200 GCTCTCACTCAGAACCCAGAGACCTGTATGCTTGATCGGATGCTTAGGCTACTTGC 259

Qy 1886 CAGTACTCTCGTCTCAGTGCACCCCTCCGCGACCTCCCGATGGCAAGGTTCGAGCGCT 1945

Db 260 TTCTTACTCTCTCAATGTACTCTTAGAACACTGCTGTAGACAGTGTGAGAGGCT 319

Qy 1946 CTAGCGTTAGCGCGGTGTGCAAGTCTTGTTCAGAAACGAGACGCGGTCTCCATCGC 2005

Db 320 TTATAGTCTGGCTCCCGCTGTAGTACTGACTAAGAAATGCTGATGAGTGTCTGTGTC 379

Qy 2006 CGCACTCACTTGATGAACCGAGGACAAATCTCTCATGAAAGCTGGTATTACCTGAAAGA 2065

|    |      |                                                                |      |
|----|------|----------------------------------------------------------------|------|
| Db | 380  | CCCACTTTTGGCTTATGAATCAAGATAAAGTCTTATGGAGAGTGGTACACATTAAAGA     | 439  |
| Qy | 2066 | TGGGTCCTTTGAAGGCGGAATCCATTCAACAAGGCGTACGGATGACCGGTCGAGTA       | 2125 |
| Db | 440  | TGCAGTACTAGATGGCGGAATCCATTCAACAAGCCTATGGAAATGACGACATTTGAGTA    | 499  |
| Qy | 2126 | TCATGGCACCGACCCCGGATTCACAAAGATCTTTAAACCGGGAAATGCTGATCACTCCAC   | 2185 |
| Db | 500  | CCATGGCACAGATCCAAAGATTCAAACAAGTGTCAACCGTGGAAATGCTGATCACTCCAC   | 559  |
| Qy | 2186 | CATTACTATGAAGNAGTACTGGAACATACAAAGGCTTCAGAGGCTCGAGACCCGGT       | 2245 |
| Db | 560  | TATGTCAAATGAAGNAGATTCCTGAGGACTCAAAAGGATTTGAAGGCGCTAAATTCCAATGT | 619  |
| Qy | 2246 | CGATGTCGGAGGCGGCACTCGGGCGGTGCTCAGCATGATCGTTGCCAAATACCCATCAAT   | 2305 |
| Db | 620  | TGATGTTGGTGGGAACGGGTGCTACAGTTTACATGATTTGCTCTTAATATCCCTCTAT     | 679  |
| Qy | 2306 | GAAGGGATCAACTTCGA - CGGCCCCAACGGATTTGAAGCGCCCCACCCCTTCCTGGTGT  | 2364 |
| Db | 680  | TAAGGCATTAACTTTGATTTGCCACATGTAAATGGAGATGCTCCAACTTACCCCGGTGT    | 739  |
| Qy | 2365 | CAACGCGTCGGAGCGCACATGTTCTGTCAGGCTTCCAAAGGGAGATGCCATTTTCATGAA   | 2424 |
| Db | 740  | CGAGCAGTTGGTGGCGCACATGTTGCTAGTGTGCCAAAGCAGATGCCATTTTCATGAA     | 799  |
| Qy | 2425 | GTGGATATGCCATGACTGGAGTGACGACCATTTGGCGGAAGTTCCTCAAGAACTGCTACGA  | 2484 |
| Db | 800  | GTGGATTTGTCAATGATTTGGACGATGAGCATTTGCTAAATCTTTGAAGAAATTCCTATGA  | 859  |
| Qy | 2485 | TGCGCTTTCCCAACAAATGAAAGGTGATGTTTGCAGAGTGGGTACTCCTGTGTACCCAGA   | 2544 |
| Db | 860  | AGCACTACTCGAAATGGGAAGGTGATAATTGCAGATGTCATCTTCAGAGAGGCCCCAGA    | 919  |
| Qy | 2545 | CACGAGCCTAGCGACCAAGATGTGATCCACATCGATGTCATCATGTGTGCCCCACACCC    | 2604 |
| Db | 920  | TACATCACTTGCACCTAAGAAATCAGTACATGTTGATTTGTGATGTTAGCACATAACCC    | 979  |
| Qy | 2605 | AGGCGGGAAGAGAGGACACAAAGGAGTTTCAGGCGAATGGCCAAAGGGCGGATTTCA      | 2664 |
| Db | 980  | AGHAGGCAAGAAAGGACTGAGAGGAAATTTGAGGCTTTGGCTAAGGGCGCTGGTTTAC     | 1039 |
| Qy | 2665 | GGGCTTCCAAGTCATGTCTCGCTTTCCGGCACTCACGTCATGAGGATTCCTGGAAG       | 2719 |
| Db | 1040 | TGTTTTCGCAAGGCT - TCTTCGGCTTACAAACACTTGGCTCATGGAATTCACAAAG     | 1093 |

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:25:56 ; Search time 3876.36 Seconds  
(without alignments)  
9604.757 Million cell updates/sec

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Perfect score: 3030  
Sequence: 1 cacctgttcagttgatcc.....acttcgaacaaaaaa 3030

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:

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- 2: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq\*
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- 9: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq\*
- 10: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq\*
- 11: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq\*
- 12: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq\*
- 13: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq\*
- 14: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq\*
- 15: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq\*
- 16: /EMC Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | ID | Description         |
|------------|-------------|-------|--------|----|---------------------|
| 1          | 3030        | 100.0 | 3070   | 6  | US-10-137-036-113   |
| 2          | 3030        | 100.0 | 3070   | 9  | US-10-702-319A-113  |
| 3          | 3030        | 100.0 | 3070   | 10 | US-10-927-641-113   |
| 4          | 2020.4      | 66.7  | 2096   | 6  | US-10-137-036-60    |
| 5          | 2020.4      | 66.7  | 2096   | 9  | US-10-702-319A-60   |
| 6          | 2020.4      | 66.7  | 2096   | 10 | US-10-927-641-60    |
| 7          | 1429.6      | 47.2  | 1630   | 7  | US-10-174-693-107   |
| 8          | 638.2       | 21.1  | 661    | 6  | US-10-137-036-12    |
| 9          | 638.2       | 21.1  | 661    | 9  | US-10-702-319A-12   |
| 10         | 638.2       | 21.1  | 661    | 10 | US-10-927-641-12    |
| 11         | 631         | 20.8  | 1503   | 3  | US-09-947-027-5     |
| 12         | 631         | 20.8  | 1503   | 6  | US-10-091-009-5     |
| 13         | 631         | 20.8  | 1503   | 13 | US-11-057-518-5     |
| 14         | 613.4       | 20.2  | 2037   | 8  | US-10-424-599-20299 |
| 15         | 613         | 20.2  | 1486   | 8  | US-10-469-993-11    |
| 16         | 603.8       | 19.9  | 1370   | 8  | US-10-464-610-3     |
| 17         | 589         | 19.4  | 1380   | 3  | US-09-796-256A-5    |

ALIGNMENTS

RESULT 1  
US-10-137-036-113  
; Sequence 113, Application US/10137036  
; Publication No. US20030101478A1  
; GENERAL INFORMATION:  
; APPLICANT: Perera, Rajan  
; APPLICANT: Rice, Stephen  
; APPLICANT: Eagleton, Clare  
; APPLICANT: Lasham, Annette  
; APPLICANT: Wood, Marion  
; APPLICANT: Visser, Elizabeth  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Expression  
; FILE REFERENCE: 11000.1036c4  
; CURRENT APPLICATION NUMBER: US/10137.036  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 113  
; LENGTH: 3070  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-10-137-036-113

Query Match 100.0%; Score 3030; DB 6; Length 3070;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 41 CACCTGTTCACTTTGATTCCCTTCAGATGACCTACAGTATAGCTTCGATGAATAAGATGG 100  
QY 61 GATAATAGATTCAACAGAGGATAAAAGGTAGGAGATAGGGGATCTCCCGCTCTGATG 120  
DB 101 GATAATAGATTCAACAGAGGATAAAAGGTAGGAGATAGGGGATCTCCCGCTCTGATG 160  
QY 121 CCTCGGTAGGTTGAAATAAGCAAAAGTTTCGCCGTTGAAATTTGACAGCAAAAGACACC 180  
DB 161 CCTCGGTAGGTTGAAATAAGCAAAAGTTTCGCCGTTGAAATTTGACAGCAAAAGACACC 220  
QY 181 GTCGTTATGCAATTCGATGATCCATTTGACCATGTCAGGTGAAATCTTAGAGTGAGGAGA 240  
DB 221 GTCGTTATGCAATTCGATGATCCATTTGACCATGTCAGGTGAAATCTTAGAGTGAGGAGA 280  
QY 241 TAGTCCCTTTGAAAGTCCCATTTCCACCTCATATAGGCTTTCTGCATATCCATTTTAAGA 300  
DB 281 TAGTCCCTTTGAAAGTCCCATTTCCACCTCATATAGGCTTTCTGCATATCCATTTTAAGA 340  
QY 301 ACAGCCCGGAATTCAGCTCAATTTCTGACTTTGAAATTCGATGTAGAACTCTTAGACT 360  
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DB 401 ATTAAATATTTGCTCTGAAATTTGAGTCCACTGACAAAGCGCTTTCCTCTGGAATA 460  
QY 421 AGTACAGCAGTAGGGCTTAAGGCGATTGGCAATCACCTTAGAAATGATCTTATATGCG 480  
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QY 481 TAAATPACAAAGACTGATGGGGGTTATGGTCTAAATTTGTTCCAGGATGGTGTGGGT 540  
DB 521 TAAATPACAAAGACTGATGGGGGTTATGGTCTAAATTTGTTCCAGGATGGTGTGGGT 580  
QY 541 ATTAGGGCTATGATGGTTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 600  
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QY 601 TGCACGTATGAGAAATAGTTTCATCTCTGGAGTATATCCCAATGATGCTGTAGAGAGTCCA 660  
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DB 701 TTCAAGCCATCTGACCCGGGGCTTGGTAACTCCAGTTCGAAAGTACCTCTTAAT 760  
QY 721 TCCTTCTTTGGTAAACAGGAGCTATTAGGACATATTCATCTCATTAGTAAACCTTAAGGA 780  
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DB 821 CACTGGTTTCAAGATAGGCAAGTGTCTCGATGTCCCACTGTCTGAAATPAGATGTGAAAG 880  
QY 841 TAACTATCGTCAATCTTCAAAATTTTCCAGATCGCGCAATCCAGCTTGTATGTCATCC 900  
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QY 961 GTATTTTGTCTCCCGCAGCTGAGCCATTTAATTCGAGAGCAATCCGCCAAATTTATCT 1020  
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DB 1061 TCTTGTGCAATACTGTCGAATTTTCTTTTGTAGTAACTAATGATGCGCATGT 1120  
QY 1081 TGACAAAAGGCTGATTAGTATGATCTTGGAGTTGTTGGTGAATTTTGAAGCTGACGA 1140

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QY 1381 AGAGAGAGAGAGAGAGAGTTTCTCTATATTTCTGGTTTCAACCGTTGGAGTCAATGGCA 1440  
DB 1421 AGAGAGAGAGAGAGAGAGTTTCTCTATATTTCTGGTTTCAACCGTTGGAGTCAATGGCA 1480  
QY 1441 TGGCTGACCAATGTACATATTTGGTGTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACC 1500  
DB 1481 TGGCTGACCAATGTACATATTTGGTGTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACC 1540  
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QY 1861 TCGACCGGATCTTCGCCGCTCGCCAGCTACTCCGTGCTCAGTGCACCTCCGCGACC 1920  
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QY 1921 TCCCGGATGCAAGGTTCGAGCGGCTCTACCGGCTTAGCGCGGTTGCAAGTCTTGTGTC 1980  
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QY 1981 AGAACGAGGACGGGGTCTCCATCGCGCACTCAATTTGATGAACCCAGGACAAATCTCTCA 2040  
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QY 2041 TGGAAAGCTGGTATTAATCTGAAAGTGGGTTCTTGAAGCGGAAATCCCAATTTCAACAGG 2100  
DB 2081 TGGAAAGCTGGTATTAATCTGAAAGTGGGTTCTTGAAGCGGAAATCCCAATTTCAACAGG 2140  
QY 2101 CGTACGGGATGACCGCGTTTCGAGTATCATGCGCACCGACCCCGGATTCACAAAGATCTTTA 2160  
DB 2141 CGTACGGGATGACCGCGTTTCGAGTATCATGCGCACCGACCCCGGATTCACAAAGATCTTTA 2200  
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Db 2261 GCTTCGAGGGCTCGAGACCGTGTGCGATGTCGAGGCGGCACTGGGCGCTGTCTCAGCA 2320  
Qy 2281 TGATCGTTGCCAAATPACCATCAATGAAGGGATCAACTTCGACCGGCCCAACCGAATTGA 2340  
Db 2321 TGATCGTTGCCAAATPACCATCAATGAAGGGATCAACTTCGACCGGCCCAACCGAATTGA 2380  
Qy 2341 AGAGCCCCACCCCTTCTGTGTCAAGCAGTGTGAGGCGGACATGTTTCGTCAGGTTCC 2400  
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Qy 2461 GAAAGTTCCTCAAGAACTGCTACGATGCGCTTCCCAACAATGGAAGGTGATCGTTGCAGA 2520  
Db 2501 GAAAGTTCCTCAAGAACTGCTACGATGCGCTTCCCAACAATGGAAGGTGATCGTTGCAGA 2560  
Qy 2521 GTGCGTACTCCTGTGTACCCAGACACGAGCTAGCGACCAAGAAATGTGATCCACATCGA 2580  
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Db 3041 TCAGTAAATCACTTCGAAACAAAAA 3070

RESULT 2  
US-10-702-319A-113  
; Sequence 113, Application US/10702319A  
; Publication No. US20050026162A1  
; GENERAL INFORMATION:  
; APPLICANT: Perera, Ranjan  
; APPLICANT: Rice, Stephen  
; APPLICANT: Eagleton, Clare  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE OF INVENTION: Modification of Gene Expression  
; FILE REFERENCE: 11000.1036C5  
; CURRENT APPLICATION NUMBER: US/10702,319A  
; CURRENT FILING DATE: 2003-11-06  
; PRIOR APPLICATION NUMBER: U.S. No. 10/291,447

; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: U.S. No. 60/425,087  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: U.S. No. 10/137,036  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 113  
; LENGTH: 3070  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-10-702-319A-113

Query Match 100.0%; Score 3030; DB 9; Length 3070;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 41 CACCTGTTCAAGTTGATTCCTTCAGATGACCTACAGTACCTGATAGCTTCTGATGAATGAATGG 100  
Qy 61 GATAATAGATTACACGAGGAGTAAAGAGGTAGGAGATAGGGGATCTCCCGTCTGATG 120  
Db 101 GATNATAGATTACACGAGGAGTAAAGAGGTAGGAGATAGGGGATCTCCCGTCTGATG 160  
Qy 121 CCTCGGTAGTTGAAATTAAGCAAAAGTTGCGCGTTGAATTTGACAGCAAAAGACACC 180  
Db 161 CCTCGGTAGTTGAAATTAAGCAAAAGTTGCGCGTTGAATTTGACAGCAAAAGACACC 220  
Qy 181 GTGCTTATGATTCATGATGATCCATTTACCATGATAGGTTGAATCTTAGATGAGGAGA 240  
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Qy 241 TAGTCTTTTGAAGTCCCATTCACCTCATCATAGGCTTCTGCATATCCATTTTAAAGA 300  
Db 281 TAGTCTTTTGAAGTCCCATTCACCTCATCATAGGCTTCTGCATATCCATTTTAAAGA 340  
Qy 301 ACAGCCCGGAATTGACGCTCTACATTTTCTGACTTTAAATTTGAATGATAGAACCTTTAGACT 360  
Db 341 ACAGCCCGGAATTGACGCTCTACATTTTCTGACTTTAAATTTGAATGATAGAACCTTTAGACT 400  
Qy 361 ATTAAATATTTGCTGATTTGACGTCCTCACTGACAAAGGCTTTGCTCTGAGAAATA 420  
Db 401 ATTAAATATTTGCTGATTTGACGTCCTCACTGACAAAGGCTTTGCTCTGAGAAATA 460  
Qy 421 AGTACAGCGAGTGGGCTTAAGGCGATTGCGCAATCACCTTAGAAATGATCTTATATGCG 480  
Db 461 AGTACAGCGAGTGGGCTTAAGGCGATTGCGCAATCACCTTAGAAATGATCTTATATGCG 520  
Qy 481 TAATTACAAAGACTGATGGGCGGTATTGGTCTAATTTGTTTCTAGGATGGTACCTTGGGT 540  
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Db 641 TGCACTGATGAGATAGTTTCATCTCGAGTATATCCCAATGATCTGTAAGAGTCCA 700  
Qy 661 TTCAAGGCATCTGGACCGGGGCGCTTGTGTAAGTCCCGAGTTGGAAAGTAGGCTCTTAAGT 720



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|----|------|----------------------------------------------------------------|------|
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| Qy | 721  | TCCTTTCTGGTAACAGAGAGCTATTAGGACATATTCATCTCATTTAGTAACAACCTTAAGGA | 780  |
| Db | 761  | TCCTTTCTGGTAACAGAGAGCTATTAGGACATATTCATCTCATTTAGTAACAACCTTAAGGA | 820  |
| Qy | 781  | CACCTGGTTCAAGATAGCAAGTAGTCTCGATGTCCCACTCTCTGAAATAGATGTGAAAG    | 840  |
| Db | 821  | CACCTGGTTCAAGATAGCAAGTAGTCTCGATGTCCCACTCTCTGAAATAGATGTGAAAG    | 880  |
| Qy | 841  | TAACTATCGTCATCATCTTCAAAATTTAGGATCGGCACCCAAAGCTTGATGTATCC       | 900  |
| Db | 881  | TAACTATCGTCATCATCTTCAAAATTTAGGATCGGCACCCAAAGCTTGATGTATCC       | 940  |
| Qy | 901  | TGCAACATACATCTTCTTGTGTGTCTTGTATAGTTGTGATGAAAAATTTA             | 960  |
| Db | 941  | TGCAACATACATCTTCTTGTGTGTCTTGTATAGTTGTGATGAAAAATTTA             | 1000 |
| Qy | 961  | GTATTTTGTCCCGGAGCTGAGCAATTAATTCGAGAGCAATCGCCCAAAATTTCT         | 1020 |
| Db | 1001 | GTATTTTGTCCCGGAGCTGAGCAATTAATTCGAGAGCAATCGCCCAAAATTTCT         | 1060 |
| Qy | 1021 | TCCTGCTGCCATACCTGTCGAATTTCTCTTTTAGGTAAAGTAAGTAACTGATGCGCCATGT  | 1080 |
| Db | 1061 | TCCTGCTGCCATACCTGTCGAATTTCTCTTTTAGGTAAAGTAAGTAACTGATGCGCCATGT  | 1120 |
| Qy | 1081 | TGCAAAAAAGGCTGATAGTATGATCTTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGA  | 1140 |
| Db | 1121 | TGCAAAAAAGGCTGATAGTATGATCTTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGA  | 1180 |
| Qy | 1141 | TGGCCCTCTCAGGAAATTAAGCGGCAACCCAGATGCAAGAGACCAAGAGCAGCACC       | 1200 |
| Db | 1181 | TGGCCCTCTCAGGAAATTAAGCGGCAACCCAGATGCAAGAGACCAAGAGCAGCACC       | 1240 |
| Qy | 1201 | CAACCTTTCTTAAACAAGATCATCACAGATCGGCCAGTAAAGGTAATTAATTTAAACA     | 1260 |
| Db | 1241 | CAACCTTTCTTAAACAAGATCATCACAGATCGGCCAGTAAAGGTAATTAATTTAAACA     | 1300 |
| Qy | 1261 | AATAGCTCTTGTACCGGGAACCTCGTATTTCTCTCACTTCCATATAACCCCTGATTAATTT  | 1320 |
| Db | 1301 | AATAGCTCTTGTACCGGGAACCTCGTATTTCTCTCACTTCCATATAACCCCTGATTAATTT  | 1360 |
| Qy | 1321 | GGTGGAAAGCAGACAGCAACCCCAAAAGGTGATGTCATCTCCACGAGAGAGAGAG        | 1380 |
| Db | 1361 | GGTGGAAAGCAGACAGCAACCCCAAAAGGTGATGTCATCTCCACGAGAGAGAGAG        | 1420 |
| Qy | 1381 | AGAGAGAGAGAGAGAGATTTCTCTCTATATTTCTGTTTCACTGTTGAGTCAATGGCA      | 1440 |
| Db | 1421 | AGAGAGAGAGAGAGAGATTTCTCTCTATATTTCTGTTTCACTGTTGAGTCAATGGCA      | 1480 |
| Qy | 1441 | TGCGTGACGAATGTACATATTTGGTGTAGGTCATATTTTTCGGGAGGGTTGGTGAACC     | 1500 |
| Db | 1481 | TGCGTGACGAATGTACATATTTGGTGTAGGTCATATTTTTCGGGAGGGTTGGTGAACC     | 1540 |
| Qy | 1501 | GCAAGTTCTATATATTCGAACCTCCACCAACATCTCACTTCAATCCCACTTTAT         | 1560 |
| Db | 1541 | GCAAGTTCTATATATTCGAACCTCCACCAACATCTCACTTCAATCCCACTTTAT         | 1600 |
| Qy | 1561 | CCGTTTTATTTCTCTGCTTTCTTGTGCTCGAGTCTCGCGGAGAGAGAGAGAGAG         | 1620 |
| Db | 1601 | CCGTTTTATTTCTCTGCTTTCTTGTGCTCGAGTCTCGCGGAGAGAGAGAGAGAG         | 1660 |
| Qy | 1621 | AGGAGAGATGGGTTGACCGGCTCCGAGACCCAGATGACCCGACCCAAAGTCTCGGAG      | 1680 |
| Db | 1661 | AGGAGAGATGGGTTGACCGGCTCCGAGACCCAGATGACCCGACCCAAAGTCTCGGAG      | 1720 |
| Qy | 1681 | ACGAGGCAACCTCTTCCGATCGAGTGGCGAGCGCTCCGCTGCTCCCATGGTCTCTAA      | 1740 |
| Db | 1721 | ACGAGGCAACCTCTTCCGATCGAGTGGCGAGCGCTCCGCTGCTCCCATGGTCTCTAA      | 1780 |
| Qy | 1741 | AGGCGGCAATCGAGATCGACCTCTCGAGATCATGCGCAAGAGCAGGCGCGGCTTCC       | 1800 |
| Db | 1781 | AGGCGGCAATCGAGATCGACCTCTCGAGATCATGCGCAAGAGCAGGCGCGGCTTCC       | 1840 |
| Qy | 1801 | TCTCCACGGGGAATCGCGCACAGCTCCGACCCAGAACCCCGAGGCAACCCGCTCATGC     | 1860 |
| Db | 1841 | TCTCCACGGGGAATCGCGCACAGCTCCGACCCAGAACCCCGAGGCAACCCGCTCATGC     | 1900 |
| Qy | 1861 | TCGACCGGATCTTCCGGCTGCTGGCCAGCTACTCCGTCCTCACTGCAACCCCTCCGCGACC  | 1920 |
| Db | 1901 | TCGACCGGATCTTCCGGCTGCTGGCCAGCTACTCCGTCCTCACTGCAACCCCTCCGCGACC  | 1960 |
| Qy | 1921 | TCCTCCGATGGCAAGGTTCAGCGGCTTACGGCTTAGCGCCGGTGTGCAAGTCTTGGTCA    | 1980 |
| Db | 1961 | TCCTCCGATGGCAAGGTTCAGCGGCTTACGGCTTAGCGCCGGTGTGCAAGTCTTGGTCA    | 2020 |
| Qy | 1981 | AGAACGAGGAGGGGTCTCCATCGCGCACTCAACTTGATGAACCCAGGACAAAATCTCTCA   | 2040 |
| Db | 2021 | AGAACGAGGAGGGGTCTCCATCGCGCACTCAACTTGATGAACCCAGGACAAAATCTCTCA   | 2080 |
| Qy | 2041 | TGGAAGCTGTGTATTACCTGAAAGATGCGGTCTTTGAAAGCGGAATCCATTTCAACAAG    | 2100 |
| Db | 2081 | TGGAAGCTGTGTATTACCTGAAAGATGCGGTCTTTGAAAGCGGAATCCATTTCAACAAG    | 2140 |
| Qy | 2101 | CGTACGGGATGACCGGCTTCGAGTATCATGGCACCGCCGCGATTCAACAAGATCTTTTA    | 2160 |
| Db | 2141 | CGTACGGGATGACCGGCTTCGAGTATCATGGCACCGCCGCGATTCAACAAGATCTTTTA    | 2200 |
| Qy | 2161 | ACCGGGATGTCTGATCACTCCACATTTACTATGAAGAAGATACTGGAACATACAAGG      | 2220 |
| Db | 2201 | ACCGGGATGTCTGATCACTCCACATTTACTATGAAGAAGATACTGGAACATACAAGG      | 2260 |
| Qy | 2221 | GCTTCGAGGGCTCGAGACCGTGTGATGTCGAGGGGGGCACTGGGGCGGTGCTCAGCA      | 2280 |
| Db | 2261 | GCTTCGAGGGCTCGAGACCGTGTGATGTCGAGGGGGGCACTGGGGCGGTGCTCAGCA      | 2320 |
| Qy | 2281 | TGATCGTTCGCAAAATACCATCAATGAAAGGATCAACTTCGACCCGCCAACGGAATGA     | 2340 |
| Db | 2321 | TGATCGTTCGCAAAATACCATCAATGAAAGGATCAACTTCGACCCGCCAACGGAATGA     | 2380 |
| Qy | 2341 | AGACGGCCCAACCCCTTCTGCTGTCAAGCACGCTCGAGGGCGACATGTTGCTCAGCGTTC   | 2400 |
| Db | 2381 | AGACGGCCCAACCCCTTCTGCTGTCAAGCACGCTCGAGGGCGACATGTTGCTCAGCGTTC   | 2440 |
| Qy | 2401 | AAAGGAGATGCGCATTTTTCATGAAGTGTATGTCCTGATGAGTGAAGGATGCTGCGC      | 2460 |
| Db | 2441 | AAAGGAGATGCGCATTTTTCATGAAGTGTATGTCCTGATGAGTGAAGGATGCTGCGC      | 2500 |
| Qy | 2461 | GAAGTTCCTCAAGAACTGCTTACGATCGCTTCCCAACAAATGGAAGGTGATCGTTGCAGA   | 2520 |
| Db | 2501 | GAAGTTCCTCAAGAACTGCTTACGATCGCTTCCCAACAAATGGAAGGTGATCGTTGCAGA   | 2560 |
| Qy | 2521 | GTGCGTACTCCCTGTGTACCCAGACACGAGCTTAGCGACCAAGATGTGATCCACATCGA    | 2580 |
| Db | 2561 | GTGCGTACTCCCTGTGTACCCAGACACGAGCTTAGCGACCAAGATGTGATCCACATCGA    | 2620 |
| Qy | 2581 | CTGCATCATGTTGGCCCAACCCAGCGGGAAGAGAGACACAGAGAGTTCGAGGC          | 2640 |
| Db | 2621 | CTGCATCATGTTGGCCCAACCCAGCGGGAAGAGAGACACAGAGAGTTCGAGGC          | 2680 |
| Qy | 2641 | ATTGGCAAAAGGGGCGGATTTTCAGGGCTTCCAAAGTCACTGCTGCGCTTTTCGGCACTCA  | 2700 |
| Db | 2681 | ATTGGCAAAAGGGGCGGATTTTCAGGGCTTCCAAAGTCACTGCTGCGCTTTTCGGCACTCA  | 2740 |
| Qy | 2701 | CGTCATCGAGTTCCTGAAGACCGCTTGATCTGCTCTCTGCTGATGTTGATGTTCTT       | 2760 |
| Db | 2741 | CGTCATCGAGTTCCTGAAGACCGCTTGATCTGCTCTCTGCTGATGTTGATGTTCTT       | 2800 |
| Qy | 2761 | GGATTTGAAGGTCGTCAAGGAGCCCTTTCTCACAGTTCGGCTTCGGCATACCAAGTTCT    | 2820 |
| Db | 2801 | GGATTTGAAGGTCGTCAAGGAGCCCTTTCTCACAGTTCGGCTTCGGCATACCAAGTTCT    | 2860 |
| Qy | 2821 | TCTCATAAAAGGAACCAATTAAGAGCGACTGTATGATGGCGCAAGTGGAGATTAAGAT     | 2880 |
| Db | 2861 | TCTCATAAAAGGAACCAATTAAGAGCGACTGTATGATGGCGCAAGTGGAGATTAAGAT     | 2920 |





1381 AGAGAGAGAGAGAGAGAGTTTCTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCA 1440  
1421 AGAGAGAGAGAGAGAGAGTTTCTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCA 1480  
1441 TGGGTGACGAATGACATATTTGGTGTAGGTTCCAAATATTTTGGGAGGAGTTGGTGAACC 1500  
1481 TGGGTGACGAATGACATATTTGGTGTAGGTTCCAAATATTTTGGGAGGAGTTGGTGAACC 1540  
1501 GCAAGTTCCTATATATGCAACCTCCACCACTACCTCACTTCAATCCCACTTTAT 1560  
1541 GCAAGTTCCTATATATGCAACCTCCACCACTACCTCACTTCAATCCCACTTTAT 1600  
1561 CGGTATTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620  
1601 CGGTATTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1660  
1621 AGGAGAGAAATGGGTTTCGACCGGCTCCGAGACCCAGATGACCCCGACCCAAAGTCTCGGACG 1680  
1661 AGGAGAGAAATGGGTTTCGACCGGCTCCGAGACCCAGATGACCCCGACCCAAAGTCTCGGACG 1720  
1681 AGGAGGCAACCTCTTTCGCAATGCACTGGCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
1721 AGGAGGCAACCTCTTTCGCAATGCACTGGCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 1780  
1741 AGGCGCGCATCGAGATCGACCTCTCTCGAGATCATGGCCAGGACGGGCGGGCGGCTTCC 1800  
1781 AGGCGCGCATCGAGATCGACCTCTCTCGAGATCATGGCCAGGACGGGCGGGCGGCTTCC 1840  
1801 TCTTCAACGGGGAAATCGGGGCAAGCTCCCGACCCAGAACCCCGAGGCAACCGGTCATGC 1860  
1841 TCTTCAACGGGGAAATCGGGGCAAGCTCCCGACCCAGAACCCCGAGGCAACCGGTCATGC 1900  
1861 TCGACGGATCTTTCGGGCTGCTGGGCGAGCTACTCGGCTCACTGCAACCTCCCGGACG 1920  
1901 TCGACGGATCTTTCGGGCTGCTGGGCGAGCTACTCGGCTCACTGCAACCTCCCGGACG 1960  
1921 TCCCGCATCGCAAGTTCGAGCGGCTCTACGGGTTAGCGCGGTTGCAAGTCTTGGTCA 1980  
1961 TCCCGCATCGCAAGTTCGAGCGGCTCTACGGGTTAGCGCGGTTGCAAGTCTTGGTCA 2020  
1981 AGAACGAGACGGGTTCTCATCGCGGCTCACTGATGAAACGAGGATCCCTCA 2040  
2021 AGAACGAGACGGGTTCTCATCGCGGCTCACTGATGAAACGAGGATCCCTCA 2080  
2041 TGGAAAGCTGGTATTAACCTGAAAGATCGCGTCTTTGAAAGCGGAAATCCATTTCAACAAGG 2100  
2081 TGGAAAGCTGGTATTAACCTGAAAGATCGCGTCTTTGAAAGCGGAAATCCATTTCAACAAGG 2140  
2101 CGTACGGGATGACCGGTTTCGAGTATCATGGACCGGACCGGATTCACAGATCTTTA 2160  
2141 CGTACGGGATGACCGGTTTCGAGTATCATGGACCGGACCGGATTCACAGATCTTTA 2200  
2161 ACCGGGAATGTCGTATCACTCCACCTATGAAAGATGATCTGGAACATACAAAGG 2220  
2201 ACCGGGAATGTCGTATCACTCCACCTATGAAAGATGATCTGGAACATACAAAGG 2260  
2221 GCTTTCGAGGCGCTCGAGACCGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280  
2261 GCTTTCGAGGCGCTCGAGACCGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2320  
2281 TGATCGTTGCAAAATACCAATCAATGAAGGATCACTTCGACCGGCGGCGGCGGATTCGA 2340  
2321 TGATCGTTGCAAAATACCAATCAATGAAGGATCACTTCGACCGGCGGCGGCGGATTCGA 2380  
2341 AGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2400  
2381 AGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2440  
2401 AAAGGGAGATGCCATTTTCTATGAAGTGGATATGCGCATGATGAGTGAACCATTTGCCG 2460  
2441 AAAGGGAGATGCCATTTTCTATGAAGTGGATATGCGCATGATGAGTGAACCATTTGCCG 2500

2461 GAACTTCTCAAGAACTGCTACGATCGCTTCCAAACAATGGAAGGTGATCGTTGCAGA 2520  
2501 GAAGTTCTCAAGAACTGCTACGATCGCTTCCAAACAATGGAAGGTGATCGTTGCAGA 2560  
2521 GTGGGTACTCTCTCTGTGTACCCAGACACGAGCTAGCGACCAAGAATGTGATCCACATCGA 2580  
2561 GTGGGTACTCTCTCTGTGTACCCAGACACGAGCTAGCGACCAAGAATGTGATCCACATCGA 2620  
2581 CTGCATCATGTGTGGCCCAACAACCCAGCGGGAAGAGAGGACACAGAAGAGTTTCGAGGC 2640  
2621 CTGCATCATGTGTGGCCCAACAACCCAGCGGGAAGAGAGGACACAGAAGAGTTTCGAGGC 2680  
2641 ATTGGCCAAAGCGGCGGATTTTCAGGGCTTCCAAAGTCACTGTGTGCTGCGCTTTTCGGCACTCA 2700  
2681 ATTGGCCAAAGCGGCGGATTTTCAGGGCTTCCAAAGTCACTGTGTGCTGCGCTTTTCGGCACTCA 2740  
2701 CGTCATGAGGTTTCTGAAAGACCGCTTGATCTGCTCTCTGTGGTGATGTTTCATCGTCTTT 2760  
2741 CGTCATGAGGTTTCTGAAAGACCGCTTGATCTGCTCTCTGTGGTGATGTTTCATCGTCTTT 2800  
2761 GGAATTGAAAGTTCGTGAGGAGCGCTTTCTCAGTTTGGCTTCGGCATACCAAGTTCT 2820  
2801 GGAATTGAAAGTTCGTGAGGAGCGCTTTCTCAGTTTGGCTTCGGCATACCAAGTTCT 2860  
2821 TCTCTAAAGGAAACAATAAGAGCGACTGATGATGCGGCAAGTGAAGTTTCAAGAT 2880  
2861 TCTCTAAAGGAAACAATAAGAGCGACTGATGATGCGGCAAGTGAAGTTTCAAGAT 2920  
2881 TTGTTGTTTATGCTATATAAGTTTGTGATCTCTCTGTGGTGATGTTTCATCGTCTTT 2940  
2921 TTGTTGTTTATGCTATATAAGTTTGTGATCTCTCTGTGGTGATGTTTCATCGTCTTT 2980  
2941 AGAAACGGGCTATATGATGCTCTGATGATGCTCTGATGATGCTCTGATGATGCTCTGATGAT 3000  
2981 AGAAACGGGCTATATGATGCTCTGATGATGCTCTGATGATGCTCTGATGATGCTCTGATGAT 3040  
3001 TCAGTAAATCACTTCGAAACAAAAA 3030  
3041 TCAGTAAATCACTTCGAAACAAAAA 3070

RESULT 4

US-10-137-036-60  
; Sequence 60, Application US/10137036  
; Publication No. US20030101478A1  
; GENERAL INFORMATION:  
; APPLICANT: Perera, Ranjan  
; APPLICANT: Rice, Stephen  
; APPLICANT: Eggleston, Claire  
; APPLICANT: Lasham, Annette  
; APPLICANT: Wood, Marion  
; APPLICANT: Visser, Elizabeth  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE OF INVENTION: Modification of Gene Expression  
; FILE REFERENCE: 11000.1036c4  
; CURRENT APPLICATION NUMBER: US/10/137,036  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60  
; LENGTH: 2096

|                                                                |      |                                                                |      |  |  |  |  |  |  |
|----------------------------------------------------------------|------|----------------------------------------------------------------|------|--|--|--|--|--|--|
| : TYPE: DNA                                                    |      |                                                                |      |  |  |  |  |  |  |
| ; ORGANISM: Eucalyptus grandis                                 |      |                                                                |      |  |  |  |  |  |  |
| US-10-137-036-60                                               |      |                                                                |      |  |  |  |  |  |  |
| Query Match 66.7%; Score 2020.4; DB 6; Length 2096;            |      |                                                                |      |  |  |  |  |  |  |
| Best Local Similarity 99.3%; Pred. No. 0;                      |      |                                                                |      |  |  |  |  |  |  |
| Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1; |      |                                                                |      |  |  |  |  |  |  |
| Qy                                                             | 979  | CTGAGCCATTTAATTCGAGAGCACATCGCCCAAAATTATCTCTCTGCTGCCATAACTGT    | 1038 |  |  |  |  |  |  |
| Db                                                             | 41   | CTGAGCCATTTAATTCGAGAGCACATCGCCCAAAATTATCTCTCTGCTGCCATAACTGT    | 100  |  |  |  |  |  |  |
| Qy                                                             | 1039 | CGAATTTTCTCTTTTAGGTAAAGTAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA  | 1098 |  |  |  |  |  |  |
| Db                                                             | 101  | CGAATTTTCTCTTTTAGGTAAAGTAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA  | 160  |  |  |  |  |  |  |
| Qy                                                             | 1099 | GTATGATCTTTGGAGTTTGGTGCAAATTTGCAAGCTGACGATGGCCCTCAGAGGAATT     | 1158 |  |  |  |  |  |  |
| Db                                                             | 161  | GTATGATCTTTGGAGTTTGGTGCAAATTTGCAAGCTGACGATGGCCCTCAGAGGAATT     | 220  |  |  |  |  |  |  |
| Qy                                                             | 1159 | AAGGCGCCAAACCGAGTTTCAAGAGGACAAAGAGCACGACCCAACTTTCTTTAAACAAG    | 1218 |  |  |  |  |  |  |
| Db                                                             | 221  | AAGGCGCCAAACCGAGTTTCAAGAGGACAAAGAGCACGATCCAACTTTCTTTAAACAAG    | 280  |  |  |  |  |  |  |
| Qy                                                             | 1219 | ATCATCACAGATCGGCCAGTAAAGGGTAATATTAATTTAAACAATAGCTCTTGACCGGG    | 1278 |  |  |  |  |  |  |
| Db                                                             | 281  | ATCATCACAGATCGGCCAGTAAAGGGTAATATTAATTTAAACAATAGCTCTTGACCGGG    | 340  |  |  |  |  |  |  |
| Qy                                                             | 1279 | AACCTCGTATTTCTCATCTCCATTAACCCCTGATTAATTTGGTGGAAAGCCACAGCC      | 1338 |  |  |  |  |  |  |
| Db                                                             | 341  | AACCTCGTATTTCTCATCTCCATTAACCCCTGATTAATTTGGTGGAAAGCCACAGCC      | 400  |  |  |  |  |  |  |
| Qy                                                             | 1339 | AACCCACAAAAGGTCCAGATGTTCATCCAC- - -GAGAGAGAGAGAGAGAGAGAGAG     | 1394 |  |  |  |  |  |  |
| Db                                                             | 401  | AACCCACAAAAGGTCCAGATGTTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAG        | 460  |  |  |  |  |  |  |
| Qy                                                             | 1395 | AGAGTTTTCTCTATATTTCTGGTTTCAACGGTTGAGTCAATGGCATGCGTGACGAATGT    | 1454 |  |  |  |  |  |  |
| Db                                                             | 461  | AGAGTTTTCTCTATATTTCTGGTTTCAACGGTTGAGTCAATGGCATGCGTGACGAATGT    | 520  |  |  |  |  |  |  |
| Qy                                                             | 1455 | ACATATTTGGTGTAGGTTCCAAATATTTTGGGGAGGGTTGGTGAACCGCAAAAGTTCTTATA | 1514 |  |  |  |  |  |  |
| Db                                                             | 521  | ACATATTTGGTGTAGGTTCCAAATATTTTGGGGAGGGTTGGTGAACCGCAAAAGTTCTTATA | 580  |  |  |  |  |  |  |
| Qy                                                             | 1515 | TATCGAACTTCCACACCATACCTCATCTTCAATCCCAACCATTTATCCGTTTATTTTCTCT  | 1574 |  |  |  |  |  |  |
| Db                                                             | 581  | TATCGAACTTCCACACCATACCTCATCTTCAATCCCAACCATTTATCCGTTTATTTTCTCT  | 640  |  |  |  |  |  |  |
| Qy                                                             | 1575 | CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATCGGT     | 1634 |  |  |  |  |  |  |
| Db                                                             | 641  | CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATCGGT     | 700  |  |  |  |  |  |  |
| Qy                                                             | 1635 | TCGACCGGCTCCGAGACCCAGATGACCCGACCCAGTCTCGAGAGAGAGAGAGAGAGAGAG   | 1694 |  |  |  |  |  |  |
| Db                                                             | 701  | TCGACCGGATCCGAGACCCAGATGACCCGACCCAGTCTCGAGAGAGAGAGAGAGAGAGAG   | 760  |  |  |  |  |  |  |
| Qy                                                             | 1695 | TTGCGCATGCGAGTGGCGAGCCCTCCGTCCTCCCATGTCCTTAAGGCGCCCATCGAG      | 1754 |  |  |  |  |  |  |
| Db                                                             | 761  | TTGCGCATGCGAGTGGCGAGCCCTCCGTCCTCCCATGTCCTTAAGGCGCCCATCGAG      | 820  |  |  |  |  |  |  |
| Qy                                                             | 1755 | ATCGACCTCTCGAGATCATGTCGCAAGGACGCGCGCGGGTTCCTCTCCACGGGGGAA      | 1814 |  |  |  |  |  |  |
| Db                                                             | 821  | CTCGACCTCTCGAGATCATGTCGCAAGGACGCGCGCGGGTTCCTCTCCCGGGGGAA       | 880  |  |  |  |  |  |  |
| Qy                                                             | 1815 | ATCGGGGACAGTCTCCGACCCAGAAACCCGAGAGCACCGGTCATGCTCGACCGGATCTTC   | 1874 |  |  |  |  |  |  |
| Db                                                             | 881  | GTGCGGGCCAGTCTCCGACCCAGAAACCCGAGAGCACCGGTCATGCTCGACCGGATCTTC   | 940  |  |  |  |  |  |  |
| Qy                                                             | 1875 | CGGCTGCTGGCAGGTACTCCGTCGTCAGTGCACCTCCGCGACCTCCCGATGGCAAG       | 1934 |  |  |  |  |  |  |
| Db                                                             | 941  | CGGCTGCTGGCAGGTACTCCGTCGTCAGTGCACCTCCGCGACCTCCCGATGGCAAG       | 1000 |  |  |  |  |  |  |
| Qy                                                             | 1935 | GTGAGCGGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGGACGGG    | 1994 |  |  |  |  |  |  |

[illegible]

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Db 1541 ACTGCTACGATGCGCTTCCCAACAATGGAAGAGTGATGTTGCAGAGTGCCTACCTCCCTG 1600
Qy 2535 TGTACCCAGACACGAGCCTAGCGACCAAGAATGTGATCCACATGACATGCATCATGTGG 2594
Db 1601 TGTACCCAGACACGAGCCTAGCGACCAAGAATGTGATCCACATGACATGCATCATGTGG 1660
Qy 2595 CCCAACCCAGCGCGGGAAGAGAGGACACAGAAGAGTTCGAGGCATTTGGCCAAAGGGG 2654
Db 1661 CCCAACCCAGCGCGGGAAGAGAGGACACAGAAGAGTTCGAGGCATTTGGCCAAAGGGG 1720
Qy 2655 CGGATTTTCAGGCTTCCAAAGTCATGTCGTGGCTTTTCGGCACTCAAGTTCATGAGATTCC 2714
Db 1721 CGGATTTTCAGGCTTCCAAAGTCATGTCGTGGCTTTTCGGCACTCAAGTTCATGAGATTCC 1780
Qy 2715 TGAAGACCGCTTGATCTGCTCTCTGTCGTGATGTTTCATGTTCTTGGATTGGAAGGTC 2774
Db 1781 TGAAGACCGCTTGATCTGCTCTCTGTCGTGATGTTTCATGTTCTTGGATTGGAAGGTC 1840
Qy 2775 GTGAAGGAGCCCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTCCTCTCATAAAGGAA 2834
Db 1841 GTGAAGGAGCCCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTCCTCTCATAAAGGAA 1900
Qy 2835 ACATAAGACGACGATGATGATGCGCAAGTGGAAAGTTACAGATTGTTGTTTATGT 2894
Db 1901 ACATAAGACGACGATGATGATGCGCAAGTGGAAAGTTACAGATTGTTGTTTATGT 1960
Qy 2895 CTATAAGCTTTGAGTCTTCTGCATCTGATGTTTCACAGATGTTGTAAGCAAGCGGTAT 2954
Db 1961 CTATAAGCTTTGAGTCTTCTGCATCTGATGTTTCACAGATGTTGTAAGCAAGCGGTAT 2020
Qy 2955 ATGATGTCCTGATGATGGAATTTGATGATTTCTGCTCTCTTTTTCAGTAAATCACTT 3014
Db 2021 ATGATGTCCTGATGATGGAATTTGATGATTTCTGCTCTCTTTTTCAGTAAATCACTT 2080
Qy 3015 CGAACAAAAA 3030
Db 2081 CGAACAAAAA 2096

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RESULT 6

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; US-10-927-641-60
; Sequence 60, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2096

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; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; US-10-927-641-60

Query Match 66.7%; Score 2020.4; DB 10; Length 2096;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;

Qy 979 CTGAGCATTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTTGTGTCATAACTGT 1038
Db 41 CTGAGCATTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTTGTGTCATAACTGT 100
Qy 1039 CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATCGCCATGTTGACAAAAAGGCTGATTA 1098
Db 101 CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATCGATCATGTTGACAAAAAGGCTGATTA 160
Qy 1099 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCCCTCAGGGAAATTT 1158
Db 161 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCCCTCAGGGAAATTT 220
Qy 1159 AAGCGCCCAACCCAGATTGCAAAAGACACAAAGAGCAGCCCAACCTTTCTTCTTAAACAAG 1218
Db 221 AAGCGCCCAACCCAGATTGCAAAAGAGCAGCAAAAGAGCAGATCCAACTTTCTTCTTAAACAAG 280
Qy 1219 ATCATACACGATCGGCCAGTAAAGGTAATTAATTAATTTAAACAAATAGCTCTTGTACCGGG 1278
Db 281 ATCATACACGATCGGCCAGTAAAGGTAATTAATTAATTTAAACAAATAGCTCTTGTACCGGG 340
Qy 1279 AACTCGGATTTCTCTCATTTCAATAAACCCCTGATTAATTTGGTGGGAAAGCAGACCC 1338
Db 341 AACTCGGATTTCTCTCATTTCAATAAACCCCTGATTAATTTGGTGGGAAAGCAGACCC 400
Qy 1339 AACCACCAAAAGGTCAGATGTCATCCAC ---CAGAGAGAGAGAGAGAGAGAGAGAGAG 1394
Db 401 AACCACCAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
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Db 461 AGAGTTTTCTCTATATTTCTGGTTTCCCGGTTTGGAGTCAATGTCATGTCGTCGATGATGT 520
Qy 1455 ACATATTTGGTGTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACCCGAAAGTTCTTATA 1514
Db 521 ACATATTTGGTGTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACCCGAAAGTTCTTATA 580
Qy 1515 TATCGAACCTCCACCCATACCTCACTCAATCCCACTTCTTATCGTTTATTTTCTTCT 1574
Db 581 TATCGAACCTCCACCCATACCTCACTCAATCCCACTTCTTATCGTTTATTTTCTTCT 640
Qy 1575 CTGCTTTCTTGTCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 1634
Db 641 CTGCTTTCTTGTCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 700
Qy 1635 TCGACCGGCTCCGAGACCCAGATGACCCGACCCAAAGTCTCGGACGAGAGGCGAACCTC 1694
Db 701 TCGACCGGATCCGAGACCCAGATGACCCGACCCAAAGTCTCGGACGAGAGGCGAACCTC 760
Qy 1695 TTCCGCATGAGCTGGCGAGGCTCCGTCCTCCCATGCTCTTAAGGCGCGCATCGAG 1754
Db 761 TTCCGCATGAGCTGGCGAGGCTCCGTCCTCCCATGCTCTTAAGGCGCGCATCGAG 820
Qy 1755 ATCGACCTCTTCGAGATCATGGCCAGGCGCGGCGGCTTCTCTTCCACCGGGGAA 1814
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Qy 1815 ATCGCGCACAGCTTCCGACCCAGAACCCGAGGACCCCGTATGCTCGACCGGATCTTC 1874
Db 881 GTGCGGCGCCAGCTCCCGACCCAGAACCCCGAGGACCCCGTATGCTCGACCGGATCTTC 940
Qy 1875 CGGCTGCTGGCCAGCTACTCGTGCTCACTGACCTTCCGACCTTCCCGATGGCAAG 1934
Db 941 CGGCTGCTGGCCAGCTACTCGTGCTCACTGACCTTCCGACCTTCCCGATGGCAAG 1000
Qy 1935 GTCGAGCGGCTCTACGGCTTAGCGCGGTTGCAAGTTCTTGGTCAAGAACGAGGACGGG 1994

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|----|------|-----------------------------------------------------------------|------|
| Db | 1001 | GTGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGGTCAAGAACGAGACGGG        | 1060 |
| QY | 1995 | GTCTCCATCGCGCAGCTCAACTGTTGTAACACGAGCAAAATCTCATGGAAGCTGTAT       | 2054 |
| Db | 1061 | GTCTCCATCGCGCAGCTCAACTGTTGTAACACGAGCAAAATCTCATGGAAGCTGTAT       | 1120 |
| QY | 2055 | TACTGAAAGATGCGGTCTTGAAGCGGAATCCCATTCACCAAGCGGTACGGGATGACC       | 2114 |
| Db | 1121 | TACTGAAAGATGCGGTCTTGAAGCGGAATCCCATTCACCAAGCGGTACGGGATGACC       | 1180 |
| QY | 2115 | CGGTTCGAGTATCATGCGACCGACCGCGGATTCACCAAGATCTTTAACCGGGGAATGTCT    | 2174 |
| Db | 1181 | CGGTTCGAGTATCATGCGACCGACCGCGGATTCACCAAGATCTTTAACCGGGGAATGTCT    | 1240 |
| QY | 2175 | GATCACTCCACATTAATGAAAGATATGAAAGATATGAAACATACAGGGCTTCGAGGGCTC    | 2234 |
| Db | 1241 | GATCACTCCACATTAATGAAAGATATGAAAGATATGAAACATACAGGGCTTCGAGGGCTC    | 1300 |
| QY | 2235 | GAGACGTTGGTGTGATGTCGAGGGCGGCACTGGGGCGGTGCTCAGCATGATCGTTGCCAA    | 2294 |
| Db | 1301 | GAGACGTTGGTGTGATGTCGAGGGCGGCACTGGGGCGGTGCTCAGCATGATCGTTGCCAA    | 1360 |
| QY | 2295 | TACCCATCAATGAAAGGATCAACTTCGACCGCCCCCAACGGAATTGAAGACCCGCCCCC     | 2354 |
| Db | 1361 | TACCCATCAATGAAAGGATCAACTTCGACCGCCCCCAACGGAATTGAAGACCCGCCCCC     | 1420 |
| QY | 2355 | TTCTCTGGTGTCAAGCAGCTCGGAGCGGACATGTTGTCGAGCGTTCCTCAAGGAGATGCCA   | 2414 |
| Db | 1421 | TTCTCTGGTGTCAAGCAGCTCGGAGCGGACATGTTGTCGAGCGTTCCTCAAGGAGATGCCA   | 1480 |
| QY | 2415 | TTTTTCATGAAGTGGATATGCCATGATGAGTGCAGCAATTCGCGGAGTTCCTCAAGA       | 2474 |
| Db | 1481 | TTTTTCATGAAGTGGATATGCCATGATGAGTGCAGCAATTCGCGGAGTTCCTCAAGA       | 1540 |
| QY | 2475 | ACTGCTACGATGGCTTCCCAACATGGAAGGTGATCGTTGCGAGTGCCTACCTCCCTG       | 2534 |
| Db | 1541 | ACTGCTACGATGGCTTCCCAACATGGAAGGTGATCGTTGCGAGTGCCTACCTCCCTG       | 1600 |
| QY | 2535 | TGTAACCCAGACAGCGCTAGCGACCAAGAAATGTATCCACATCGCATGCTATGTTGG       | 2594 |
| Db | 1601 | TGTAACCCAGACAGCGCTAGCGACCAAGAAATGTATCCACATCGCATGCTATGTTGG       | 1660 |
| QY | 2595 | CCCAACACCGCGGGGAAAGAGAGACACAGAGAGTTCGAGGATTCGCGCAAGAGGG         | 2654 |
| Db | 1661 | CCCAACACCGCGGGGAAAGAGAGACACAGAGAGTTCGAGGATTCGCGCAAGAGGG         | 1720 |
| QY | 2655 | CCGGATTTAGGGGCTTCCAAAGTCAATGTCGCGCTTTCCGGCACTCAACGTCATGGATTCC   | 2714 |
| Db | 1721 | CCGGATTTAGGGGCTTCCAAAGTCAATGTCGCGCTTTCCGGCACTCAACGTCATGGATTCC   | 1780 |
| QY | 2715 | TGAAGACCGCTTGATCTGCTCCTCTGTTGGTGTATGTTTCGCGCACTCAACGTCATGGATTCC | 2774 |
| Db | 1781 | TGAAGACCGCTTGATCTGCTCCTCTGTTGGTGTATGTTTCGCGCACTCAACGTCATGGATTCC | 1840 |
| QY | 2775 | GTGAAGGAGCCCTTTCTCAGAGTTCGCTTCGCGATACCAAGTTCCTTCATAAAAGGAA      | 2834 |
| Db | 1841 | GTGAAGGAGCCCTTTCTCAGAGTTCGCTTCGCGATACCAAGTTCCTTCATAAAAGGAA      | 1900 |
| QY | 2835 | ACAATGAAGACGACTGATGATGCGCAAGTGAAGTTACAGATTTGTTGTTTATGT          | 2894 |
| Db | 1901 | ACAATGAAGACGACTGATGATGCGCAAGTGAAGTTACAGATTTGTTGTTTATGT          | 1960 |
| QY | 2895 | CTATAAAGTTTGTAGTCTTCGCATACGTATTCACAGATGCTGAACGAAACGGCGTAT       | 2954 |
| Db | 1961 | CTATAAAGTTTGTAGTCTTCGCATACGTATTCACAGATGCTGAACGAAACGGCGTAT       | 2020 |
| QY | 2955 | ATGGATGTGCTGATGATGAAATTTGTGATATTCGTCTTTTTCAGTAAATCATCTT         | 3014 |
| Db | 2021 | ATGGATGTGCTGATGATGAAATTTGTGATATTCGTCTTTTTCAGTAAATCATCTT         | 2080 |
| QY | 3015 | CGAACAAAAA 3030                                                 |      |

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|----|------|-------------------------------------------------------------|------|
| Db | 2081 | CGAACAAAAA 2096                                             |      |
| QY | 1561 | CGGTTTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAG     | 1620 |
| Db | 1621 | AGGAGAGATGGGTTCCGACCGCTCCGAGCCAGATGACCCGACCCAGCTCCGAGG      | 1680 |
| QY | 1681 | ACGAGGCAACCTTTTCGCGATGCGAGTCCGCGAGCGCTCCGCTGCTCCCGATGGTCTAA | 1740 |
| Db | 1741 | AGGAGAGATGGGTTCCGACCGCTCCGAGCCAGATGACCCGACCCAGCTCCGAGG      | 1800 |
| QY | 1801 | TCTCCACGGGGAAATCGCGGACAGCTCCGACCCAGAACCCGAGGCAACCGTCAATGC   | 1860 |
| Db | 1861 | TCTCCACGGGGAAATCGCGGACAGCTCCGACCCAGAACCCGAGGCAACCGTCAATGC   | 1920 |
| QY | 1921 | TCCCGGATGGCAAGTTCGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGTGCA  | 1980 |
| Db | 1981 | TCCCGGATGGCAAGTTCGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGTGCA  | 2040 |
| QY | 2041 | TGAAGAGTGGTATTTACTGTAAGATGCGGTCTTTGAAGCGGATCCCATTTCAACAGG   | 2100 |
| Db | 2101 | CGTACGGATGACCGGTTTCGAGTATCATGGCACCGACCCCGGATTCACAAAGATCTTTA | 2160 |

Db 541 CGTACGGGATGACCGCGTTCGAGTATCATGGCACCGACCGCGATTCACCAAGATCTTTA 600  
Qy ACCGGGGAATGTCATCACTCCACATTTACTATCAAGAAGATATCTGGAACATACAAAGG 2220  
Db ACCGGGGAATGTCATCACTCCACATTTACTATCAAGAAGATATCTGGAACATACAAAGG 660  
Qy GCTTCGAGGGCTCGAGACCGGTGTCGATGTCGAGGGCGGCACTGGGCGCGTGTCTAGCA 2280  
Db GCTTCGAGGGCTCGAGACCGGTGTCGATGTCGAGGGCGGCACTGGGCGCGTGTCTAGCA 720  
Qy TGATCGTTGCCAAATACCAATCAATGAAGGGATCACTTCGACC-GCCCAACGGATG 2339  
Db TGATCGTTGCCAAATACCAATCAATGAAGGGATCACTTCGACCCTGCTCAGCGTATG 780  
Qy AAGACGCGCCACCCCTCTCTGTGTCAAGCAGCTCGGAGGGGACATGTTCTGTCAGCGTTC 2399  
Db AAGACGCTCCACCCCTCTCTGTGTCAAGCAGCTCGGAGGGGACATGTTCTGTCAGCGTTC 840  
Qy CAAAGGAGATGCCCCATTTTCATGAAGTGGATATGCCATGCTGGAGTGACCACTTCGG 2459  
Db CAAAGGAGATGCCCCATTTTCATGAAGTGGATATGCCATGCTGGAGTGACCACTTCGG 900  
Qy CGAAGTCTCTAAGAACTCTACGATCGCTTCCCAACAATGAAGGTGATCGTTGCGAG 2519  
Db CGAAGTCTCTAAGAACTCTACGATCGCTTCCCAACAATGAAGGTGATCGTTGCGAG 960  
Qy AGTGGTACTCCCTGTGTACACAGACAGCGCTAGCGACCAAGAAATGTATCCACATCG 2579  
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Db ACTGCATCATGTTGGCCCAACCCAGCGGGGAAAGAGAGAGACACAGAAAGGATTCGAGG 1080  
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Db CATTGGCCAAAGGGCGCGGATTTTCAGGGCTTCCAAAGTCAATGCTGCGCTTCGCGCACTC 1140  
Qy ACGTCATCGAGTTCCTGAAGACCGCTTGATCTGCTCCTCTGTGGTGATGTTTCATGTTCT 2759  
Db ACGTCATCGAGTTCCTGAAGACCGCTTGATCTGCTCCTCTGTGGTGATGTTTCATGTTCT 1200  
Qy TGGATTTCAAAGGTCGTGAAGGAGCGCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTC 2819  
Db TGGATTTCAAAGGTCGTGAAGGAGCGCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTC 1260  
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Db TTCTCATAAAGGAAACAATAAGAGCGACTGTATGATGGCGCAAGTGGAAAGTTACAAGA 1320  
Qy TTTGTGTTTATGTCATTAAGTTTTCAGTCTTCGATCTGCTGATGTTTCACAGATGTT 2939  
Db TTTGTGTTTATGTCATTAAGTTTTCAGTCTTCGATCTGCTGATGTTTCACAGATGTT 1380  
Qy AACGAAACCGGCTATATGATGTCGCTGAATGATGGAATTTGTGATATTTCTGTTCTTT 2999  
Db AACGAAACCGGCTATATGATGTCGCTGAATGATGGAATTTGTGATATTTCTGTTCTTT 1440  
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Db 1441 TTCAGTAAATCACTTCGAAACAAA 1464

RESULT 8

US-10-137-036-12  
; Sequence 12, Application US/10137036  
; Publication No. US20030101478A1  
; GENERAL INFORMATION:  
; APPLICANT: Perera, Ranjan  
; APPLICANT: Rice, Stephen  
; APPLICANT: Eagleton, Clare  
; APPLICANT: Lasham, Annette  
; APPLICANT: Wood, Marion

; APPLICANT: Visser, Elizabeth  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1036c4  
; CURRENT APPLICATION NUMBER: US/10/137,036  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 661  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
; US-10-137-036-12  
  
Query Match 21.1%; Score 638.2; DB 6; Length 661;  
Best Local Similarity 98.9%; Pred. No. 4.8e-185;  
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;  
  
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Qy 1039 CGAATTTTCTCTTTAGTAAAGTAAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 1098  
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Qy 1099 GTATGATCTTGGAGTGTGTTGGTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 1158  
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Db 241 ATCATACACAGATCGGCGCAGTAAAGGTAATTAATTAATTAACAAATAGCTCTTGTACCGGG 300  
  
Qy 1279 AACTCCGTTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGTTGGGAAAGCGACAGCC 1338  
Db 301 AACTCCGTTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGTTGGGAAAGCGACAGCC 360  
  
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Db 361 AACCACCAAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
  
Qy 1395 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTCCAGTCAATGCGATCGGTGAGCAATGT 1454  
Db 421 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTCCAGTCAATGCGATCGGTGAGCAATGT 480  
  
Qy 1455 ACATATTTGGTGTAGGTTCCATATTTTTCGGGAGGGTTGGTGAACCCGCAAGTTCCCTATA 1514  
Db 481 ACATATTTGGTGTAGGTTCCATATTTTTCGGGAGGGTTGGTGAACCCGCAAGTTCCCTATA 540  
  
Qy 1515 TATCGAACTCCACCACTACCTCACTTCAATCCCACTTATTCGTTTATTTTCTTCTTCT 1574  
Db 541 TATCGAACTCCACCACTACCTCACTTCAATCCCACTTATTCGTTTATTTTCTTCTTCT 600  
  
Qy 1575 CTGCTTTCTTTTCTGCTGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1634  
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[illegible]





2247 GATGTGGAGCGGCACTGGGCGGCTGCTCAGCATGATCGTTGGCCAAATACCCATCAATG 2306  
 680 GATGTTGGTGGTGGGACTGGAGCGGCTGTTAAACACCATCGTCTCTAAATACCCCTTCAATC 739  
 2307 AAAGGGATCAACTTGA-CGCCCCCAACCGGATTGAAGCGCCCCCCTTCTTGGTGTC 2365  
 740 AAGGCAATTAATTCGATCTGCCACGCTCATTTGAGGATGCCCATCTTATCCCGAGTG 799  
 2366 AAGCAGTCGGAGCGGACATGTTGTCAGCGTTTCCAAAGGAGATGCATTTTTCATGAAG 2425  
 800 GAGCATGTTGGTGGGACATGTTTGTAGTGTGCCAAAGCAGATGCCGTTTTCATGAAG 859  
 2426 TGGATATGCGATGATGAGTGAAGCGGCTGCTTAAATTTCTTGAAGAAATTCATGAC 919  
 860 TGGATATGCGATGATGAGTGAAGCGGCTGCTTAAATTTCTTGAAGAAATTCATGAC 919  
 2486 GCGCTTCCCAACAATGGAAGGATGATGTTGAGAGTGGTACTTCTTGGTGTACCCAGAC 2545  
 920 GCGTTGCCGGAAGGCAAGGATGATGTTGAGTGGTACTTCTTGGTGTACCCAGAC 979  
 2546 ACGAGCTTAGGACCAAGATGTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605  
 980 ACAAGCTTGGCACCAGGAGTGTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039  
 2606 GCGCGGAAAGAGAGACACAGAGGAGTTCGAGGATTCGAGGATTCGAGGATTCGAGGATTCGAG 2665  
 1040 GGTGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1099  
 2666 GCGTTCACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2725  
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 2726 TGA 2728  
 1160 TAA 1162

RESULT 13  
 US-11-057-518-5  
 ; Sequence 5, Application US/11057518  
 ; Publication No. US20050166283A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chiang, Vincent Lee C.  
 ; APPLICANT: Li, Laigeng  
 ; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION  
 ; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS  
 ; FILE REFERENCE: 066040-9718  
 ; CURRENT APPLICATION NUMBER: US/11/057,518  
 ; CURRENT FILING DATE: 2005-02-14  
 ; PRIOR APPLICATION NUMBER: US/09/947,027  
 ; PRIOR FILING DATE: 2001-09-05  
 ; PRIOR APPLICATION NUMBER: 60/230,086  
 ; PRIOR FILING DATE: 2000-09-05  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1503  
 ; TYPE: DNA  
 ; ORGANISM: aspen populus tremuloides  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: AldomT; GenBank accession number: X62096  
 ; US-11-057-518-5

Query Match 20.8%; Score 631; DB 13; Length 1503;  
 Best Local Similarity 74.5%; Pred. No. 1.4e-182; Indels 1; Gaps 1;  
 Matches 807; Conservative 0; Mismatches 275;  
 1647 GAGACCCAGATGACCCGACCCAAAGTCTCGGACGACGAGGCGAACCTCTTGGCATGAG 1706  
 80 GAAACTCAGATGACTTCCAACTCAGGTATCAGATCAGATGAGGAGGACACCTCTTGGCATGCAA 139  
 1707 CTGGCGAGCGCTCGTGTCTCCCATGTCCTAAAGGCGCCATCGAGATCGACCTCTC 1766

US-10-091-009-5  
 ; Sequence 5, Application US/10091009  
 ; Publication No. US20020138870A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chiang, Vincent Lee C.  
 ; APPLICANT: Li, Laigeng  
 ; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND  
 ; TITLE OF INVENTION: COMPOSITION, AND  
 ; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS  
 ; FILE REFERENCE: 066040-9718  
 ; CURRENT APPLICATION NUMBER: US/10/091,009  
 ; CURRENT FILING DATE: 2002-03-06  
 ; PRIOR APPLICATION NUMBER: 09/947,027  
 ; PRIOR FILING DATE: 2001-09-05  
 ; PRIOR APPLICATION NUMBER: 60/230,086  
 ; PRIOR FILING DATE: 2000-09-05  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1503  
 ; TYPE: DNA  
 ; ORGANISM: aspen populus tremuloides  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: AldomT; GenBank accession number: X62096  
 ; US-10-091-009-5

Query Match 20.8%; Score 631; DB 6; Length 1503;  
 Best Local Similarity 74.5%; Pred. No. 1.4e-182; Indels 1; Gaps 1;  
 Matches 807; Conservative 0; Mismatches 275;  
 1647 GAGACCCAGATGACCCGACCCAAAGTCTCGGACGACGAGGCGAACCTCTTGGCATGAG 1706  
 80 GAAACTCAGATGACTTCCAACTCAGGTATCAGATGAGGAGGACACCTCTTGGCATGCAA 139  
 1707 CTGGCGAGCGCTCGTGTCTCCCATGTCCTAAAGGCGCCATCGAGATCGACCTCTC 1766  
 140 CTAGCAGTGTCTAGTCTTACCAATGATCTCTCAAAACAGCATTGAACCTGACCTTCTT 199  
 1767 GAGATCATGCCAAGACCGGCGGCGGCTCTCCAGCGGGAATCGCGCACAG 1826  
 200 GAAATCATGGCTAAAGCTGGCTGTCTTGTGTCACATCTGAGATGCTCTCAC 259  
 1827 CTCCCGACCCAGAACCCGAGGACCGGCTCATGCTCGACCGGATCTTCGGCTGTGGCC 1886  
 260 CTCCCTACCAAAACCTGATGCGCTGTATGATGATGATGATGATGATGATGATGATGATG 319  
 1887 AGCTACTCGTGTCTACGTGACCCCTCCGAGACCTCCCGATGGCAAGTTCGAGCGGCTC 1946  
 320 AGCTACTCCATCTTACCTGCTCTCTGAAAGATCTTCTGATGGGAGGTTGAGAGACTG 379  
 1947 TAGGCTTAGCGCGGTGTCAAGTCTTGTGTCAGAACGAGGCGGGTCTCCATCGCC 2006  
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 2007 GCATCAACTTGTAAACACGAGCAAAATCTCATGAAAGCTGTGATTAACCTGAAAGT 2066  
 440 CCTCTCTCTCATGAACACGAGCAAGGCTCTCATGAAAGCTGTGATTAATTTGAAGAT 499  
 2067 GCGGTCTTGAAGCGGAATCCCATCAACAGCGGTACGGGATGACCGGTTTCGAGTAT 2126  
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 2127 CATGGCACCGACCGGATTCACCAAGATCTTTAAACCGGGAATGTGTATCTACCTCAC 2186  
 560 CATGGCAGGATTCACCAAGTCTTCAACAGGGAATGTGTGACCACTCTTACC 619  
 2187 ATTACTATGAAGAGATCTGGAACATACAGGCTTCCGAGGCGCTTCGAGACCGGTGTC 2246  
 620 ATTACCATGAAGAGATCTTGTGAGACCTTACAAAGGCTTTGAAGGCTTCAAGCTCTTGGTG 679

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Db 140 CTAGCCAGTGTTCAGTTCTACCAATGATCCTCAAAACAGCATTGAACCTGCACCTTCTT 199
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Db 200 GAAATCATGGTAAAGCTGGCCCTGGTCTTCTTGTCACATCTGAGATAGCTTCTCAC 259
Qy 1827 CTCCGACCCAGAACCCCGAGGCACCCCGTCATGCTCGACCGGATCTTCGGCTGTGCGC 1886
Db 260 CTCCCTACCAAAACCCTGATGGCTGTCTATGTTAGACCGTATCTCTGGCTCTCTGGCT 319
Qy 1887 AGCTACTCCGTGCTCACTGTCACCTCTCGACCTCCCGACCTCCCGATGGCAAGGTGCGAGCGCTC 1946
Db 320 AGCTACTCCATCTTACCTGCTCTCTGAAGATCTTCTGTGATGGGAAGTTTGAGAGACTG 379
Qy 1947 TACGCTTAGCGCGGTGTGCAAGTCTTGTGTCAAGCAGGAGCGGGTCTCATCGCC 2006
Db 380 TATGCGCTCGCTCTCTGTTGTAATTTCTTGACCAAGAACGAGGACGGGTCTCTGTGACG 439
Qy 2007 GCACCTCAACTTGTATGAACAGGACAAATCTCTATGGAAGCTGTATTAACCTGAAGAT 2066
Db 440 CCTCTCTGCTCTATGAACAGGACAGGCTCTCTATGGAAGCTGTATTAATTTGAAGAT 499
Qy 2067 CGCGTCTCTGAAGCGGAATCCCATTTCAAGGCGTACGGGATGACCGGCTTCGAGTAT 2126
Db 500 GCAATTTCTTGATGGAGGAATTCATTTAAACAGGCTATGGGATGACTGCAATTTGAATAT 559
Qy 2127 CATGGCACCGACCGCGATTTCAACAGATCTTTAAACCGGGAATGTCTGATCATCTCAC 2186
Db 560 CATGGCACCGATCCAAAGATTTCAACAGGCTTTCAACAGGGAATGTCTGACCACTCTACC 619
Qy 2187 ATTACTATGAAGAAGATATCTGMAACATACAAAGGCTTCGAGGCGCTTCGAGACCGTGTG 2246
Db 620 ATTACCATGAAGAAGATTTCTTGAGACCTTCAAAAGCTTTGAAGGCTCACTGCTCTGGTG 679
Qy 2247 GATGTCGAGCGGCACCTGGGCGCGTGTCTCAGCATGATGCTGTGCAAAATACCCATCAATG 2306
Db 680 GATGTTGTTGTTGGGACTGGAGCGCTGCTTAAACCATCGTCTCTAAATACCCCTTCAATC 739
Qy 2307 AAAGGGATCAACTTCGA-CCGCGCCACAGGATTTGAAGCGCCACCCCTTCTCTGGTGTG 2365
Db 740 AAGGCGATTAACCTTCGATCTGCCCCACGTCATTTGAGGATGCCCCATCTTATCCCGGAGTG 799
Qy 2366 AAGCAGCTCGGAGCGGACATGTTGTCAGCGCTTCCAAAGGAGATGCCATTTTCATGAAG 2425
Db 800 GAGCATGTTGTTGGGACATGTTTGTAGTGTGCCCAAGCAGATGCCGTTTTTCATGAAG 859
Qy 2426 TGGATATGCCATGACTGGAGTGAAGCCATTTGCGCGAAGTTTCTCAAGAACTGTACGAT 2485
Db 860 TGGATATGCCATGATTGGAGCGACGCCCATCTGCTTAAATTTCTTGAAGAAATTGCTATGAC 919
Qy 2486 GCGCTTCCCAACAATGGAAGGTGATGTTGCAAGTGCATGCTCTCTGTTGTATCCAGAC 2545
Db 920 GCGTTGCGGAAAACGGCAAGGTGATATCTTGTGATGTCATTTCTCCGCTGGCTCCTGAC 979
Qy 2546 ACGAGCTTAGGACCAAGAAATGTGATCCACATGCACTGTCATCATGTTGGGCCCAACCCCA 2605
Db 980 ACAAGCCTTGCCACCAAGGGAGTGTGACAGCTGTGATGTCATCATGCTGTGGCGCACAACCCC 1039
Qy 2606 GCGCGGAAAGAGAGGACACAGAAGGATTTGAGGCTTGGCCAAAGGGGCGGGAATTTTCAG 2665
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Qy 2726 TGA 2728
Db 1160 TAA 1162
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RESULT 14

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US-10-424-599-20299
; Sequence 20299, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 20299
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118334C.1
US-10-424-599-20299
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Query Match 20.2%; Score 613.4; DB 8; Length 2037;  
Best local Similarity 72.5%; Pred. No. 4.7e-177;  
Matches 808; Conservative 0; Mismatches 306; Indels 1; Gaps 1;

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Qy 1707 CTGCGCAGAGCCCTCCGTGCTCCCATGCTCTAAAGCGCCCATCGAGATCGACCTCTC 1766
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Db 713 GAAATCATAGCAAGGCTGGCGCTGTGTTTCACTTTCCCGCTCCGACATTTGCTTCGG 772
Qy 1827 CTCCGACCCAGAACCCCGAGGCGACCGTCACTGTCAGCCGATCTTCGCGCTGCTCGCC 1886
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Db 833 TGCTACATATCTCTCTTTTCTCTCGCACTCTCCCTCATGGAAGGTTGAGAGGCTC 892
Qy 1947 TACGCTTAGCGCGGTGTGCAAGTTCCTGCTCAAGAACGAGGACGGGTCTCCATCGCC 2006
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Qy 2007 GCACTCAACTGTATGAACAGGACCAAAATCCTCATGGAAGCTGGTATTACCTGAAAGAT 2066
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Qy 2067 GCGTCTCTCAAGCGGGAATCCCATTCACAAAGCGTACCGGATGACCGGCTTCGAGTAT 2126
Db 1013 GCACTCTTGAAGGGGTATTCATTTAAACAGCATATGGAATGACAGCTTTGAATAC 1072
Qy 2127 CATGGCACCGACCGCGGATTCACAAAGATCTTTAAACCGGGAATGTCTGATCACTCAC 2186
Db 1073 CATGGAACCGGATCCAAAGGTTTAAACAAAGGTTTCAAAGGGATGGGTGATCACTCTACC 1132
Qy 2187 ATTACTATGAAGAAGTACTGGAACATACAAAGGCTTCGAGGCGCTTCGAGACCGTGTG 2246
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Qy 2247 GATGTCGAGGCGGCACTGGGCGGTGCTCAGCATGATGCTGTGCAAAATACCCATCAATG 2306
Db 1193 GATGTTGGTGAGGAACCTGGAGCTGTAGTCAACATGATGTCTCAAGATATCCCATTT 1252
Qy 2307 AAAGGGATCAACTTCGA-CCGCGCCCAACCGGATTTGAAGACGCCCCCTTTCCTGGTGTG 2365
Db 1253 AAGGCGATTAATTTTGAATTTGCCCATGTCTATTGAAGATGCCCATCTTATTCAGGAGTG 1312
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|                                                                |      |                                                               |      |
|----------------------------------------------------------------|------|---------------------------------------------------------------|------|
| Qy                                                             | 2366 | AAGCAGTCGGAGGCGACATGTTGTCAGCGTTCCAAAGGAGATGCCATTTTCATGAAG     | 2425 |
| Db                                                             | 1313 | GAACATGTTGGTGAGATATGTTGTGTCAGTGTCCAAAGCTGATGCTATTTTATGAAG     | 1372 |
| Qy                                                             | 2426 | TGGATATGCCATCAGCTGGAGTACGACCAATTTGGCGAAGTTCCTCAAGAACTGCTACCAT | 2485 |
| Db                                                             | 1373 | TGGATTTGCCACAGATTGGAGTGATGAGCACTGCTGAAGTTTGAAGAACTGCTATGAG    | 1432 |
| Qy                                                             | 2486 | GCGCTTCCCAACATGAAAGGTGATGTTGTCAGAGTGGGTACTCCTGTGTACCCAGAC     | 2545 |
| Db                                                             | 1433 | GCACTACCAATATGGAAGGTGATTTGTGGCGGAATGCAATCTCCGGTGGTCCAGAC      | 1492 |
| Qy                                                             | 2546 | ACGAGCTTAGCCACCAAGATGTATCCACATCGACTGATCATGTTGTGGCCCAACACCA    | 2605 |
| Db                                                             | 1493 | TCTAGCTTGGCCCAAAAGGTGTTGCATTCGATGTGATCATGTTGGCTCATATCCA       | 1552 |
| Qy                                                             | 2606 | GGCGGAAAGAGAGACACAGAAAGGATTCGAGGCATTTGCCAAAGGGCCGGATTCAG      | 2665 |
| Db                                                             | 1553 | GGTGGAAAGAGAGACACAGAAAGGATTTGAGGCTCTGGCCAAAGGGTCTGGATTTCCAA   | 1612 |
| Qy                                                             | 2666 | GGCTTCCAAATCATGTGTCGGCTTTCGGCACTCACGTGATGAGTTTCTTGAAGACCGGT   | 2725 |
| Db                                                             | 1613 | GGTTTCCAGATCTGTGCTGCTTTCAATACCTACGTCATGGAAATTTCTCAAAAGGTT     | 1672 |
| Qy                                                             | 2726 | TGATCTGCTCCTCTGTGTGATGTTTCATGGTTCTT 2760                      |      |
| Db                                                             | 1673 | TAAATTTCTTGGCGGTGGATTCATATCAAGTTGCAT 1707                     |      |
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| US-10-469-993-11                                               |      |                                                               |      |
| ; Sequence 11, Application US/10469993                         |      |                                                               |      |
| ; Publication No. US2004007847A1                               |      |                                                               |      |
| ; GENERAL INFORMATION:                                         |      |                                                               |      |
| ; APPLICANT: Paldi, Nitzan                                     |      |                                                               |      |
| ; TITLE OF INVENTION: METHOD OF ENHANCING ENTOMOPHILOUS        |      |                                                               |      |
| ; FILE REFERENCE: 26678                                        |      |                                                               |      |
| ; CURRENT APPLICATION NUMBER: US/10/469,993                    |      |                                                               |      |
| ; CURRENT FILING DATE: 2003-09-16                              |      |                                                               |      |
| ; NUMBER OF SEQ ID NOS: 22                                     |      |                                                               |      |
| ; SOFTWARE: PatentIn version 3.1                               |      |                                                               |      |
| ; SEQ ID NO 11                                                 |      |                                                               |      |
| ; LENGTH: 1486                                                 |      |                                                               |      |
| ; TYPE: DNA                                                    |      |                                                               |      |
| ; ORGANISM: Clarkia breweri                                    |      |                                                               |      |
| US-10-469-993-11                                               |      |                                                               |      |
| Query Match 20.2%; Score 613; DB 8; Length 1486;               |      |                                                               |      |
| Best Local Similarity 73.9%; Pred. No. 5e-177;                 |      |                                                               |      |
| Matches 804; Conservative 0; Mismatches 280; Indels 4; Gaps 2; |      |                                                               |      |
| Qy                                                             | 1645 | CCGAGACCCAGATGACCCCGACCAAGTCTTCGGACGACGAGGCGAACCTTTCGCCATGC   | 1704 |
| Db                                                             | 62   | CAGAGATCCAGATTAATCCCAACCACTCTCCGACGAGGAAGCCAACTCTTCGCCATGC    | 121  |
| Qy                                                             | 1705 | AGCTGGCGAGCGCTCCGTGTCCTCCATGTCCTTAAGCGCGCATTCGAGATCGACCTCC    | 1764 |
| Db                                                             | 122  | AGCTGGCGAGCGCGCGCTTCTCCCATGCGCTTAAGCGCGCATTCGAGATCGACCTCC     | 181  |
| Qy                                                             | 1765 | TCGAGATCMTGGCCAAAG--GAGCGCGCGCGGTTCCTCTCCACGCGGGAATTCGCG      | 1821 |
| Db                                                             | 182  | TTGAGATCATGGCAAGTTCCTCTCCAGCGGCTACATCTCTCCGGGGAGATTCGCG       | 241  |
| Qy                                                             | 1822 | CACAGCTCCGACCCAGAACCCCGAGGACCCGTCATGCTCGACCGGATCTTCGGGTGC     | 1881 |
| Db                                                             | 242  | CGAGCTTCTTACCACCAACCTCGAAGCTCCGGTGATGCTTGAACCGGTCTCCGGCTCC    | 301  |
| Qy                                                             | 1882 | TGGCCAGCTACTCCGTGTCACGTGCACCTCCGCGACCTCCCGATGGCAAGGTTCGAGC    | 1941 |
| Db                                                             | 302  | TAGCCAGCTACTCCGTGTCACGTGCACCTCCGCGACCTCCCGATGGCAAGGTTCGAGC    | 361  |
| Qy                                                             | 1942 | GGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGGACGGGGTCTCCA   | 2001 |

|    |      |                                                               |      |
|----|------|---------------------------------------------------------------|------|
| Db | 362  | GGCTGTACGGCTCGCCCTGTCTCAAGTTCTTGACCAAGAACGAGATGAGGTTTCTC      | 421  |
| Qy | 2002 | TCGCCGACATCAAACTGTATGTAACACAGGACAAATCCTCATGGAAGCTGGTATTACCTGA | 2061 |
| Db | 422  | TTGCTCTTTTTCGTCAAGGCTACCGACAAAGGTCCTTTTGGAGCCCTGTTTACTTGA     | 481  |
| Qy | 2062 | AGATGGGTCTTGAAGGCGGAATCCCATTCACAAAGCGGTACGGGATGACCGGTTTCG     | 2121 |
| Db | 482  | AGATGGGTCTTGAAGGCGGAATCCCATTCACAAAGCGGTATGGAATGAATGAATTCG     | 541  |
| Qy | 2122 | AGTATCATGTCACCGCCCGGATTCACAAAGATCTTTTAAACCGGGAATGTCTGATCACT   | 2181 |
| Db | 542  | ATTACCATGGAACAGACACAGATTCACAAAGGTGTTCAACAGGGAATGTCCAGCAACT    | 601  |
| Qy | 2182 | CCACATTTATGAAGAAGATATCTGGAACATATCAAGGCTTCGAGGGCTTCGAGCCG      | 2241 |
| Db | 602  | CTACCATCATCATGAAGAAGATCTTGAATGTATCAACCGATTCGAGGGCTTAAACAGA    | 661  |
| Qy | 2242 | TGCTCGATGTCGAGGCGGCACTGGGGCCGTCTCAGCATGATCGTTTGCCTTCCATATCCAT | 2301 |
| Db | 662  | TTGTCGATGTTGGGGCGGTACAGTCCGCTGGCTAGCATGATTTGTCTAAGTATCTCT     | 721  |
| Qy | 2302 | CAATGAAGGATCAACTTTCGACC-GCCCCAAACGATTTGAAGACGCCACCCCTTCTCG    | 2360 |
| Db | 722  | CCATCAACGCCATCAACTTCGACCTCACTGTTTTCAGGATGCTCCAGCTTTTCTG       | 781  |
| Qy | 2361 | GTGTCAGCACGTTCGAGGCGACATGTTGTCAGCGTTTCCAAAGGGAGATGCTTTCAT     | 2420 |
| Db | 782  | GTGTTGAACATCTTGGAGGAGATGTTTGTATGCGGTACCCAAAGGCGAGCTATATTC     | 841  |
| Qy | 2421 | TGAAGTGGATATGCGATGACAGACCAATTTGGCGGAAGTTCTCTCAAGAACTGCT       | 2480 |
| Db | 842  | TCAAGTGGATTTGCCACGACTGGAGCGATGAGCATTTGCTGAAGTTGCTGAAAACCTGCT  | 901  |
| Qy | 2481 | ACGATGCGCTTCCCAACATGGAAGGTGATCGTTTGCAGAGTGGGTACTCCCTGTGTACC   | 2540 |
| Db | 902  | ATGCTGCACTTCCCGACCATGGCAAGGTTCATTTTGCAGATACATCTTCTCCGTCTC     | 961  |
| Qy | 2541 | CAGACACGAGCTTAGCGACCAAGAAATGTATCCATCGACTGCACTGATCATGTGGCCACA  | 2600 |
| Db | 962  | CTGACCCGAGTATCGCCACCAAGGTAGTTCATCATACCGACGCTCATGTGGCTTACA     | 1021 |
| Qy | 2601 | ACCCAGCGGGAAGAGAGGACACAGAAAGGTTCGAGGCAATTTGGCCAAAGGGCGCGAT    | 2660 |
| Db | 1022 | ACCCAGCGGGAAGAGAGGACCTGAGAAAGGTTCAGGCTTTGGCTATGGCTTCGCGAT     | 1081 |
| Qy | 2661 | TTCAGGGCTTCCAAAGTCACTGTGCTGCGCTTTTCGGCACTCACTCATGAGGATTCCTGA  | 2720 |
| Db | 1082 | TCAGGGGTTTCAAGGTAGCATCTTGTGCTTCAACACTTACGTCATGGAGTTCTCAAAA    | 1141 |
| Qy | 2721 | CCGCTTGA 2728                                                 |      |
| Db | 1142 | CCGCTTAA 1149                                                 |      |

Search completed: November 1, 2006, 14:26:09  
Job time : 3878.36 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:48:44 ; Search time 657.143 Seconds  
(without alignments)  
8946.617 Million cell updates/

Title: US-10-702-319A-113 COPY 41 3070

Perfect score:

Sequence: 1 cacctgttcagtttgattcc.....acttcgaacacaaaaaaaaa 3030

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2461376 seqs, 970166171 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Local processing: Minimum Match 0% Maximum Match 100%

## Listing first 45 summaries

Database : Published Applications NA New:\*

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8: /ENC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1.*
9: /ENC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
10: /ENC_Celerra_SIDS3/ptodata/2/pubpna/US6_NEW_PUB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1429.6	47.2	1630	7	US-11-397-533-107	Sequence 107, App	
2	610.6	20.2	1410	8	US-11-216-545-7471	Sequence 7471, Ap	
3	566.4	18.7	1266	9	US-11-174-307B-477	Sequence 477, App	
4	566.4	18.7	1266	9	US-11-056-355B-22559	Sequence 22559, A	
5	564.8	18.6	1394	6	US-10-953-349-3948	Sequence 3948, Ap	
6	564.8	18.6	1394	9	US-11-174-307B-2145	Sequence 2145, Ap	
7	564.8	18.6	1394	9	US-11-056-355B-36626	Sequence 36626, A	
8	485	16.0	1485	8	US-11-229-858-78	Sequence 78, Appl	
9	437.6	14.4	1425	6	US-10-449-902-14143	Sequence 14143, A	
10	419.6	13.8	1522	9	US-11-056-355B-5836	Sequence 5836, Ap	
11	418	13.8	1227	6	US-10-449-902-4559	Sequence 4559, Ap	
12	404	13.3	1219	6	US-10-532-464-1	Sequence 1, Appli	
13	398.2	13.1	1531	9	US-11-056-355B-5315	Sequence 5315, Ap	
14	391.4	12.9	421	7	US-11-397-533-24	Sequence 24, Appl	
15	391	12.9	407	7	US-11-397-533-106	Sequence 106, App	
16	388	12.8	1024	8	US-11-216-545-7470	Sequence 7470, Ap	
17	345.2	11.4	608	7	US-11-292-078-17322	Sequence 17322, A	
18	306	10.1	306	8	US-11-229-856-80	Sequence 80, Appl	
19	294.2	9.7	1366	6	US-10-953-349-20948	Sequence 20948, A	
20	283.2	9.3	1387	6	US-10-953-349-13681	Sequence 13681, A	
21	264.6	8.7	1228	9	US-11-056-355B-26750	Sequence 26750, A	
22	261.6	8.6	1302	8	US-11-216-545-6368	Sequence 6368, Ap	
23	259.4	8.6	1744	7	US-11-397-533-51	Sequence 51, Appl	

ALIGNMENTS

RESULT 1

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US-11-397-533-107
; Sequence 107, Application US/11397533
; Publication No. US2006018395A1
; GENERAL INFORMATION:
; APPLICANT: Blockberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c6
; CURRENT APPLICATION NUMBER: US/11/397,533
; CURRENT FILING DATE: 2006-04-03
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/143,833
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/615,192
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 10/174,693
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 407
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-107

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Query Match 47.2%; Score 1429.6; DB 7; Length 1630;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1449: Conservative 0; Mismatches 14; Indels 1; Gaps 1;

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Qy	1621	AGCAGAGATGGGTTTCGACCGGCTCCGAGACCCAGATGACCCGACCCAAAGTCTCGGACG	1680
Db	61	AGCAGAGATGGGTTTCGACCGGATTCGAGACCCAGATGACCCGACCCAAAGTCTCGGACG	120
Qy	1681	ACGAGGCGAACCTCTTTCGCCATCAGCTGGCAGCGCTCCGTCGCTCCCATCGTCTCTAA	1740

121 AGGAGCGGAACCTTTTCGCGCATGACGCTGGCGAGCGCCCTCCGTGCTCCCGATGCTCTCA 180
1741 AGCGCGCATCGAGATCGACCTCTCGAGATCATGGCCAAAGACGGCGCGCGGTTC 1800
181 AGCGCGCATCGAGCTCGACCTCTCGAGATCATGGCCAAAGACGGCGCGCGGTTC 240
1801 TCTCCACGGGGGAAATCGGGGACAGCTCCGACCCAGAACCCCGAGGACCGGTTCAGC 1860
241 TCTCCCGGGGAAATCGGGGACAGCTCCGACCCAGAACCCCGAGGACCGGTTCAGC 300
1861 TCGACCGGATCTTCGGCTGCTGGCGAGCTACTCCGTGCTCAGCTGCACTCCCGGACC 1920
301 TCGACCGGATCTTCGGCTGCTGGCGAGCTACTCCGTGCTCAGCTGCACTCCCGGACC 360
1921 TCCCGGATGCGAGGTCGAGCGGCTCTACGGCTTAGCGCGGTGTCGAAAGTTCGCTCA 1980
361 TCCCGGATGCGAGGTCGAGCGGCTCTACGGCTTAGCGCGGTGTCGAAAGTTCGCTCA 420
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2041 TGGAAAGCTGTAATTAACCTGAAAGATCGGTCTCTTGAAGCGGAAATCCCAATCAAGG 2100
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2161 ACCGGGAAATGTCGATCACTCCACATTAATGTAAGAAATGATCTGAAACATACAAAG 2220
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961 AGTGGTACTCCCTGTGTACCAAGACGAGCTAGGACCAAGATGATGATGATGATGATGATG 1020
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1321 TTGTGTTTATGCTATATAAGTTTTCAGTCTTCTGCATATCTGATTTCAAGAAATGTGT 1380
2940 AACGAAACGCGGTATATGATGTCCTGAAATGATGAAATTTGATATTTCTGCTTCTTT 2999
1381 AACGAAACGCGGTATATGATGTCCTGAAATGATGAAATTTGATATTTCTGCTTCTTT 1440
3000 TCCAGTAAATCACTTCGAACAAA 3023
1441 TCCAGTAAATCACTTCGAACAAA 1464

RESULT 2
US-11-216-545-7471
; Sequence 7471, Application US/11216545
; Publication No. US20060135758A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO Technology, LLC
; APPLICANT: McLaird, Paul L
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53659)B
; CURRENT APPLICATION NUMBER: US/11/216,545
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: US 60/606,062
; PRIOR FILING DATE: 2004-08-31
; NUMBER OF SEQ ID NOS: 8783
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7471
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Glycine max
US-11-216-545-7471

Query Match 20.2%; Score 610.6; DB 8;
Best Local Similarity 72.0%; Pred. No. 3.2e-166;
Matches 810; Conservative 0; Mismatches 314; Indels 1; Gaps 1;

1645 CCAGACCCAGATGACCCGACCCCAAGTCTCGAGACGAGCGGAACTCTTCGCCATGC 1704
73 CTGAGACTCAGATTACTCCAAACCATGTATCTGATGAAGAGGCAAACTTTTGGCATGC 132
1705 AGCTGGGAGCGCTCCGTGCTCCCATGCTCTTAAAGCCGCCATCGAGATCGACCTCC 1764
133 AACTAGCAGTGCCTCTGACTCTCCCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 192
1765 TCGAGATCATGGCCAAAGGACCGGCGCGGCGGTCTCTCCACGGGGGAAATCGCGGAC 1824
193 TGGAAATCATAGCCAGGCTGGCCCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 252
1825 AGCTCCGACCCAGAACCCCGAGGACCCGTCTGCTGATGCTCGACCGGATCTTCCGGCTGCTGG 1884
253 AGCTTCCAAACACACAAACCCCTGATGACCCCGTTATGTTGGACCCGATTTTGGCGCTCTTGG 312
1895 CAGGCTACTCGTCTCAGCTGACCCCTCCGCGACCTCCCGGATGCGCAAGGTGAGCGGC 1944
313 CTGCTCAAAATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 372
1945 TCTACGGCTTAGCGCGGTGTCGAAAGTCTTGGTCAAGAACGAGGACGGGTCTCCATCG 2004
373 TCTATGCTCTGCGCCCGCTTCTTAAAGTACCTGCTGTCGAGACCGAGATGCTGCTTCTTCT 432
2005 CCGCATCACTGATGTAACGAGGACAAATCTCATGAAAGCTGCTATTTACCTGAAAG 2064
433 CTGCTCTTAACTATGAAACGAGGACAAAGTCTCTCATGAAAGCTGCTTCTTCTTCTTCTTCT 492

Thu Nov 2 13:35:57 2006

1825 AGCTCCGACCCAGAACCCCGAGGACCCGTCATGCTCGACCGGATCTTCGGGTGCTGG 1884
 266 AACTTCCGACCAAAACCCCTGAAAGCTCCGTCATGCTCGACCGTATCTCTCGTCTTCTTA 325
 1885 CCAGCTTACTCCGTCGTCACGTCGACCCCTCCGCGACCTCCCGATGGCAGGTCGAGCGGC 1944
 326 GCTCTTACTCCGTCCTAACTGCTCAAACCGTAAACTTTCGGGTGATGGCGGTGAACCGGA 385
 1945 TCTACGGCTTAGCGCGGTGTCAGAGTCTTGGTCAAGAACGAGGACGGGTCTCCATCG 2004
 386 TTTACGGGCTTGCTCGGTTTGGAAATTTGACCAAGATTTGACCAAGATGGTGTTCCTCAATG 445
 2005 CCCACTCAACTTGTATGAACACGAGCAAAATCCTCATGAAAGCTGGTATACCTGAAAG 2064
 446 CTGCTCTTTGTCTTATGAACCAAGACCAAGGTTCTCATGAAAGCTGGTATACCTGAAAG 505
 2065 ATGCGGTCTTGAAGCGGGAATCCCAATTCAAAGGCGTACGGGATGACCGGTCGAGT 2124
 506 ATGCAATTTCTGATGGGATTCCTCAACAGGCTTATGGAATGAGCGGTCGAGT 565
 2125 ATCATGCGACCGACCGCGGATTCAAAGATCTTTAAACCGGGGAATGTCTGATCACTCA 2184
 566 ACCACGGGACTGACCTTAGATTCACCAAGGCTTTTAAACATGGAATGTCTAACCATTTCA 625
 2185 CCATTACTATGAAGAGATATCTGAAACATACAGGGCTTCGAGGCGCTCGAGACCGTGG 2244
 626 CAATCACCATGAAGATTTCTGAGACCTTAAAGGTTTTGAAGGATTCGATCTCTTTGG 685
 2245 TCGATGTCGAGGCGGCACTGGGCGCTGTCTGACGATGATCGTTGGCAATACCCATCAA 2304
 686 TTGATGTTGGTGGGCAATGGTGTCTACATCAAAATGATTGTCTCCAAAGTACCCTAATC 745
 2305 TGAAAGGATCAACTTCGACCGCCC - CAACGGATTTGAAGCGGCGCCACCCCTCTCTGGT 2363
 746 TTAAGGCGATCACTTTGATCTCCACATGTCTTGAAGATGCTCTCTCATCTGCTGTA 805
 2364 TCAAGCAGTCGAGGCGACATGTCGTCAGCGTTCCAAAGGAGATGCCATTTTCATGA 2423
 806 TTGAGCATGTTGGGAGATATGTTTGAAGTGTCCCTTAAAGGTGATGCCATATTCATGA 865
 2424 AGTGGATATGCCATGCTGAGTGAACCAATTCGCGCAAGTTCCTCAAGAACCTGCTACG 2483
 866 AGTGGATATGCTGATGCTGAGTGAACCAATTCGCGCAAGTTCCTCAAGAACCTGCTACG 925
 2484 ATGCGCTTCCCAACATGAAAGGTCATGCTGTCAGAGTGGCTACTCCCTGTGTACCCAG 2543
 926 AGTCACTTCCAGAGGATGAAAGTGAATATGACGAGTGTATATCTCCAGAGACACAG 985
 2544 ACACGAGCTTAGCGACCAAGAAATGTGATCCATCGATCATGTTGGCCCAACAC 2603
 986 ACTCAAGCTTCAACCAACCAAGTAGTCCATGTCGATTTATGTTGGCTCAATC 1045
 2604 CAGCGGGAAGAGAGACACAGAGGATTCGAGGCAATTTGGCCAAAGGGCGGATTTTC 2663
 1046 CCGGAGGCAAGAAACCAACCGAAGAGATTTGAGGCATTTAGCCAAAGCATCAGGCTTCA 1105
 2664 AGGCTTCCAGTCATGCTGCGCTTTGCGCACTCAGCTCATGAGTTCCTGGAAGACCG 2723
 1106 AGGCGATCAAGTGTCTGCGAGCGCTTTTGGTGTAAACCTTATTGATTTACTCAGAGC 1165
 2724 CTTGATCTGCTCTCTGCTGGTGTGATTTTCATGGTT 2757
 1166 TCTAAACAAACAAATGTTCTTATGAAGATGATT 1199

RESULT 5
 US-10-953-349-3948
 ; Sequence 3948, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; TITLE OF INVENTION: ENCODED THERBY

2484 ATGCGCTTCCCAACATGAAAGGTGATGTTGTCAGAGTGGTACTCCTGTGTACCCAG 2543
 926 AGTCACTTCCAGAGGTGAAAGTATATTAGCAGAGTGTATATCTCCAGAGACACCG 985
 2544 ACACGAGCTTAGCGACCAAGATGATCCATCGACTGATCATGTTGGGCCCAACAC 2603
 986 ACTCAAGCTTCTCAACCAACAAAGTAGTCCATGTCGATTCGATTTATGTTGGCTCAATC 1045
 2604 CAGCGGGAAGAGAGACACAGAGTTCGAGGATTTGAGGCAATTTAGCCAAAGCATCAGGCTTCA 1105
 1046 CCGGAGGCAAGAAACGACCGAAGAGTTCGAGGCAATTTAGCCAAAGCATCAGGCTTCA 1105
 2664 AGGCTTCCAGTCATGCTGCGCTTTTGGCACTCAGCTCATGAGTTCCTGGAAGACCG 2723
 1106 AGGCGATCAAGTGTCTGCGAGCGCTTTTGGTGTAAACCTTATTGATTTACTCAGAGC 1165
 2724 CTTGATCTGCTCTCTGCTGGTGTGATTTTCATGGTT 2757
 1166 TCTAAACAAACAAATGTTCTTATGAAGATGATT 1199

US-11-056-355B-22559
 ; Sequence 22559, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; PRIOR FILING DATE: 2005-02-14
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 22559
 ; LENGTH: 1266
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1266)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12338255
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1266)
 ; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 14304148
 ; OTHER INFORMATION: as cited in SEQ ID NO 57313
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1266)
 ; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13598513
 ; OTHER INFORMATION: as cited in SEQ ID NO 64102
 ; OTHER INFORMATION: as cited in SEQ ID NO 64102
 ; US-11-056-355B-22559

Query Match 18.7%; Score 566.4; DB 9; Length 1266;
 Best Local Similarity 70.6%; Pred. No. 2e-153;
 Matches 786; Conservative 0; Mismatches 321; Indels 7; Gaps 2;

1645 CCGAGACCGAGTACCCGACCAAGTCTCGAGACGAGGCGAAGCTCTTCGCCATGC 1704
 92 CCGAGACCAATTAATCTCCGTTGCAAGTACCGACGAGAGCTGCTTCGCCATGC 151
 1705 AGCTGCGAGCGCTCCGTCGTCCTCCCATGTCCTTAAGGCGCGCATCGAGTCGACCTCC 1764
 152 AACTAGCAGTCTCGTCTCTTCGATGGCTTTAAATCCGCTTAGAGCTTACCTTC 211
 1765 TCGAGATCATGCCAAGAGCGGCGGCTTCTCTCCACGGGGAAATCCGCGCAC 1824
 212 TTGAGATTTATGGCAAGATGTTCTTCCATGCTCTCTACC-----GAGATCGCTCTA 265

2305	Qy	TGAAGGAGTCACTTCGACGGCCC - CAACGAGATTGAAGACGCCCAACCCCTTCCTGGT	2363
788	Db	TTAAAGGATCAACTTTTGATCTCCACATGTCATCGAAGATGCTCTTCTCATCTCGGTA	847
2364	Qy	TCAAGACGTCGGAGGCGCATGTTGCTCAGCGTTCCAAAGGGAGATGCCATTTTCATGA	2423
848	Db	TTGAGCATGTTGGAGGAGATATGTTTGAAGTGTCCTTAAAGGTGATGCCATATTTCATGA	907
2424	Qy	AGTGGATATGCGATGATCGGAGTGACGACCAATTGCGCGAAGTTCCTCAAGAACTGCTACG	2483
908	Db	AGTGGATATGTCATGACTGGAGTGACGAACATTTGCGTGAATACTTTGAAGAACTGCTACG	967
2484	Qy	ATCGCTTCCCAACAATGGAAAGGTGATCGTTGCAGAGTCGGTACTCCCTGTGTACCACG	2543
968	Db	AGTCACATTCAGAGGATGGAAAGTGAATTTTAGCAGAGTGATATCTTCCAGAGACACG	1027
2544	Qy	ACACGAGCTAGCGACCAAGAATGTGATCCACATCGACTGCATCATGTTGGCCCCACAAC	2603
1028	Db	ACTCAAGCCTCTCAACCACAAAGTAGTCCATGTCGATTGCATTTATGTTGGCTCACAATC	1087
2604	Qy	CAGCGGGAAGAGAGACACAGNAGAGTTCGAGGCAATTGGCCAAAGGGGCCGGAATTC	2663
1088	Db	CCGAGGCCAAGAAACGAACCCGAGAAAGAGTTTGAGGCAATTAGCCAAAGCATCAGGCTTCA	1147
2664	Qy	AGGCTTCCAAAGTCACTGCTGGCGTTTCGGCACTCACGTCATGGAGTTCCTCGAAGACCG	2723
1148	Db	AGGGCATCAAGTTGCTCGACGCTTTTGGTGTAACTTATTGAGTTTACTCAAGAAC	1207
2724	Qy	CTTGATCTGCTCCTCTGCTGGTGATGTTTCATGGTT	2757
1208	Db	TCTAAAAACAAACAAATGTTCTCTATGAAGATGATT	1241

RESULT 8

US-11-229-856-78
; Sequence 78, Application US/11229856
; Publication No. US20060130183A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: ROTTMANN, WILLIAM H.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: SANDERS, PAUL
; APPLICANT: ZHANG, GARY
; APPLICANT: FITZGERALD, SANDRA JOANNE
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
; FILE REFERENCE: 044463-0441
; CURRENT APPLICATION NUMBER: US/11/229,856
; CURRENT FILING DATE: 2005-09-20
; PRIOR APPLICATION NUMBER: 10/946,650
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 10/946,644
; PRIOR FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 78
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-229-856-78

	Query Match	16.0%;	Score 485;	DB 8;	Length 485;
	Best Local Similarity	100.0%;	Pred. No. 4,6e-130;		
	Matches 485;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1119	GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATTTAAGCGCCAACCCAGATTGC	1178		
Db	1	GTGCAAAATTTTGAAGCTGACGATGGCCCTCAGGGAATTTAAGCGCCAACCCAGATTGC	60		
Qy	1179	AAAGAGCACAAAGAGCAGCAAGCCAAACCTTTCTTTAAACAAGATCATCAACAGATCGGCCAG	1338		
Db	61	AAAGAGCACAAAGAGCAGCAAGCCAAACCTTTCTTTAAACAAGATCATCAACAGATCGGCCAG	130		

Qy	1239	TAAGGGTAATATTAATTTAA	CAAAATAGCTCTTG	TACGGGAAC	TCCGTA	TTTCTCTCACT	1298
Db	121	TAAGGGTAATATTAATTTAA	CAAAATAGCTCTTG	TACGGGAAC	TCCGTA	TTTCTCTCACT	180
Qy	1299	TCCATAAACCCCTGATTAA	TTTGGTGGGAAAGCGA	CAGCCAA	CCCAAAAGGTCAGATG	1358	
Db	181	TCCATAAACCCCTGATTAA	TTTGGTGGGAAAGCGA	CAGCCAA	CCCAAAAGGTCAGATG	240	
Qy	1359	TCATCCACGAGAGAGAGAG	GAGAGAGAGAGAGAG	GAGAGAG	AGAGAGAGAGAGAGAG	1418	
Db	241	TCATCCACGAGAGAGAGAG	GAGAGAGAGAGAGAG	GAGAGAG	AGAGAGAGAGAGAGAG	300	
Qy	1419	TCACCGGTTGGAGTCAAT	TGCGATGCGTGACGA	ATGTACAT	ATTGGTGTAGGGTCCAAATAT	1478	
Db	301	TCACCGGTTGGAGTCAAT	TGCGATGCGTGACGA	ATGTACAT	ATTGGTGTAGGGTCCAAATAT	360	
Qy	1479	TTTTCGGGAGGGTTGGTGA	ACCGCAAGTTCCCTAT	TATATCGAA	CCCTCCACCAACATACCT	1538	
Db	361	TTTTCGGGAGGGTTGGTGA	ACCGCAAGTTCCCTAT	TATATCGAA	CCCTCCACCAACATACCT	420	
Qy	1539	CACCTCAATCCCAACCAAT	TTTATCCGTTTATTTAT	TTCTCTCTGCTTTT	CCCTTTGCTCGAGTCTCG	1598	
Db	421	CACCTCAATCCCAACCAAT	TTTATCCGTTTATTTAT	TTCTCTCTGCTTTT	CCCTTTGCTCGAGTCTCG	480	
Qy	1599	CGGAA	1603				
Db	481	CGGAA	485				

RESULT 9
 US-10-449-902-14143
 ; Sequence 14143, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14143
 ; LENGTH: 1425
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: AK064768
 ; DATABASE ENTRY DATE: 2001-12-06
 ; US-10-449-902-14143

RESULT 9

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US-10-449-902-14143
; Sequence 14143, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14143
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK064768
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-14143

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	Query Match	14.4%	Score 437.6;	DB 6;	Length 1425;
	Best Local Similarity	66.0%;	Pred. No. 5.3e-116;		
	Matches 706;	Conservative 0;	Mismatches 339;	Indels 25;	Gaps 4;
Qy	1675	CGACGACGAGGCGGAACCTCTTCGCCATCCAGCTGCGGAGCGCTCCGTGCTCCCCCATGG	1734		
Db	117	CCGACGAGGAGGGTGCATGTACGCGCTCAGCTGGCGTCTCGTGCATCTCTGCCCATGA	176		
Qy	1735	TCCTAAAGGCGCGCATCGAGATCGACTCTCTCGAGATCATGGCCAAAGGAC	1784		
Db	177	CGCTCAGAACGCATCGAGCTGGGCTGCTCGAGACGCTGCAGTCCGCGCGCTCGCGG	236		
Qy	1785	-----GGCGCGGCGCGTTCTCTCCACGCGGGGAATTCGGGCACAGCTCCCGACCC	1836		
Db	237	GAGGAGGGGGAAGCGGCGCTCTCAGCGCGCGGAGGTGGCCGACAGCTCCCGTCCA	296		

Db 800 CGGGGTCAACTTCGACCTGCGCACGTCACTCTCCGAGGCGCGCGTTCCCGGGGTGCG 859
Qy 2368 GCACCTCGGAGCGCATGTTTGGTTCAGCGTTCCAAAGGAGATGCCATTTTCATGAAGTG 2427
Db 860 CCACGTGGCGGGGACATGTTTCGCGTCCGTCGCGCGCGGACGCGCATCTCTCATGAAGTG 919
Qy 2428 GATATGCCATGACTGAGTGACGACCATTTGCGCGAAGTTCTCAAGAACTGCTACGATGC 2487
Db 970 GATCTTCAAGCTGAGGAGCGCGCATCTGCGCCACGCTGCTCAAGAACTGCTACGACGC 979
Qy 2488 GCTTCCCAACAATGGAAGGATGATCGTTGCGAGAGTGCCTGCTGTGTATCCCAAGACAC 2547
Db 980 GCTGCGCGAAATGCAAGGTCACTGCTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1039
Qy 2548 GAGCTAGCGACCAAGATGATCCATCGACTGATCATGTTGGGCGCCCAACCCAGG 2607
Db 1040 CACCCCAAGGCGGAGCGGCGTCTTCCAGTGCATGATCATGCTCGGCGCAACCCCGG 1099
Qy 2608 CGGAAAGAGAGGACACAGAAGGAGTTGAGGCAATGGCCAAAGGGCGGATTTTCAGGG 2667
Db 1100 CGGAGAGCGGTACGAGCGGAGTTCCGCGAGCTCGCAAGGCGCGGCTTCTCCGG 1159
Qy 2668 GTTCAAGTCAATGCTGCTGCTGCTTTCGCGCACTCACTCATGAGTTCCTGAAG 2719
Db 1160 GTTCAAGGCCACCTGCATCTACGCCAACCGCTGGGCCCATCGAGTTTCATCAAG 1211

RESULT 11

US-10-449-902-4559
; Sequence 4559, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4559
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK061859
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-4559

Query Match 13.8%; Score 418; DB 6; Length 1227;

Best Local Similarity 67.4%; Pred. No. 2.4e-110;
Matches 635; Conservative 0; Mismatches 300; Indels 7; Gaps 3;
Qy 1785 GGGCGGGCGCGTCTCTCCACGGGGGAAATCGCGCACAGCTCCCGACCCA---GAAC 1841
Db 43 GGAAGGGCGGCGCTGCTACGCGCGGGAGGTGGCGGACAGCTCGCTCCNAGGCGAAC 102
Qy 1842 CCCGAGGACCCGTCATGCTCGACCGGATCTTCGCGCTGCTGGCGAGTACTCCGTCGTC 1901
Db 103 CGGCGGGCGCGGACATGTGACCGCATGCTCCGCGCTGCTCGCTCTCTACAACTGCTC 162
Qy 1902 AGCTGCACCTCCGCGACCTCCCGATGGCAAGGTTCGAGCGGCTCTACGGCTTAGCGCG 1961
Db 163 AGGTGCGAGATGAGGAGGGGGCGCCGACGCAAGCTCTCCCGCGCTACGCGCGCGCGCG 222
Qy 1962 GTGTGCAAGTCTTGTGTCAGAACGAGGAGGGGTCTCCATCGCGCACTCACTTGATG 2021

Db 223 GTGTGAAGTGGCTGACGCGCCCAACGAGGACGCGCTCTCCATGGCGCGCTCGCCCTCATG 282
Qy 2022 AACGAGGACAAATCTCTCATGGAAGCTGGTATTACCTGAAGATGCGGTCTCTTGAAGGC 2081
Db 283 AACGAGGACAAAGTCTCTCATGAGAGCTGGTACTACCTTAAGGACGCACTCTCGACGCG 342
Qy 2082 GGAATCCCATTCACAAAGGCGTACGGGATGACCGGTTTCGAGTATCATGGCACGACCGCG 2141
Db 343 GGCATCCGTTTCAACAAGGCGTACGGGATGACGGGTTTCGAGTACCACGCGACGAGCGCC 402
Qy 2142 CGATTCAACAAGATCTTTAAACCGGGAAATGCTCATCTCCACCATTTACTATGAAGAAG 2201
Db 403 CGCTTCAACCGCTCTTCAACGAGGCGATGAAGAACCACTCCGTCTCATCAACAAGAAG 462
Qy 2202 ATACTGGAACATACAGGCGCTTCGAGGCGCTCGAGACCGGTGCTGATGTCGAGGCGGC 2261
Db 463 CTGCTCGACCTCTACACCGGCTTCGAGCGCGCTTCACCGCTGCTCGAGCTCGGCGCGCG 522
Qy 2262 ACTGGGCGCGTCTCAGCATGATGTTGCCAAATACCCATCAATGAAGGATCAACTTC 2321
Db 523 GTGGGCGCACTGTGGCGCGCTGCTCTCCGCGCACCGGCACATCCGCGGGATCAACTAC 582
Qy 2322 GACGCGCCCAACG-GATTGAAGACGCGCCACCTTCTCTGCTGTCAAGACAGCTCGGAGGC 2380
Db 583 GACCTCCCGCACGTCATCTCCGAGGCGCGCGCTTCCCGGGGTGGAGCACGTCGGCGCGC 642
Qy 2381 GACATGTTCTGTCAGCGTTCC---AAAGGAGATGCCATTTTCATGAAGTGCATATGCCAT 2437
Db 643 GACATGTTTCGCTCTCCGCGCGCGGCGACGCCATCTCTGATGAAGTGCATCTCTCCAC 702
Qy 2438 GACTGGAGTACGACCACTTTCGCGCAAGTTCTCTCAAGAACTGCTACGATGCGCTTCCCAAC 2497
Db 703 GACTGGAGCGGACGACACTGCGCGCGCTGCTCAAGAACTGCTACGACGCGCTGCGGAG 762
Qy 2498 AATGGAAGGTGATGCTGTTGAGAGTGGCTACTCTCCTGTGTACCCAGACACAGGCTAGCG 2557
Db 763 CACGGGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 822
Qy 2558 ACCAAGATGTGATCCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2617
Db 823 GAGCAGGGGGTGTTCACGTCGACATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Qy 2618 AGGACACAGAAGGAGTTCGAGGCAATGGCCAAAGGGCGCGGATTTTCAGGGCTTCCAGTC 2677
Db 883 AGGTACGAGGAGGAGTTCAGGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 942
Qy 2678 ATGTGCTCGCGCTTTCGCGCACTCAGCTCATGAGTTCCTGAAG 2719
Db 943 ACCTACATCTACGCCAACGCGCTGGGCCATCGAGTTCCACCAAG 984

RESULT 12

US-10-532-464-1
; Sequence 1, Application US/10532464
; Publication No. US20060172402A1
; GENERAL INFORMATION:
; APPLICANT: Hawkin-Frenkel, Daphna
; APPLICANT: Zylstra, Gerben J.
; APPLICANT: Frenkel, Chaim
; APPLICANT: Belanger, Faith
; TITLE OF INVENTION: PRODUCTION OF VANILLIN IN MICROBIAL CELLS
; FILE REFERENCE: RUCC-0064
; CURRENT APPLICATION NUMBER: US/10/532,464
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/412,649
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: PCT/US2003/034011
; PRIOR FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1219

TYPE: DNA
; ORGANISM: Vanilla planifolia
US-10-532-464-1

Query Match
Best Local Similarity 13.3%; Score 404; DB 6; Length 1219;
Matches 700; Conservative 59.5%; Pred. No. 2.7e-106; Indels 1; Gaps 1;

1666 CCACAGTCTCGGACGACGAGCGGAACTCTTTCGCCATGAGTGGGAGCGGCTCGTGC 1725
Db 1004 AGAAGAGTTTAAAGAAATGGCTATGCTATCTGGTTCTCTAAATTCAGGCACTTTTA 1063
QY 2685 GCGCTTTTCGGCACTCAAGTTCATGAGTTCCTGAAAGCCGCTGATCTGCTCTCTGTGT 2744
Db 1064 GTTATGCTAATGTTTGGGTTCATGGAATTCACAAATAGTAATCTTGAACCTCCATATGT 1123
QY 2745 GATGTTTCATGTTCTTGGATTTGAAGGTCGTGAAGGAGCCCTTTTCTCACATGTTGGCTT 2804
Db 1124 GTGCTAAATTTGGATGCTATTTTTCATGCAAGGATGTGTCTCTTATTATATGAATG 1183
QY 2805 CGGCATACCAAGTCTTCTCTCATAAAGAGAAACAATA 2840
Db 1184 TATGCATATTTTCTTAAATAAAAAAAAAAAAAA 1219

RESULT 13
US-11-056-355B-5315
; Sequence 5315, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 5315
; LENGTH: 1531
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: Ceres seq. ID no. 12435048
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14304148
; OTHER INFORMATION: as cited in SEQ ID NO 57313
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598513
; OTHER INFORMATION: as cited in SEQ ID NO 64102
US-11-056-355B-5315

Query Match 13.1%; Score 398.2; DB 9; Length 1531;
Best Local Similarity 64.2%; Pred. No. 1.5e-104; Indels 25; Gaps 5;
Matches 688; Conservative 0; Mismatches 358;

1664 GACCAAGTCTCGGACGACGAGCGGAACTCTTTCGCATGACGCTCGGAGCGCTCGGT 1723
Db 141 GCGCGCGGTGTGACGAGGAGGCGGTGCTGATGACGAGTGCAGCTGGCGTCTGCTCAT 200
QY 1724 GCTCCCATGTTCTCTAAGGCGCGCATCGAGATGACCTCTCGAGATCATGGCCAAGGA 1783
Db 201 CCT-----GCCCTGAAGAACGCCATCGAGCTGGGCTCTGGAGGTGCTGAGAAGGA 253
QY 1784 CG-----GGCGGGCGGTTCCTCTCCACGGGGGAAATCGCGGCACAGCTCCGACC 1835
Db 254 GGCGCGCGCGCGCAAGGCGGCGGTGGCGCCGAGAGGTGGTGGCGGATGCCCGCGCG 313
QY 1836 CAGAACCCCGAGGACACCCGTC-----ATGCTCAGCCGATCTTCCGGTCTCGCCAGC 1889
Db 314 CCCAGGACCCCGCGCGCGCGCNATTTGGTGAACCGCATGCTCCGCTCTCGCTCC 373
QY 1890 TACTCGGTCTCAGGTGACCTCCCGACCTCCCGATGGCAAGGTCCAGCGGCTCTAC 1949

1666 CCACAGTCTCGGACGACGAGCGGAACTCTTTCGCCATGAGTGGGAGCGGCTCGTGC 1725
Db 44 CCAAGAGGTGGACGAGGAGCGGTGATGATGACCCATGCAATGTTGTGAGCATGTTGCTCC 103
QY 1726 TCCCATGTTCTTAAAGCGCGCATCGAGATGACACTCTCGAGATCATGGCCAGGAGC 1785
Db 104 TCCGATGACGCTTAGGGTAGCGGTGAGTCTGAGTCTGCAACAAATCCAGGCGGG 163
QY 1786 GGCGGGCGGCTTCTCTCCACGGGGGAAATCGCGGCACAGCTCCCGACCCAGACCCCG 1845
Db 164 GCCAGATTCGATCTTACTCTCCAGGATTTGGCGGCGAGGCTCGGCAACTCCAACCCCT 223
QY 1846 AGGCACCCGTCATGCTCGACCGGATCTTCCGGCTGTGGCCAGTACTCGTCTCAGCT 1905
Db 224 TAGTCCGTCATGATCGAGCGGATCTTCCGCTGCTCACGAGTACTTCCATCTTAAT 283
QY 1906 GACCCCTCGGACCTCCCGATGCGAGGTCGAGCGGCTCTACGGCTTAGCGGCGGTGT 1965
Db 284 TCACCGACACCGTCCGACGGGAGGTAGACCGTCCGAGTACGGCGCGCGCATGCT 343
QY 1966 GCAAGTCTTGTGCAAGAACGAGGACGGGTCTCCATCGCGCATCACTTGTATGAACC 2025
Db 344 GCAAGTACCTGACTCCCAACGAGGACGGGTCTCCATGGCGCTCTCGTCTCATGAACA 403
QY 2026 AGGACAAATCTCATGGAAGCTGATTAACCTGAAAGATGCGGTCTCTGAAGCGGAA 2085
Db 404 CGGATAAGTCTTATGAGAGCTGATACCAATGAGAGTGCAGTGACAAATGTTGAA 463
QY 2086 TCCCATTCACAGGCGTACGGGATGACCGGTTTCGAGTATCATGGCACCCAGCCGGAT 2145
Db 464 TACATTCATCTAGCATATGGATGACAGCTTTTGAATGATCATGGGAAAGATCTAAGGT 523
QY 2146 TCACCAAGATCTTTTAAACCGGGAATGCTGATCACTCCACCAATTAATGAGAGATAC 2205
Db 524 TTAATAAGGTGTTCAACGAGGCGATGACAGCTTTTGAATGATGTTGGTGGAAATG 583
QY 2206 TGGACATACAGGCTTCGAGGCTCGAGACCGTGTGATGATGCGAGCGGCTCGGAGCGGCTG 2265
Db 584 TAGAGATACAAAGTTTGAAGATGTCATGTTTAAATGATGTTGGTGGAAATG 643
QY 2266 GGGCGGTCTCAGCATGATCGTTGCCAATACCATCAATGAAGGATCAACTTCGACC 2325
Db 644 GTGGAATATCAGTATGATTAATGCAAGTATCCATATACATGAGGATTAATTTGACC 703
QY 2326 -GCCCAACGATTAAGAGCCGCCCTCTCTGTTGTAAGACGCTCGGAGGCGACA 2384
Db 704 TTTCTCATGTTGTTCTGAGCTCCACTTTCAGAGGTTAGACATGTCGGTGGAAACA 763
QY 2385 TGTTCGTGAGGTTCCAAAGGAGATGCTTTTTCATGAAAGTGAATGCAATGCACTGGA 2444
Db 764 TGTGAAAGTGTCCCATGTTGATGCAATCTTTCATAAAGTGAATCTTTCATGATGGA 823
QY 2445 GTGACGACATGCGGAGTTCCTCAAGACTGCTAGCTGCGCTTCCCAACAATGGAA 2504
Db 824 GTGATGAGCATTTGTTGAGCTCTTAAGAAATTTGCAAAATCTTTTACCTGACAAAGGA 883
QY 2505 AGGTGATGTTGAGAGTGGTACTCTCTGTGTATCCAGACA CAGGCTTAGCGACCAAGA 2564
Db 884 AGTCAATGTTGTGAATGATCTTCTCCGATGACCTTTTGGTACGCGCAGAGGCTAAG 943
QY 2565 ATGTGATCACAATCGATGATCATGTTGGCCCAACACCCAGGCGGGAAGAGAGACAC 2624
Db 944 GTGTCTTTCAVTTGACATGATAATTTGTTGGTCTCAATCTCTGGGGGAAGAGAGACAA 1003
QY 2625 AGAAGGATTCGAGGATTTGGCCAAAGGGCGGATTTTCAGGGCTTTCAGAGTCAATGTGCT 2684

Db 374 TACGACGTCGTCGGTGCAGATGAGGACCGG---GACGGCCGCTACGAGCGCGCTAC 430
Qy 1950 GCTTTAGCGCGGTCGCAAGTCTTGTGTCAGAACGAGGAGCGGCTCTCCATCGCGCA 2009
Db 431 TCCGCGCGCGGTCGCAAGTCTTGTGTCAGAACGAGGAGCGGCTCTCCATCGCGCC 490
Qy 2010 CTCAACTGTATGAACAGGACAAAATCTCATGAAAGCTGCTATTAATCTGAAAGATGCG 2069
Db 491 CTCGGCTCATGAACAGGACAAAGTCTCTCATGAGAGCTGCTATCTCAAGGACGCG 550
Qy 2070 GTCCTTGAAGCGGATCCCAATCAACAGGCTACGAGGATCGCGGCTTCGAGTATCAT 2129
Db 551 GTGTGGACGGCGGCTCCGCTTCAACAGGCTACGAGGATCGCGGCTTCGAGTATCCAC 610
Qy 2130 GGCACCGACCGCGGATCAACAGGATCTTAACCGGGGAATGTCTGATCACTTCCACCAATT 2189
Db 611 GGCACGAGCGGCTTCAACCGGCTTCAACGAGGCGCATGAGAACCATCTCGTGATC 670
Qy 2190 ACTATGAAGAAGATACCTGAAACATACAAAGGCTTCGAGGCGCTCGAGACCGTGGTGCAT 2249
Db 671 ATCACCAGAAGCTGCTGACTTCTACACGGCTTCGAGGCGGCTGCGACGCTGGTGAC 730
Qy 2250 GTGAGGCGGCGACTGGGCGCGTGTCTAGCATGATGCTTGGCAATACCATCAATGAAA 2309
Db 731 GTGGCGGCGGCTGGGCGCGCACGCTGCACGCCATCAGCTCCCGCCACCCCGCACATCTCC 790
Qy 2310 GGGATCAACTTCGACC-CCCCCAACGGATTGAAGACGCCCAACCCCTTCTCGGTGTCAAG 2368
Db 791 GGGGTCAACTTCGACCTCCCGGACGTCATCTCCGAGGCGCGCGCTTCCCGGCGGTGGCG 850
Qy 2369 CACGTCGAGGCGGACATCTTCTGTCAGCGTTTCCAAAGGAGATGCGCATTTTCATGAAGTG 2428
Db 851 CACGTGGCGGAGCATGTTCCGCTCCGTCGCGCGCGCGAGCATCTCTCATGAGTGG 910
Qy 2429 ATATGCCATGATGAGTGAAGCAATTTGGCGGAGTTCTTCAAGAACTGTCATGATGCG 2488
Db 911 ATCTTCCACGATGAGGCGGCGCACTGCGCCACGCTGCTCAAGAACTGCTACGACGCG 970
Qy 2489 CTTCACCAATGAAAGTGATCGTTGACAGTGCCTGCTGTCAGTGCCTGCTGTCACCGACACG 2548
Db 971 CTCGCGGAAATGGAAGTTCATGCTGTCGAGTGCCTGCTGCGCGCTCAACAGGAGGCC 1030
Qy 2549 AGCTTAGCGCAAGAAATGTATCCATCGACTGCATCATGTTGGCCCAACACCCAGGC 2608
Db 1031 ACCCGAGGCGGAGGCTGTTCCACGTCACATGATCATGCTCGCGCAACACCCGCGC 1090
Qy 2609 GGGAAAGAGAGACACAGAGGTTGAGGATTTGGCCAAAGGGCGCGGATTTACGGGC 2668
Db 1091 GCGAAGGAGCGGTACGAGCGGAGTTCCGCGAGCTCGCAAGGCGCGCGCTTCTCCGGG 1150
Qy 2669 TTCCAAGTCATGTCGCGCTTTCGGCACTCAGCTCATGGAGTTCCTGAAG 2719
Db 1151 TTCAAGGCCCTACATCATACGCCCAACGCTTGGGCCATCGAGTTTCATCAAG 1201

RESULT 14

US-11-397-533-24
; Sequence 24, Application US/11397533
; Publication No. US20060183895A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c6
; CURRENT APPLICATION NUMBER: US/11397,533
; PRIOR FILING DATE: 2006-04-03
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: US 60/143,833
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/615,192
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 10/174,693
; PRIOR FILING DATE: 2002-06-18
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-24

Query Match 12.9%; Score 391.4; DB 7; Length 421;
Best Local Similarity 97.3%; Pred. No. 6.2e-103;
Matches 398; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1559 ATCCGTTTTTATTTCTCTCTGCTTTCTTTGTCGAGTCTCGCGAAGAGAGAGAGG 1618
Db 13 AGCGTTTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGG 72
Qy 1619 AGAGAGAGAAATGGGTTTCGACCGGCTCCGAGACCCAGATGACCCCGACCCCAAGTCTCGGA 1678
Db 73 AGAGAGAGAAATGGGTTTCGACCGGATCCGAGACCCAGATGACCCCGACCCCAAGTCTCGGA 132
Qy 1679 CGAGAGCGCAACTCTTTCCGCAATGACAGTGGGAGCGCTTCGCTGCTCCCATGCTCT 1738
Db 133 CGAGAGAGCAACTCTTTCCGCAATGACAGTGGGAGCGCTTCGCTGCTCCCATGCTCT 192
Qy 1739 AAAGCGCGCATCGAGATCGACCTCTTCGAGATCATGCGCAAGGACCGGCGCGCGTT 1798
Db 193 CAAGCGCGCATCGAGCTCGACCTCTTCGAGATCATGCGCAAGGCGCGCGCGCGTT 252
Qy 1799 CTTCTCACCGGGGAAATTCGCGCAGCTCCGACCCAGACCCCGACCCCAAGTCTCAT 1858
Db 253 CTTCTCCCGGGGAAAGTCGCGCCAGCTCCGCGCCAGTCCCGACCCAGACCCCGGTAAT 312
Qy 1859 GCTCGACCGGATCTTCGCGCTGCTGGCGAGTACTCGTGTCTACGTGACCCCTCCGCGA 1918
Db 313 GCTCGACCGGATCTTCGCGCTGCTGGCGAGTACTCGTGTCTACGTGACCCCTCCGCGA 372
Qy 1919 CTTCCCGGATGCGAAGTTCGAGCGGCTTACGGCTTAGCGCGCGTGTGTC 1967
Db 373 CTTCCCGGATGCGAAGTTCGAGCGGCTTACGGCTTAGCGCGCGTGTGTC 421

RESULT 15

US-11-397-533-106
; Sequence 106, Application US/11397533
; Publication No. US20060183895A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c6
; CURRENT APPLICATION NUMBER: US/11397,533
; PRIOR FILING DATE: 2006-04-03
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/143,833
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/615,192
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 10/174,693
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 407
; SOFTWARE: Fast-SEQ for Windows Version 3.0

Thu Nov 2 13:35:57 2006

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; SEQ ID NO 106
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-106

Query Match      12.9%; Score 391; DB 7; Length 407;
Best Local Similarity 97.5%; Pred. No. 8e-103; Indels 0; Gaps 0;
Matches 397; Conservative 0; Mismatches 10;

QY 1561 CCGTTTATTTCCTCTCTCTTTCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAG 1620
Db      1 CCGTTTATTTCCTCTCTCTTTCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAG 60

QY 1621 AGGAGAGAAATGGGTTCGACCGGCTCCGAGACCCGATGACCCGACCCAGTCTCGGACG 1680
Db      61 AGGAGAGAAATGGGTTCGACCGGATCCGAGACCCGATGACCCGACCCAGTCTCGGACG 120

QY 1681 ACGAGGCGAACCTCTTCGCCATGCGCTGGCGAGCGCTCCGTCTCCCATGGTCTCTAA 1740
Db      121 AGGAGGCGAACCTCTTCGCCATGCGCTGGCGAGCGCTCCGTCTCCCATGGTCTCTCA 180

QY 1741 AGGCCGCCATCGAGATCGACCTCTCTCGAGATCATGCGCAAGGAGCGGCGCGGCTTC 1800
Db      181 AGGCCGCCATCGAGCTCGACCTCTCTCGAGATCATGCGCAAGGCGGCGGCGGCTTC 240

QY 1801 TCTCCACGGGGGAATCGGGGACAGCTCCCGACCCGAGAACCCGAGGACCCCGTCAATGC 1860
Db      241 TCTCCCGGGGGAATCGCGGCGGAGCTCCCGACCCGAGAACCCGAGGACCCCGTAAATGC 300

QY 1861 TCGACCGGATCTTCGGGCTGTGGCCAGCTACTCGTGCTCACTGTCACCTCCGCGACC 1920
Db      301 TCGACCGGATCTTCGGGCTGTGGCCAGCTACTCGTGCTCACTGTCACCTCCGCGACC 360

QY 1921 TCCCGGATCGCAAGTTCGAGCGGCTCTACGGCTTAGCGCGGTGTGC 1967
Db      361 TCCCGGATGGCAAGTTCGAGCGGCTCTACGGCTTAGCGCGGTGTGC 407
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Search completed: November 1, 2006, 14:52:56
Job time : 659.143 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:27:09 ; Search time 3753.23 Seconds
(without alignment)
1193.945 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1675

Perfect score: 657

Sequence: 1 ctgagccatttaattcgaga.....aggagagagaagaatgggtt 657

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb env.*

2: gb pat.*

3: gb ph.*

4: gb pl.*

5: gb pr.*

6: gb ro.*

7: gb sts.*

8: gb sv.*

9: gb un.*

10: gb vi.*

11: gb ov.*

12: gb htg.*

13: gb in.*

14: gb om.*

15: gb ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	657	100.0	3070	2	AR360987 Sequence
2	638.2	97.1	661	2	BD262120 Compositi
3	638.2	97.1	661	2	AR360905 Sequence
4	638.2	97.1	2096	2	BD262168 Compositi
5	638.2	97.1	2096	2	AR360953 Sequence
6	75	11.4	1630	2	BD224383 Materials
7	75	11.4	1630	2	AR216433 Sequence
8	75	11.4	1630	2	AR432835 Sequence
9	73.8	11.2	421	2	AR074115 Sequence
10	73.8	11.2	421	2	BD005663 Materials
11	73.8	11.2	421	2	BD224300 Materials
12	73.8	11.2	421	2	BD273002 Materials
13	73.8	11.2	421	2	AR216350 Sequence
14	73.8	11.2	421	2	AR432752 Sequence
15	73.4	11.2	407	2	BD224382 Materials
16	73.4	11.2	407	2	AR216432 Sequence
17	73.4	11.2	407	2	AR432834 Sequence
18	67.4	10.3	1452	4	EGOMTRN X74814 E.gunni OM

19	53.2	8.1	249121	12	AC096843	AC096843 Rattus no
20	50.2	7.6	198450	12	AC110357	AC110357 Rattus no
21	50.2	7.6	218614	12	AC123243	AC123243 Rattus no
22	50.2	7.6	252137	12	AC107438	AC107438 Rattus no
23	50	7.6	193795	12	AC069535	AC069535 Mus muscu
24	49.4	7.5	5235	12	AC012735	AC012735 Drosophil
25	49.4	7.5	5626	2	CQ591632	CQ591632 Sequence
26	49.4	7.5	137544	12	AC018487	AC018487 Drosophil
27	49.4	7.5	165118	13	AC018488	AC018488 Drosophil
28	49.4	7.5	182416	13	AC022345	AC022345 Drosophil
29	49.4	7.5	204000	6	AC136645	AC136645 Rattus no
30	49.4	7.5	341520	13	AE003498	AE003498 Drosophil
31	49	7.5	74587	5	HSDJ90205	ALI09750 Human DNA
32	48.8	7.4	221729	12	AC094575	AC094575 Rattus no
33	48.8	7.4	248722	12	AC095781	AC095781 Rattus no
34	48.2	7.3	231530	6	AL671975	AL671975 Mouse DNA
35	48	7.3	230763	12	AC129875	AC129875 Rattus no
36	48	7.3	244684	12	AC114841	AC114841 Rattus no
37	48	7.3	298672	12	AC108330	AC108330 Rattus no
38	47.6	7.2	231	4	AJ865169	AJ865169 Cocos nuc
39	47.6	7.2	192583	6	AL671782	AL671782 Mouse DNA
40	47.6	7.2	306749	12	AL590310	AL590310 Homo sapi
41	47.4	7.2	127293	12	AC026917	AC026917 Homo sapi
42	47.4	7.2	167483	5	AC115540	AC115540 Homo sapi
43	47.4	7.2	182375	12	AC105920	AC105920 Homo sapi
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ALIGNMENTS

RESULT 1
AR360987
LOCUS AR360987 3070 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 113 from patent US 6596925.
ACCESSION AR360987
VERSION AR360987.1 GI:33768497

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3070)

Perera,J.R., Eagleton,C. and Rice,S.J.

Compositions and methods for the modification of gene expression

Patent: US 6596925-A 113 22-JUL-2003;

Genensis Research & Development Corp. Ltd. and Rubicon Forests

Holdings Ltd.; Parnell;

NZX;

FEATURES

Location/Qualifiers

1..3070

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 657; DB 2; Length 3070;

Best Local Similarity 100.0%; Pred. No. 2.8e-208;

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Qy 61 CGAATTTTCTTTTAGTAAAGTAACCAATGATCGCCATGTTGACAAAAGGCTGATTA 120

1079 CGAATTTTCTTTTAGTAAAGTAACCAATGATCGCCATGTTGACAAAAGGCTGATTA 1138

Qy 121 GTATGATCTTGGAGTTCTTGTGCAAAATTTTGAAGCTGACATGCGCCCTCAGGGAATT 180

1139 GTATGATCTTGGAGTTCTTGTGCAAAATTTTGAAGCTGACATGCGCCCTCAGGGAATT 1198

Qy 181 AAGCGCGCAACCCAGATGTCAAAGAGACACAAAGAGACGACCCCAACCTTCTTCTTAAACAAG 240

|||||

Thu Nov 2 13:35:55 2006

Matches	654;	Conservative	0;	Mismatches	3;	Indels	4;	Gaps	1;
QY	1	CTGAGCCATTAATTCGAGACACATCGCCCAAAATTAATTCCTTCTGCTGCCATAACTGT	60						
Db	1	CTGAGCCATTAATTCGAGACACATCGCCCAAAATTAATTCCTTCTGCTGCCATAACTGT	60						
QY	61	CGAATTTCTCTTTAGGTAACTTAACCAATGATGCGCATGTTGACAAAAAGGCTGATTA	120						
Db	61	CGAATTTCTCTTTAGGTAACTTAACCAATGATGCGCATGTTGACAAAAAGGCTGATTA	120						
QY	121	GTATGATCTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT	180						
Db	121	GTATGATCTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT	180						
QY	181	AAGCGCCAAACCCAGATTTGCAAGAGACACAAAGAGACACCAACCTTTTCCCTTAACAAG	240						
Db	181	AAGCGCCAAACCCAGATTTGCAAGAGACACAAAGAGACACCAACCTTTTCCCTTAACAAG	240						
QY	241	ATCATCACAGATCGGCCAGTAAAGGGTAAATTAATTAATTAACAAATAGCTCTTGACCGGG	300						
Db	241	ATCATCACAGATCGGCCAGTAAAGGGTAAATTAATTAATTAACAAATAGCTCTTGACCGGG	300						
QY	301	AATCCCGTATTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGAAAGCGACAGC	360						
Db	301	AATCCCGTATTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGAAAGCGACAGC	360						
QY	361	AACCCACAAAAGGTGAGATGTCATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420						
Db	361	AACCCACAAAAGGTGAGATGTCATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420						
QY	417	AGAGTTTCTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGAAAGCGACAGC	476						
Db	421	AGAGTTTCTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGAAAGCGACAGC	480						
QY	477	ACATATTTGGTGTAGGTTCCATATTTTGGCGGAGGGTGGTGAACCCGAAAGTTCTTATA	536						
Db	481	ACATATTTGGTGTAGGTTCCATATTTTGGCGGAGGGTGGTGAACCCGAAAGTTCTTATA	540						
QY	537	TATCGAACCTCCACCAACCATACCTCACCTTCAATCCCAACCAATTTATTCGGTTTATTCCT	596						
Db	541	TATCGAACCTCCACCAACCATACCTCACCTTCAATCCCAACCAATTTATTCGGTTTATTCCT	600						
QY	597	CTGCTTTCCTTCTGCTGAGTCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGT	656						
Db	601	CTGCTTTCCTTCTGCTGAGTCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGT	660						
QY	657	T 657							
Db	661	T 661							
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LOCUS	AR360905	Sequence 12 from patent US 6596925.	661 bp	DNA	linear				PAT 17-AUG-2003
DEFINITION									
ACCESSION	AR360905								
VERSION	AR360905.1	GI:33768415							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 661)								
AUTHORS	Perera, J.K., Bagleton, C. and Rice, S.J.								
TITLE	Compositions and methods for the modification of gene expression								
JOURNAL	Patent: US 6596925-A 12 22-JUL-2003; and Rubicon Forests								
	Genesis Research & Development Corp. Ltd. and Rubicon Forests								
	Holdings Ltd.; Parnell;								
FEATURES	NZX,								
source	Location/Qualifiers								
	1..661								
	/organism="unknown"								
	/mol_type="genomic DNA"								
ORIGIN									
Query Match	97.1%	Score 638.2;	DB 2;	Length 661;					
Best Local Similarity	98.9%	Pred. No. 3.4e-202;							

Query Match 97.1%; Score 638.2; DB 2; Length 661;
Best Local Similarity 98.9%; Pred. No. 3.4e-202;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTGCTGCCATAACTGT 60
Db 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTGCTGCCATAACTGT 60

Qy 61 CGAATTTCTCTTTAGTAAATTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 120
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Qy 121 GTATGATCTTGAGTGTGTGGTGCATAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 180
Db 121 GTATGATCTTGAGTGTGTGGTGCATAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 180

Qy 181 AAGCGCCCAACCCAGATTGCAAGAGCAACAAGAGCAGCACCACCTTCTTAAACAAG 240
Db 181 AAGCGCCCAACCCAGATTGCAAGAGCAACAAGAGCAGCACCACCTTCTTAAACAAG 240

Qy 241 ATCATCAGCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTGTACCGGG 300
Db 241 ATCATCAGCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTGTACCGGG 300

Qy 301 AACTCCGTATTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 360
Db 301 AACTCCGTATTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 360

Qy 361 AACCACAAAAGGTCAGATGTCATCCAC- - - -GAGAGAGAGAGAGAGAGAGAGAG 416
Db 361 AACCACAAAAGGTCAGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 417 AGAGTTTCTCTATATTCTGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 476
Db 421 AGAGTTTCTCTATATTCTGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 480

Qy 477 ACATATTGGTGTAGGTCCTAATTTTCGGGAGGTTGGTGAACCGCAAAAGTTCCCTATA 536
Db 481 ACATATTGGTGTAGGTCCTAATTTTCGGGAGGTTGGTGAACCGCAAAAGTTCCCTATA 540

Qy 537 TATCGAACCCTCCACCAATACCTCATTCAATCCCAACCAATTTATCGTTTTATTTCCCT 596
Db 541 TATCGAACCCTCCACCAATACCTCATTCAATCCCAACCAATTTATCGTTTTATTTCCCT 600

Qy 597 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 656
Db 601 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 660

Qy 657 T 657
Db 661 T 661

RESULT 4
BD262168
LOCUS BD262168 2096 bp DNA linear PAT 17-JUL-2003
DEFINITION Composition and methods for the modification of gene expression.
ACCESSION BD262168
VERSION BD262168.1 GI:33071936
KEYWORDS JP 2002539834-A/60.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 2096)
Perera,R., Rice,S.J. and Bagleton,C.K.
Composition and methods for the modification of gene expression
Patent: JP 2002539834-A 60 26-NOV-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS INDUSTRIES LTD
OS Eucalyptus grandis (flooded gum)

PN JP 2002539834-A/60
PD 26-NOV-2002
PF 24-FEB-2000 JP 2000608755
PR 25-MAR-1999 US 09/276599, 30-JUL-1999 US 60/146591 PI
RANJAN PREREA, STEPHEN J RICE, CLARE KATHERINE BAGLETON PC
C12N15/09, A01H5/00, C07K14/415, C12N5/10, C12Q1/02, C12Q1/68, PC
C12N15/00,
PC C12N5/00
CC Composition and methods for the modification of gene CC
expression
FH Key Location/Qualifiers
FT source 1..2096
FT /organism="Eucalyptus grandis (flooded gum)"
FEATURES
source 1..2096
Location/Qualifiers
1..2096
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ORIGIN
Query Match 97.1%; Score 638.2; DB 2; Length 2096;
Best Local Similarity 98.9%; Pred. No. 4.9e-202;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTGCTGCCATAACTGT 60
Db 41 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTGCTGCCATAACTGT 100

Qy 61 CGAATTTCTCTTTAGTAAATTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 120
Db 101 CGAATTTCTCTTTAGTAAATTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 160

Qy 121 GTATGATCTTGAGTGTGTGGTGCATAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 180
Db 161 GTATGATCTTGAGTGTGTGGTGCATAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 220

Qy 181 AAGCGCCCAACCCAGATTGCAAGAGCAACAAGAGCAGCACCACCTTCTTAAACAAG 240
Db 221 AAGCGCCCAACCCAGATTGCAAGAGCAACAAGAGCAGCACCACCTTCTTAAACAAG 280

Qy 241 ATCATCAGCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTGTGACCGGG 300
Db 281 ATCATCAGCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTGTGACCGGG 340

Qy 301 AACTCCGTATTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 360
Db 341 AACTCCGTATTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 400

Qy 361 AACCACAAAAGGTCAGATGTCATCCAC- - - -GAGAGAGAGAGAGAGAGAGAGAG 416
Db 401 AACCACAAAAGGTCAGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460

Qy 417 AGAGTTTCTCTATATTCTGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 476
Db 461 AGAGTTTCTCTATATTCTGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 520

Qy 477 ACATATTGGTGTAGGTCCTAATTTTCGGGAGGTTGGTGAACCGCAAAAGTTCCCTATA 536
Db 521 ACATATTGGTGTAGGTCCTAATTTTCGGGAGGTTGGTGAACCGCAAAAGTTCCCTATA 580

Qy 537 TATCGAACCCTCCACCAATACCTCATTCAATCCCAACCAATTTATCGTTTTATTTCCCT 596
Db 581 TATCGAACCCTCCACCAATACCTCATTCAATCCCAACCAATTTATCGTTTTATTTCCCT 640

Qy 597 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 656
Db 641 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 700

Qy 657 T 657
Db 701 T 701

RESULT 5
AR360953
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
GENESIS RESEARCH & Development Corp. Ltd. and Rubicon Forests Holdings Ltd.; Parnelli;
NZX;
FEATURES
source
1..2096
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 97.1%; Score 638.2; DB 2; Length 2096;
Best Local Similarity 98.9%; Pred. No. 4.9e-202;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY 1 CTGAGCCATTAAATTCGAGACACATCGCCCAAAATTTATCTTCTGCTGCCATAACTGT 60
Db 41 CTGAGCCATTAAATTCGAGACACATCGCCCAAAATTTATCTTCTGCTGCCATAACTGT 100
QY 61 CCAATTTTCTTTTGTAGTAACTAACCAATGATGATCATCATGTTGACAAAAGGCTGATTA 120
Db 101 CCAATTTTCTTTTGTAGTAACTAACCAATGATGATCATCATGTTGACAAAAGGCTGATTA 160
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGTGCATGCGCCCTCAGGGAATTT 180
Db 161 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGTGCATGCGCCCTCAGGGAATTT 220
QY 181 AGGCGCCCAACCCAGATTGCAAGAGACAAAGAGACGACGACCCACCTTTCTTTAAACAAG 240
Db 221 AGGCGCCCAACCCAGATTGCAAGAGACAAAGAGACGACGACCTTTCTTTAAACAAG 280
QY 241 ATCATCACCAGATCGGCCAGTAAAGGTAAATTAATTAATTAACAAATAGCTCTTGACCGG 300
Db 281 ATCATCACCAGATCGGCCAGTAAAGGTAAATTAATTAATTAACAAATAGCTCTTGACCGG 340
QY 301 AACTCGGTATTTCTCTCACTTCCATAAACCCTGATTAATTTGTTGGAAAGCGACAGCC 360
Db 341 AACTCGGTATTTCTCTCACTTCCATAAACCCTGATTAATTTGTTGGAAAGCGACAGCC 400
QY 361 AACCCAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416
Db 401 AACCCAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 460
QY 417 AGAGTTTCTCTCTATATTCGTTTCAACCGTTGGAGTCAATGGCATGCTGACCAATGT 476
Db 461 AGAGTTTCTCTCTATATTCGTTTCAACCGTTGGAGTCAATGGCATGCTGACCAATGT 520
QY 477 ACATATTTGTTAGGGTCCCAATATTTTGGGAGGGTGTGTGAACCGCAAAAGTTCCTATA 536
Db 521 ACATATTTGTTAGGGTCCCAATATTTTGGGAGGGTGTGTGAACCGCAAAAGTTCCTATA 580
QY 537 TATCGAACCTCCACACCATACCTCACTCAATCCCAACCAATTTATTCCTTTTCTTCT 596
Db 581 TATCGAACCTCCACACCATACCTCACTCAATCCCAACCAATTTATTCCTTTTCTTCT 640
QY 597 CTGCTTTCTTTGTCGAGTCTCCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656
Db 641 CTGCTTTCTTTGTCGAGTCTCCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
QY 657 T 657

Db 701 T 701
RESULT 6
BD224383
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE FORESTS LTD
OS Eucalyptus grandis
PN JP 200527058-A/107
PD 27-AUG-2002
PF 06-OCT-1999 JP 2000575991
PR 09-OCT-1998 US 09/169789,14-JUL-1999 US 60/143811 PI
LEONARD NATHAN BLOKSBERG,ILKKA JAAKKO HAVUKKALA PC
C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/04,C12N9/ PC
10,C12N9/24,
PC C12N9/88,C12N15/00,C12N5/00
CC Materials and methods for the modification of plant lignin CC content
FH Key Location/Qualifiers
FT source 1..1630
/organism="Eucalyptus grandis".
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/mol_type="genomic DNA"
/db_xref="taxon:71139"
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Query Match 11.4%; Score 75; DB 2; Length 1630;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 583 CCGTTTATTTCTCTGCTTTCCTTTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAG 642
Db 1 CCGTTTATTTCTCTGCTTTCCTTTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 643 AGGAGAGATGGGTT 657
Db 61 AGGAGAGATGGGTT 75
RESULT 7
AR216433
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
GENESIS RESEARCH & Development Corporation Ltd. and Fletcher Challenge Forests Ltd.;;
NZX;
FEATURES
Location/Qualifiers
1630 bp DNA linear PAT 25-SEP-2002
Sequence 107 from patent US 6410718.
AR216433
AR216433
AR216433.1 GI:23314913
Unknown.
Unclassified.
1 (bases 1 to 1630)
Blokberg,L.N. and Havukkala,I.
Materials and methods for the modification of plant lignin content
Patent: US 6410718-A 107 25-JUN-2002;
Genesis Research & Development Corporation Ltd. and Fletcher
Challenge Forests Ltd.;;
NZX;
Location/Qualifiers

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/mol_type="genomic DNA"

ORIGIN
Query Match 11.4%; Score 75; DB 2; Length 1630;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 CCGTTTATTTCTCTGCTTTCTCTGCTTCGAGTCTCGCGAAGAGAGAGAGAGAGAG 642
Db 1 CCGTTTATTTCTCTGCTTTCTCTGCTTCGAGTCTCGCGAAGAGAGAGAGAGAGAG 60

QY 643 AGGAGAGAATGGGTT 657
Db 61 AGGAGAGAATGGGTT 75

RESULT 8
LOCUS AR432835 1630 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 107 from patent US 6653528.
ACCESSION AR432835
VERSION AR432835.1 GI:40195438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Bloksberg,L.N., and Havukkala,I.
TITLE Pinus radiata nucleic acids encoding O-methyl transferase and
methods for the modification of plant lignin content therewith
JOURNAL Patent: US 6653528-A 107 25-NOV-2003;
Genesis Research & Development Corporation Limited and Rubicon
Forests Industries Limited; Parnell;
NZX;
FEATURES
source
1..1630
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 11.4%; Score 75; DB 2; Length 1630;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 CCGTTTATTTCTCTGCTTTCTCTGCTTCGAGTCTCGCGAAGAGAGAGAGAGAGAG 642
Db 1 CCGTTTATTTCTCTGCTTTCTCTGCTTCGAGTCTCGCGAAGAGAGAGAGAGAGAG 60

QY 643 AGGAGAGAATGGGTT 657
Db 61 AGGAGAGAATGGGTT 75

RESULT 9
AR074115
LOCUS AR074115 421 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 24 from patent US 5952486.
ACCESSION AR074115
VERSION AR074115.1 GI:10000875
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 421)
AUTHORS Bloksberg,L.N., Havukkala,I., and Grierson,A.W.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 5952486-A 24 14-SEP-1999;
Location/Qualifiers
1..421
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/mol_type="unassigned DNA"

ORIGIN
Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 7.2e-13;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTATTTCTCTGCTTTCTCTGCTTCGAGTCTCGCGAAGAGAGAGAGAGAG 640
Db 13 AGCGGTTTATTTCTCTGATTTCTCTTGTCTCGAGTCTCGCGAAGAGAGAGAGAGAG 72

QY 641 AGAGGAGAGAATGGGTT 657
Db 73 AGAGGAGAGAATGGGTT 89

RESULT 10
BD005663
LOCUS BD005663 421 bp DNA linear PAT 31-JAN-2002
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD005663
VERSION BD005663.1 GI:18634034
KEYWORDS JP 2001500378-A/24.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 421)
AUTHORS Bloksberg,L.N., Grierson,A.W. and Havukkala,I.J.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: JP 2001500378-A 24 16-JAN-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS
LTD
OS Unidentified
PN JP 2001500378-A/24
PD 16-JAN-2001
PF 10-SEP-1997 JP 1998513535
PR 11-SEP-1996 US 08/713000
PI LEONARD NATHAN BLOKSBERG,ALISTAIR WALLACE GRIERSON, PI ILKKA
JAAKKO HAVUKKALA
PC C12N15/53,C12N15/54,C12N15/52,C12N15/60,C12N15/82,A01H5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..421
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ORIGIN
Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 7.2e-13;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTATTTCTCTGCTTTCTCTGCTTCGAGTCTCGCGAAGAGAGAGAGAGAG 640
Db 13 AGCGGTTTATTTCTCTGATTTCTCTTGTCTCGAGTCTCGCGAAGAGAGAGAGAGAG 72

QY 641 AGAGGAGAGAATGGGTT 657
Db 73 AGAGGAGAGAATGGGTT 89

RESULT 11
BD224300
LOCUS BD224300 421 bp DNA linear PAT 17-JUL-2003
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD224300
VERSION BD224300.1 GI:33034070
KEYWORDS JP 2002527058-A/24.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Myrtales; Myrtaceae; Eucalyptus.

1 (bases 1 to 421)

REFERENCE
AUTHORS
TITLE
JOURNAL

Bloksberg, L.N. and Havukkala, I.J.
Materials and methods for the modification of plant lignin content
Patent: JP 2002527058-A 24 27-AUG-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE FORESTS LTD

OS Eucalyptus grandis
PN JP 2002527058-A/24
PD 27-AUG-2002

PF 06-OCT-1999 JP 2000575991
PR 09-OCT-1998 US 09/169789, 14-JUL-1999 US 60/143811 PI
LEONARD NATHAN BLOKSBERG, ILKKA JAAKKO HAVUKKALA PC
C12N15/09, A01H5/00, C12N5/10, C12N9/02, C12N9/04, C12N9/PC
10, C12N9/24,
PC C12N9/88, C12N15/00, C12N5/00
CC Materials and methods for the modification of plant lignin CC

content

Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 7.2e-13;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 581 ATCCGTTTATTTCTCTGCTTTCTCTGCTCTCGAGTCTCGCGAAGAGAGAGAGAGG 640
Db 13 AGCCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGG 72

Qy 641 AGAGGAGAGATGGGTT 657
Db 73 AGAGGAGAGATGGGTT 89

FEATURES
source
1. .421
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:71139"

ORIGIN
1. .421
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:71139"

RESULT 13
LOCUS AR216350 421 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 24 from patent US 6410718.
ACCESSION AR216350
VERSION AR216350.1 GI:23314830
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 421)
AUTHORS Bloksberg, L.N. and Havukkala, I.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 6410718-A 24 25-JUN-2002;
Genesis Research & Development Corporation Ltd. and Fletcher Challenge Forests Ltd.;;
NZX;

FEATURES
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Location/Qualifiers
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ORIGIN
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Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 7.2e-13;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 581 ATCCGTTTATTTCTCTGCTTTCTCTGCTCTCGAGTCTCGCGAAGAGAGAGAGAGG 640
Db 13 AGCCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGG 72

Qy 641 AGAGGAGAGATGGGTT 657
Db 73 AGAGGAGAGATGGGTT 89

RESULT 12
BD273002 421 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Materials and methods for the modification of isoprenoid content, composition and metabolism.
ACCESSION BD273002
VERSION BD273002.1 GI:33082770
KEYWORDS JP 2002541764-A/69.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Myrtales; Myrtaceae; Eucalyptus.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 421)

Havukkala, I.J.
Materials and methods for the modification of isoprenoid content, composition and metabolism
Patent: JP 2002541764-A 69 10-DEC-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE FORESTS INDUSTRIES LTD

OS Eucalyptus grandis (flooded gum)
PN JP 2002541764-A/69
PD 10-DEC-2002

PF 16-DEC-1999 JP 2000588332
PR 17-DEC-1998 US 09/215504, 29-JUL-1999 US 60/146441 PI
ILKKA JAAKKO HAVUKKALA
PC C12N15/09, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/PC
10, C12N9/00,
PC C12N1/68, C12N15/00, C12N5/00, C12N5/00
CC Materials and methods for the modification of isoprenoid CC

content,
composition and metabolism
Key Location/Qualifiers
FT source 1. .421
/organism="Eucalyptus grandis"
/mol_type="genomic DNA"
/db_xref="taxon:71139"

FEATURES
source
1. .421
Location/Qualifiers
/organism="Eucalyptus grandis"
/mol_type="genomic DNA"
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ORIGIN
1. .421
Location/Qualifiers
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Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 7.2e-13;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 581 ATCCGTTTATTTCTCTGCTTTCTCTGCTCTCGAGTCTCGCGAAGAGAGAGAGAGG 640
Db 13 AGCCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGG 72

Qy 641 AGAGGAGAGATGGGTT 657
Db 73 AGAGGAGAGATGGGTT 89

RESULT 13
LOCUS AR216350 421 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 24 from patent US 6410718.
ACCESSION AR216350
VERSION AR216350.1 GI:23314830
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 421)
AUTHORS Bloksberg, L.N. and Havukkala, I.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 6410718-A 24 25-JUN-2002;
Genesis Research & Development Corporation Ltd. and Fletcher Challenge Forests Ltd.;;
NZX;

FEATURES
source
1. .421
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
1. .421
Location/Qualifiers
/organism="unknown"
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Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 7.2e-13;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 581 ATCCGTTTATTTCTCTGCTTTCTCTGCTCTCGAGTCTCGCGAAGAGAGAGAGAGG 640
Db 13 AGCCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGG 72

Qy 641 AGAGGAGAGATGGGTT 657
Db 73 AGAGGAGAGATGGGTT 89

RESULT 14
LOCUS AR432752 421 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 24 from patent US 6653528.
ACCESSION AR432752
VERSION AR432752.1 GI:40195355
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 421)
AUTHORS Bloksberg, L.N. and Havukkala, I.

TITLE Pinus radiata nucleic acids encoding O-methyl transferase and methods for the modification of plant lignin content therewith
JOURNAL Patent: US 6653528-A 24 25-NOV-2003;
Genesis Research & Development Corporation Limited and Rubicam Forests Industries Limited; Farnell;
NZX;
FEATURES Location/Qualifiers
source 1. 421
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/mol_type="genomic DNA"
ORIGIN
Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 7.2e-13;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 581 ATCCGTTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGG 640
Db 13 AGCCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGG 72
Qy 641 AGAGGAGAGATGGGTT 657
Db 73 AGAGGAGAGATGGGTT 89

RESULT 15
BD224382
LOCUS 407 bp DNA linear PAT 17-JUL-2003
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD224382
VERSION BD224382.1 GI:33034152
KEYWORDS JP 2002527058-A/106.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 407)
Blosberg,L.N. and Havukkala,I.J.
Materials and methods for the modification of plant lignin content
Patent: JP 2002527058-A 106 27-AUG-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS LTD
COMMENT OS Eucalyptus grandis
FN JP 2002527058-A/106
PD 27-AUG-2002
PR 06-OCT-1999 JP 2000575991 60/143811 PI
PR 09-OCT-1998 US 09/169789,14-JUL-1999 US
LEONARD NATHAN BLOKSBERG,ILKKA JAAKKO HAVUKKALA PC
C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/02,C12N9/04,C12N9/ PC
10,C12N9/24,
PC C12N9/86,C12N15/00,C12N5/00
CC Materials and methods for the modification of plant lignin CC
FH Key Location/Qualifiers
FT source 1. .407
/organism='Eucalyptus grandis'.
FEATURES Location/Qualifiers
source 1. .407
/organism="Eucalyptus grandis"
/mol_type="genomic DNA"
/db_xref="taxon:71139"
ORIGIN
Query Match 11.2%; Score 73.4; DB 2; Length 407;
Best Local Similarity 98.7%; Pred. No. 9.8e-13;
Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 583 CCGTTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGG 642
Db 1 CCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGG 60
Qy 643 AGGAGAGATGGGTT 657

Db 61 AGGAGAGATGGGTT 75
Search completed: November 1, 2006, 11:25:41
Job time : 3/57.23 secs

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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:17:03 ; Search time 277.948 Seconds
(without alignments)

16480.672 Million cell updates/sec

Title: US-10-702-319a-113_COPY_1019_1675

Perfect score: 657

Sequence: 1 ctgagccatttaattcaga.....aggagaggagaatgggtt 657

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657	100.0	3070	6	ABK17109 Eucalyptu
2	657	100.0	3070	10	ADH75529 Eucalyptu
3	657	100.0	3070	14	ADW80563 E. grand
4	638.2	97.1	661	3	AAC62762 O-methyl
5	638.2	97.1	661	6	ABK17027 Eucalyptu
6	638.2	97.1	661	10	ADH75428 Eucalyptu
7	638.2	97.1	661	14	ADW80462 E. grand
8	638.2	97.1	2096	3	AAC62810 O-methyl
9	638.2	97.1	2096	6	ABK17075 Eucalyptu
10	638.2	97.1	2096	10	ADH75476 Eucalyptu
11	638.2	97.1	2096	14	ADW80510 E. grand
12	534	81.3	534	13	ADQ88319 Eucalyptu
13	485	73.8	485	13	ADQ88320 Eucalyptu
14	306	46.6	306	13	ADQ88321 Eucalyptu
15	293	44.6	293	13	ADQ88322 Eucalyptu
16	119	18.1	119	13	ADQ88323 Eucalyptu
17	98	14.9	98	13	ADQ88324 Eucalyptu
18	75	11.4	1630	3	AAA68014 Eucalyptu

19	75	11.4	1630	10	ADD41764
20	73.8	11.2	421	2	AAV23844
21	73.8	11.2	421	2	AAZ06845
22	73.8	11.2	421	3	AAA69595
23	73.8	11.2	421	3	AAA67931
24	73.8	11.2	421	10	ADD41681
25	73.8	11.2	421	14	AED59781
26	73.4	11.2	407	3	AAA68013
27	73.4	11.2	407	10	ADD41763
28	66	10.0	66	13	ADQ88325
29	49.4	7.5	5626	4	ABL4766
30	45	6.8	1951	14	ADZ44892
31	43.4	6.6	2000	10	ADC08406
32	43.4	6.6	2000	10	ADC08416
33	43.4	6.6	2199	10	ADC08351
34	43	6.5	378	6	ABQ92788
35	42.6	6.5	2000	8	ADA71732
36	42.4	6.5	110000	11	ACN43984_3
37	42	6.4	61009	14	ADZ12537
38	41.8	6.4	385	6	ABQ92741
39	41.8	6.4	136192	11	ACN44820
40	41.8	6.4	132942	14	ADZ12611
41	41.6	6.3	53981	11	ACN44928
42	41.4	6.3	24080	9	ADA02813
43	41.4	6.3	24080	10	ADB72551
44	41.4	6.3	24080	10	ADC85293
45	41.4	6.3	24080	12	ADM74408

ALIGNMENTS

RESULT 1

ABK17109

ID ABK17109 standard; cDNA; 3070 BP.

XX

AC ABK17109;

XX

DT 26-MAR-2002 (first entry)

XX

DE Eucalyptus grandis promoter polynucleotide #51.

XX

KW Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;

KW temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;

KW PCR primer.

XX

OS Eucalyptus grandis.

XX

XX WO200198485-A1.

XX

PD 27-DEC-2001.

XX

PF 20-JUN-2001; 2001WO-NZ000115.

XX

XX 20-JUN-2000; 2000US-00598401.

XX

PR 28-NOV-2000; 2000US-00724624.

XX

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX

XX (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.

XX

XX Perera R, Rice S, Eagleston C, Lasham A;

XX

XX WPI; 2002-114583/15.

XX

XX Novel polynucleotide promoter sequences from Pine and Eucalyptus useful

XX

XX for modifying expression of endogenous and/or heterologous

XX

XX polynucleotides in transgenic plants.

XX

XX Claim 1; Page 103-104; 121pp; English.

XX

XX The invention relates to isolated promoter sequences from Pinus radiata

XX

XX and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,

XX

XX flower-, pollen-, bud-, meristem-specific promoters or temporally

CC regulated promoters such as xylogenesis-specific promoters. The promoter
CC polypeptides and their related polynucleotides are useful in the
CC production of genetic constructs, used for modifying gene expression in a
CC target organism, in particular a plant. The method is useful for
CC modifying expression of a polynucleotide that comprises an intron
CC sequence, through removal of the intron sequence. The method is useful
CC for modifying growth and development of plants, and cellular responses to
CC external stimulus, such as environmental factors and disease pathogens.
CC The sequences are useful in genome and physical mapping, in positional
CC cloning of genes, in various assays to determine biological activity, to
CC raise antibodies, to isolate corresponding interacting proteins and other
CC compounds, and to quantitatively determine levels of interacting proteins
CC or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata
CC and Eucalyptus grandis polynucleotides and PCR primers used in the method
CC of the invention
XX
SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 657; DB 6; Length 3070;
Best Local Similarity 100.0%; Pred. No. 3e-199;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 60
Db 1019 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 1078

Qy 61 CGAATTTTCTCTTTAGTAAATCAATGATCGCCCATGTTGACAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGTAAATCAATGATCGCCCATGTTGACAAAAGGCTGATTA 1138

Qy 121 GTATGATCTTGGAGTTGTGTGCAAAATTTGCAAGCTGATGCGCCATGTTGACAAAAGGCTGATTA 180
Db 1139 CGAATTTTCTCTTTAGTAAATCAATGATGCGCCCATGTTGACAAAAGGCTGATTA 1138

Qy 1139 GTATGATCTTGGAGTTGTGTGCAAAATTTGCAAGCTGATGCGCCCATGTTGACAAAAGGCTGATTA 1198
Db 1139 GTATGATCTTGGAGTTGTGTGCAAAATTTGCAAGCTGATGCGCCCATGTTGACAAAAGGCTGATTA 1198

Qy 181 AAGCGCCAAACCCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 240
Db 1199 AAGCGCCAAACCCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 1258

Qy 241 ATCATCACCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 300
Db 1259 ATCATCACCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 1318

Qy 301 AACTCCGATTTTCTCTCTATATTTCTGAGTCAATGGCATGGTGACGAATGTACAT 480
Db 1439 TTTTCTCTCTATATTTCTGAGTCAATGGCATGGTGACGAATGTACAT 1498

Qy 481 ATTGTTGAGGTCCCAATTTTGGGAGGGTGTGTAACCGCAAGTTCTCTATATC 540
Db 1499 ATTGTTGAGGTCCCAATTTTGGGAGGGTGTGTAACCGCAAGTTCTCTATATC 1558

Qy 541 GAACCTCCACCACTACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGC 600
Db 1559 GAACCTCCACCACTACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGC 1618

Qy 601 TTTTCTCTGCTGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
Db 1619 TTTTCTCTGCTGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1675

RESULT 2
ADH75529
ID ADH75529 standard; DNA; 3070 BP.
XX
AC ADH75529;
CX

DT 22-APR-2004 (first entry)
XX Eucalyptus grandis superubiquitin related sequence #49.
DE ds; Monterey pine; superubiquitin; promoter; gene expression;
XX transgenic plant.
KW Eucalyptus grandis.
XX WO2003093475-A1.
XX 13-NOV-2003.
PD 30-APR-2003; 2003WO-NZ0000076.
XX 30-APR-2002; 2002US-00137036.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (RUBI-) RUBICON FORESTS HOLDINGS LTD.
XX Rice SJ, Wood M, Eagleton CK, Visser ES, Perera R;
PI WPI; 2003-903678/82.
DR New polynucleotide of the superubiquitin promoter from Pinus radiata,
XX useful in modifying gene expression in a target organism.
PT Disclosure; SEQ ID NO 113; 123pp; English.
PS The invention relates to a new isolated polynucleotide comprising the
XX Pinus radiata (Monterey pine) superubiquitin promoter sequence, its
CC complement, reverse complement, reverse sequence or inverted repeat or a
CC sequence having at least 40, 60, 75 or 90% identity with the promoter.
CC The polynucleotide is useful in modifying gene expression in a target
CC organism, especially in transgenic plants. This sequence corresponds to a
CC superubiquitin promoter related sequence.
XX Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 657; DB 10; Length 3070;
Best Local Similarity 100.0%; Pred. No. 3e-199;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 60
Db 1019 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 1078

Qy 61 CGAATTTTCTCTTTAGTAAATCAATGATGCGCCCATGTTGACAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGTAAATCAATGATGCGCCCATGTTGACAAAAGGCTGATTA 1138

Qy 121 GTATGATCTTGGAGTTGTGTGCAAAATTTGCAAGCTGATGCGCCCATGTTGACAAAAGGCTGATTA 180
Db 1139 GTATGATCTTGGAGTTGTGTGCAAAATTTGCAAGCTGATGCGCCCATGTTGACAAAAGGCTGATTA 1198

Qy 181 AAGCGCCAAACCCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 240
Db 1199 AAGCGCCAAACCCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 1258

Qy 241 ATCATCACCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 300
Db 1259 ATCATCACCAGATTCGAGAGCACATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 1318

Qy 301 AACTCCGATTTTCTCTCTATATTTCTGAGTCAATGGCATGGTGACGAATGTACAT 360
Db 1319 AACTCCGATTTTCTCTCTATATTTCTGAGTCAATGGCATGGTGACGAATGTACAT 1378

Qy 361 AACCACAAAAGTTCAGATCTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 1379 AACCACAAAAGTTCAGATCTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438

Qy 421 TTTTCTCTCTATATTTCTGAGTCAATGGCATGGTGACGAATGTACAT 480
Db 421 TTTTCTCTCTATATTTCTGAGTCAATGGCATGGTGACGAATGTACAT 480

Db 1439 TTTTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCATGCGTGACGAATGTACAT 1498
Qy 481 ATTGCTGTAGGTCCTCAATATTTTGGGAGAGGTTGGTGAACCGCAAAAGTTCCTATATATC 540
Db 1499 ATTGCTGTAGGTCCTCAATATTTTGGGAGAGGTTGGTGAACCGCAAAAGTTCCTATATATC 1558
Qy 541 GAACCTCCACCACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGTC 600
Db 1559 GAACCTCCACCACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGTC 1618
Qy 601 TTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
Db 1619 TTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1675

RESULT 3

ADW80563
ID ADW80563 standard; cDNA; 3070 BP.

XX AC ADW80563;

XX XX 21-APR-2005 (first entry)

XX DE E. grandis caffeic acid O-methyltransferase cDNA SEQ ID NO:113.

XX KW ss; wood; plant; transcription; caffeic acid O-methyltransferase;
XX KW transgenic plant.

XX OS Eucalyptus grandis.

XX FH Key Location/Qualifiers
FT 5'UTR 1. 1643

FT FT /*tag= a

FT FT 1019. 1676

XX FT /*tag= b

XX PN US2005026162-A1.

XX XX 03-FEB-2005.

XX XX 06-NOV-2003; 2003US-00702319.

XX PR 25-MAR-1999; 99US-00276599.

XX PR 30-JUL-1999; 99US-0146591P.

XX PR 24-FEB-2000; 2000WO-NZ000018.

XX PR 20-JUN-2000; 2000US-00598401.

XX PR 28-NOV-2000; 2000US-00724624.

XX PR 09-NOV-2001; 2001US-0345397P.

XX PR 30-APR-2002; 2002US-00137036.

XX PR 08-NOV-2002; 2002US-00291447.

XX PR 08-NOV-2002; 2002US-0425087P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX PA (RUBI-) RUBICON FORESTS HOLDINGS LTD.

XX PI Perera R, Rice SJ, Eagleton CK;

XX WPI; 2005-131806/14.

XX New isolated polynucleotide sequences comprising a functional vascular

XX tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase

XX promoter, useful for modifying gene expression.

XX Claim 2; SEQ ID NO 113; 82pp; English.

XX The invention relates to a novel isolated polynucleotide sequence

XX comprising a functional vascular tissue-specific Eucalyptus grandis

XX caffeic acid O-methyltransferase (COMT) promoter (ADW80462 or ADW80563).

XX Also claimed is a genetic construct comprising the above polynucleotide

XX sequence or a sequence having 20% base pairs fully defined in the

XX specification (ADW80510), a host cell comprising the above genetic

XX construct, a plant comprising the genetic construct, a method for

XX producing a plant with modified gene expression, and a method for

CC identifying a gene responsible for a desired function or phenotype. The
CC composition and methods are useful for modifying gene expression or for
CC modifying the transcription of endogenous and/or heterologous
CC polynucleotides involved in wood formation. The present sequence is used
CC in the exemplification of the invention.

XX SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 657; DB 14; Length 3070;

Best Local Similarity 100.0%; Pred. No. 3e-199;

Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGCCATTTAAATTCGAGAGACATCGCCCAAAATTTATTTCTTCTGTCATAACTGT 60

Db 1019 CTGAGCCATTTAAATTCGAGAGACATCGCCCAAAATTTATTTCTTCTGTCATAACTGT 1078

Qy 61 CGAATTTTCTTTTAGTAAAGTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA 120

Db 1079 CGAATTTTCTTTTAGTAAAGTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA 1138

Qy 121 GTATGATCTTGGAGTTGTTGTCGCAAAATTTTGAAGCTGACGATGCCCTCAGGGAATT 180

Db 1139 GTATGATCTTGGAGTTGTTGTCGCAAAATTTTGAAGCTGACGATGCCCTCAGGGAATT 1198

Qy 181 AAGCGCGCAACCCAGATTGCAAAAGAGACACAAAGAGACGACCCCAACCTTTCTTTAAACAAG 240

Db 1199 AAGCGCGCAACCCAGATTGCAAAAGAGACACAAAGAGACGACCCCAACCTTTCTTTAAACAAG 1258

Qy 241 ATCATACAGATCGGCCAGTAAGGTAATTTAAATTTAAACAATAGCTCTTTGACCGGG 300

Db 1259 ATCATACAGATCGGCCAGTAAGGTAATTTAAATTTAAACAATAGCTCTTTGACCGGG 1318

Qy 301 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAAATTTGTTGGGAAAGCCAGACC 360

Db 1319 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAAATTTGTTGGGAAAGCCAGACC 1378

Qy 361 AACCACAAAAGGTCAGATGTCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Db 1379 AACCACAAAAGGTCAGATGTCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438

Qy 421 TTTTCTCTATATTTCTGTTTACCGTTGAGTCAATGGCATGCGTGACGAATGTACAT 480

Db 1439 TTTTCTCTATATTTCTGTTTACCGTTGAGTCAATGGCATGCGTGACGAATGTACAT 1498

Qy 481 ATTGCTGTAGGTCCTCAATATTTTGGGAGGTTGGTGAACCGCAAAAGTTCCTATATATC 540

Db 1499 ATTGCTGTAGGTCCTCAATATTTTGGGAGGTTGGTGAACCGCAAAAGTTCCTATATATC 1558

Qy 541 GAACCTCCACCACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGTC 600

Db 1559 GAACCTCCACCACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGTC 1618

Qy 601 TTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657

Db 1619 TTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1675

RESULT 4

AAC62762

ID AAC62762 standard; DNA; 661 BP.

XX AC AAC62762;

XX DT 02-FEB-2001 (first entry)

XX DE O-methyl transferase promoter coding sequence #1.

XX KW Promoter; eucalyptus; pine; gene transcription; ds.

XX OS Eucalyptus grandis.

XX XX WO200058474-A1.

XX XX

OY 61 CGAATTTCTCTTTAGGTAAAGTAAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA 120
 DB |||||
 OY 61 CGAATTTCTCTTTAGGTAAAGTAAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA 120
 DB |||||
 OY 121 GTATGATCTTGGAGTGTGTTGGTGAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 180
 DB |||||
 OY 121 GTATGATCTTGGAGTGTGTTGGTGAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 180
 DB |||||
 OY 181 AAGGGCCCAACCCAGATTGCAAGAGCAACAAAGACGACGCCACCTTCTTAAACAG 240
 DB |||||
 OY 181 AAGGGCCCAACCCAGATTGCAAGAGCAACAAAGACGACGCCACCTTCTTAAACAG 240
 DB |||||
 OY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAAATAGCTCTTGTACCGGG 300
 DB |||||
 OY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAAATAGCTCTTGTACCGGG 300
 DB |||||
 OY 301 AACTCGGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACGCC 360
 DB |||||
 OY 301 AACTCGGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACGCC 360
 DB |||||
 OY 361 AACCACAAAAGGTGAGATGTCATCCAC----GAGAGAGAGAGAGAGAGAGAGAG 416
 DB |||||
 OY 361 AACCACAAAAGGTGAGATGTCATCCAC----GAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB |||||
 OY 417 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGGCATGCGTGACGAATGT 476
 DB |||||
 OY 421 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGGCATGCGTGACGAATGT 480
 DB |||||
 OY 477 ACATATTTGGTGTAGGGTCAATATTTTTCGGGAGGGTTGGTGAACCGCAAAAGTTCTCTATA 536
 DB |||||
 OY 481 ACATATTTGGTGTAGGGTCAATATTTTTCGGGAGGGTTGGTGAACCGCAAAAGTTCTCTATA 540
 DB |||||
 OY 537 TATCGAAGCTCCACCACTACCTCACTTCAATCCCACTTATTCGGTTTATTTCTCT 596
 DB |||||
 OY 541 TATCGAAGCTCCACCACTACCTCACTTCAATCCCACTTATTCGGTTTATTTCTCT 600
 DB |||||
 OY 597 CTGCTTTCTCTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656
 DB |||||
 OY 601 CTGCTTTCTCTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB |||||
 OY 657 T 657
 DB |||||
 OY 661 T 661
 DB |||||

RESULT 6

ADH75428
 ID ADH75428 standard; DNA; 661 BP.

XX AC ADH75428;

XX DT 22-APR-2004 (first entry)

XX DE Eucalyptus grandis superubiquitin related sequence #6.

XX KW ds; Monterey pine; superubiquitin; promoter; gene expression;
 transgenic plant.

XX OS Eucalyptus grandis.

XX PN W02003093475-A1.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-NZ0000076.

XX PR 30-APR-2002; 2002US-00137036.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.
 (RUBI-) RUBICON FORESTS HOLDINGS LTD.

XX PI Rice SJ, Wood M, Bagleton CK, Visser ES, Perera R;

XX WPI; 2003-903678/82.
 XX DR New polynucleotide of the superubiquitin promoter from Pinus radiata,
 PT useful in modifying gene expression in a target organism.
 XX PS Disclosure; SEQ ID NO 12; 123pp; English.
 XX CC The invention relates to a new isolated polynucleotide comprising the
 CC Pinus radiata (Monterey pine) superubiquitin promoter sequence, its
 CC complement, reverse complement, reverse sequence or inverted repeat or a
 CC sequence having at least 40, 60, 75 or 90% identity with the promoter.
 CC The polynucleotide is useful in modifying gene expression in a target
 CC organism, especially in transgenic plants. This sequence corresponds to a
 CC superubiquitin promoter related sequence.
 XX SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 97.1%; Score 638.2; DB 10; Length 661;
 Best Local Similarity 98.9%; Pred. No. 1.5e-193;
 Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

OY 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTTATTTCTTCTGCTGCCATAACTGT 60
 DB |||||
 OY 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTTATTTCTTCTGCTGCCATAACTGT 60
 DB |||||
 OY 61 CGAATTTTCTCTTTAGGTAAAGTAAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA 120
 DB |||||
 OY 61 CGAATTTTCTCTTTAGGTAAAGTAAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTA 120
 DB |||||
 OY 121 GTATGATCTTGGAGTGTGTTGGTGAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 180
 DB |||||
 OY 121 GTATGATCTTGGAGTGTGTTGGTGAATTTGCAAGCTGACGATGCGCCCTCAGGGAAT 180
 DB |||||
 OY 181 AAGGGCCCAACCCAGATTGCAAGAGCAACAAAGACGACGCCACCTTCTTAAACAG 240
 DB |||||
 OY 181 AAGGGCCCAACCCAGATTGCAAGAGCAACAAAGACGACGCCACCTTCTTAAACAG 240
 DB |||||
 OY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAAATAGCTCTTGTACCGGG 300
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 OY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAAATAGCTCTTGTACCGGG 300
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 OY 301 AACTCGGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACGCC 360
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 OY 481 ACATATTTGGTGTAGGGTCAATATTTTTCGGGAGGGTTGGTGAACCGCAAAAGTTCTCTATA 540
 DB |||||
 OY 537 TATCGAAGCTCCACCACTACCTCACTTCAATCCCACTTATTCGGTTTATTTCTCT 596
 DB |||||
 OY 541 TATCGAAGCTCCACCACTACCTCACTTCAATCCCACTTATTCGGTTTATTTCTCT 600
 DB |||||
 OY 597 CTGCTTTCTCTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656
 DB |||||
 OY 601 CTGCTTTCTCTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB |||||
 OY 657 T 657
 DB |||||
 OY 661 T 661
 DB |||||

RESULT 7
 ADW80462

ADW80462 standard; cDNA; 661 BP.	
ADW80462;	
21-APR-2005 (first entry)	
E. grandis caffeic acid O-methyltransferase promoter SEQ ID NO:12.	
ss; wood; plant; transcription; caffeic acid O-methyltransferase;	
transgenic plant.	
Eucalyptus grandis.	
Key Location/Qualifiers	
TATA_signal 537..543	
/*tag= a	
US2005026162-A1.	
03-FEB-2005.	
06-NOV-2003; 2003US-00702319.	
25-MAR-1999; 99US-00276599.	
30-JUL-1999; 99US-0146591P.	
24-FEB-2000; 2000WO-NZ000018.	
20-JUN-2000; 2000US-00598401.	
28-NOV-2000; 2000US-00724624.	
09-NOV-2001; 2001US-0345397P.	
30-APR-2002; 2002US-00137036.	
08-NOV-2002; 2002US-00291447.	
08-NOV-2002; 2002US-0425087P.	
(GENE-) GENESIS RES & DEV CORP LTD.	
(RUBI-) RUBICON FORESTS HOLDINGS LTD.	
Perera R, Rice SJ, Eagleton CK;	
WPI; 2005-131806/14.	
New isolated polynucleotide sequences comprising a functional vascular tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase promoter, useful for modifying gene expression.	
Claim 2; SEQ ID NO 12; 82pp; English.	
The invention relates to a novel isolated polynucleotide sequence comprising a functional vascular tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase (cOMT) promoter (ADW80462 or ADW80563).	
Also claimed is a genetic construct comprising the above polynucleotide sequence or a sequence having 20% base pairs fully defined in the specification (ADW80510), a host cell comprising the above genetic construct, a plant comprising the genetic construct, a method for producing a plant with modified gene expression, and a method for identifying a gene responsible for a desired function or phenotype. The composition and methods are useful for modifying gene expression or for modifying the transcription of endogenous and/or heterologous polynucleotides involved in wood formation. The present sequence is used in the exemplification of the invention.	
Seq Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;	
Query Match 97.1%; Score 638.2; DB 14; Length 661;	
Best Local Similarity 98.9%; Pred. No. 1.5e-193;	
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;	
Qy 1 CTGAGCCATTAAATTCGAGAGCACATGCCCAAAATTAATCTCTTGCTGCCATAACTGT 60	
Db 1 CTGAGCCATTAAATTCGAGAGCACATGCCCAAAATTAATCTCTTGCTGCCATAACTGT 60	
Qy 61 CGAATTTTCTCTTTTAGGTAAAGTACCAATGATCGCCATGTTGACAAAAGGCTGATTA 120	
Db 61 CGAATTTTCTCTTTTAGGTAAAGTACCAATGATCGCATCATGTCACAAAAGGCTGATTA 120	

QY	121	GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT	180
DB	121	GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT	180
QY	181	AAGGGCCCAACCCAGATTGCAAAAGAGCAAAAGAGACGACCCAACTTTCCTTAAACAAG	240
DB	181	AAGGGCCCAACCCAGATTGCAAAAGAGCAAAAGAGACGACCCAACTTTCCTTAAACAAG	240
QY	241	ATCATCACCAGATCGGCCAGTAAGGTTATATTAATTAACAAATAGCTCTTGTACCGGG	300
DB	241	ATCATCACCAGATCGGCCAGTAAGGTTATATTAATTAACAAATAGCTCTTGTACCGGG	300
QY	301	AACCTCGTATTTCTCTCACTTCCATAAACCCCTGATTAAATTTGGTGGGAAAGCGACGCC	360
DB	301	AACCTCGTATTTCTCTCACTTCCATAAACCCCTGATTAAATTTGGTGGGAAAGCGACGCC	360
QY	361	AACCCCAAAAAGTCAAGTGTATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAG	416
DB	361	AACCCCAAAAAGTCAAGTGTATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAG	420
QY	417	AGAGTTTTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCATGCGTGACGAATGT	476
DB	421	AGAGTTTTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCATGCGTGACGAATGT	480
QY	477	ACATATTTGGTAGGGTCCAAATATTTTGGGGAGGGTTGGTGAAACCGCAAAAGTTCTCTATA	536
DB	481	ACATATTTGGTAGGGTCCAAATATTTTGGGGAGGGTTGGTGAAACCGCAAAAGTTCTCTATA	540
QY	537	TATCGAACCTCCACCAACATACCTCACTTCAATCCCAATTCCTGTTTATTTTCCT	596
DB	541	TATCGAACCTCCACCAACATACCTCACTTCAATCCCAATTCCTGTTTATTTTCCT	600
QY	597	CTGCTTTTCTTCTGCTGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	656
DB	601	CTGCTTTTCTTCTGCTGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	660
QY	657	T 657	
DB	661	T 661	
RESULT 8			
AAC62810			
ID	AAC62810 standard; DNA; 2096 BP.		
XX	AAC62810;		
AC	AAC62810;		
XX	02-FEB-2001 (first entry)		
DT	O-methyl transferase promoter coding sequence #2.		
XX	Promoter; eucalyptus; pine; gene transcription; ds.		
DE	Eucalyptus grandis.		
XX	WO200058474-A1.		
XX	05-OCT-2000.		
XX	24-FEB-2000; 2000WO-NZ000018.		
XX	25-MAR-1999; 99US-00276599.		
PR	30-JUL-1999; 99US-0146591P.		
XX	(GENE-) GENESIS RES & DEV CORP LTD.		
PA	(FLET-) FLETCHER CHALLENGE FORESTS LTD.		
XX	Perera R, Rice SJ, Eagleton CK;		
XX	WPI; 2000-647236/62.		
DR	P-PSDB; AAB28142.		
XX			

PT Novel promoter sequences useful for modulating transcription of plant DNA
 PT sequences of interest and production of polypeptides.

PS Claim 1; Page 61-62; 93pp; English.

CC The present invention relates to promoter sequences from eucalyptus and
 CC pine. The present sequence is one such promoter. This sequence is useful
 CC for modulating the transcription of DNA sequences of interest. The
 CC sequences may also be used to tag or identify an organism or its
 CC reproductive material

XX Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;

Query Match 97.1%; Score 638.2; DB 3; Length 2096;
 Best Local Similarity 98.9%; Pred. No. 2.6e-193;
 Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 CTGAGCCATTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 60
 DB 41 CTGAGCCATTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 100
 QY 61 CGAATTTTCTTTTAGTAAAGTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 120
 DB 101 CGAATTTTCTTTTAGTAAAGTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 160
 QY 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 180
 DB 161 GTATGATCTTGGAGTTGTTGGTGCAAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 220
 QY 181 AAGCGCCCAACCCAGATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 240
 DB 221 AAGCGCCCAACCCAGATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 280
 QY 241 ATCATCAGCAGATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 300
 DB 281 ATCATCAGCAGATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 340
 QY 301 AACTCCGTTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 360
 DB 341 AACTCCGTTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 400
 QY 361 AACCCACAAAAGGTGAGATTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
 DB 401 AACCCACAAAAGGTGAGATTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
 QY 417 AGAGTTTCTCTCTATATTTCTGTTTCAACGGTTGAGTCAATGGATCGGTGAGCAATGT 476
 DB 461 AGAGTTTCTCTCTATATTTCTGTTTCAACGGTTGAGTCAATGGATCGGTGAGCAATGT 520
 QY 477 ACATATTTGTTGAGGTGCAATATTTTGGGAGGTTGTTGAAACCGCAAAAGTTTCTTATA 536
 DB 521 ACATATTTGTTGAGGTGCAATATTTTGGGAGGTTGTTGAAACCGCAAAAGTTTCTTATA 580
 QY 537 TATCGAATCTCCACCAACCATCTCACTTCAATCCCACTTATTCGTTTATTTCTTCT 596
 DB 581 TATCGAATCTCCACCAACCATCTCACTTCAATCCCACTTATTCGTTTATTTCTTCT 640
 QY 597 CTGCTTTCTTCTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656
 DB 641 CTGCTTTCTTCTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
 QY 657 T 657
 DB 701 T 701

RESULT 9
 ID ABK17075
 AC ABK17075 standard; cDNA; 2096 BP.
 XX
 XX ABK17075;
 DT 26-MAR-2002 (first entry)

XX Eucalyptus grandis promoter polynucleotide #31.

XX Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;
 KW temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
 KW PCR primer.

OS Eucalyptus grandis.

XX WO200198485-A1.

XX 27-DEC-2001.

XX 20-JUN-2001; 2001WO-NZ000115.

XX 20-JUN-2000; 2000US-00598401.

XX 28-NOV-2000; 2000US-00724624.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.

XX Perera R, Rice S, Eagleton C, Lasham A;

XX WPI; 2002-114583/15.

XX P-PSDB; RAU80760.

XX Novel polynucleotide promoter sequences from pine and Eucalyptus useful
 for modifying expression of endogenous and/or heterologous
 polynucleotides in transgenic plants.

XX Claim 1; Page 78; 121pp; English.

XX The invention relates to isolated promoter sequences from Pinus radiata
 and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,
 flower-, pollen-, bud-, meristem-specific promoters or temporally
 regulated promoters such as xylogenesis-specific promoters. The promoter
 polypeptides and their related polynucleotides are useful in the
 production of genetic constructs, used for modifying gene expression in a
 target organism, in particular a plant. The method is useful for
 modifying expression of a polynucleotide that comprises an intron
 sequence, through removal of the intron sequence. The method is useful
 for modifying growth and development of plants, and cellular responses to
 external stimulus, such as environmental factors and disease pathogens.
 The sequences are useful in genome and physical mapping, in positional
 cloning of genes, in various assays to determine biological activity, to
 raise antibodies, to isolate corresponding interacting proteins and other
 compounds, and to quantitatively determine levels of interacting proteins
 or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata
 and Eucalyptus grandis polynucleotides and PCR primers used in the method
 of the invention

XX Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;

Query Match 97.1%; Score 638.2; DB 6; Length 2096;
 Best Local Similarity 98.9%; Pred. No. 2.6e-193;
 Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 CTGAGCCATTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 60
 DB 41 CTGAGCCATTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 100
 QY 61 CGAATTTTCTTTTAGTAAAGTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 120
 DB 101 CGAATTTTCTTTTAGTAAAGTAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 160
 QY 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 180
 DB 161 GTATGATCTTGGAGTTGTTGGTGCAAAATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 220
 QY 181 AAGCGCCCAACCCAGATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 240
 DB 221 AAGCGCCCAACCCAGATTCGAGAGACATCGCCAAAATTAATTCCTTCTGTCGCAATACCTGT 280

QY 241 ATCATCACCAGATCGCCAGTAAGGTAATATTAATTAACAATACTCTCTGTACCGGG 300
 Db |||||
 QY 281 ATCATCACCAGATCGCCAGTAAGGTAATATTAATTAACAATACTCTCTGTACCGGG 340
 Db |||||
 QY 301 AACTCCGTAATTTCTCTCACTTCCATAAACCCTGATTAATTTGGTGGAAAGCGACAGCC 360
 Db |||||
 QY 341 AACTCCGTAATTTCTCTCACTTCCATAAACCCTGATTAATTTGGTGGAAAGCGACAGCC 400
 Db |||||
 QY 361 AACCACAAGGTGAGATGTCATCCAC----GAGAGAGAGAGAGAGAGAGAGAG 416
 Db |||||
 QY 401 AACCACAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
 Db |||||
 QY 417 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGCGATGCGTGAAGATGT 476
 Db |||||
 QY 461 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGCGATGCGTGAAGATGT 520
 Db |||||
 QY 477 ACATATTTGGTGTAGGGTCCCAATATTTTTCGCGGAGGGTGGTGAACCCGAAAGTTTCTTATA 536
 Db |||||
 QY 521 ACATATTTGGTGTAGGGTCCCAATATTTTTCGCGGAGGGTGGTGAACCCGAAAGTTTCTTATA 580
 Db |||||
 QY 537 TATCGAACCTCCACACATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTTCT 596
 Db |||||
 QY 581 TATCGAACCTCCACACATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTTCT 640
 Db |||||
 QY 597 CTGCTTTTCTTCTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGATGGT 656
 Db |||||
 QY 641 CTGCTTTTCTTCTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGATGGT 700
 Db |||||
 QY 657 T 657
 Db 701 T 701

RESULT 10
 ADH75476
 ID ADH75476 standard; DNA; 2096 BP.
 XX
 AC ADH75476;
 XX
 XX
 DT 22-APR-2004 (first entry)
 XX
 XX Eucalyptus grandis superubiquitin related sequence #31.
 XX
 XX ds; Monterey pine; superubiquitin; promoter; gene expression;
 KW transgenic plant.
 XX
 XX Eucalyptus grandis.
 XX
 XX WO2003093475-A1.
 XX
 XX 13-NOV-2003.
 XX
 XX 30-APR-2003; 2003WO-NZ0000076.
 XX
 XX 30-APR-2002; 2002US-00137036.
 XX
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX (RUBI-) RUBICON FORESTS HOLDINGS LTD.
 XX
 XX Rice SJ, Wood M, Eagleton CK, Visser ES, Perera R;
 XX WPI, 2003-903678/82.
 XX
 XX New polynucleotide of the superubiquitin promoter from Pinus radiata,
 XX useful in modifying gene expression in a target organism.
 XX
 XX Disclosure; SEQ ID NO 60; 123pp; English.
 XX
 XX The invention relates to a new isolated polynucleotide comprising the
 CC Pinus radiata (Monterey pine) superubiquitin promoter sequence, its
 CC complement, reverse complement, reverse sequence or inverted repeat or a
 CC sequence having at least 40, 60, 75 or 90% identity with the promoter.
 CC The polynucleotide is useful in modifying gene expression in a target

CC organism, especially in transgenic plants. This sequence corresponds to a
 CC superubiquitin promoter related sequence.
 XX
 SQ Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;
 Query Match 97.1%; Score 638.2; DB 10; Length 2096;
 Best Local Similarity 98.9%; Pred. No. 2.6e-193;
 Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
 QY 1 CTGAGCCATTTAATTCGAGAGCACAATGCAATGATGCGCCATGTTGACAAAGGCTGATTA 120
 Db |||||
 QY 61 CGAATTTTCTCTTTAGGTAAGTAACTAATGATGCGCCATGTTGACAAAGGCTGATTA 160
 Db |||||
 QY 101 CGAATTTTCTCTTTAGGTAAGTAACTAATGATGCGCCATGTTGACAAAGGCTGATTA 220
 Db |||||
 QY 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGAAAT 180
 Db |||||
 QY 161 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGAAAT 240
 Db |||||
 QY 181 AAGGCGCCAAACCCAGATTTGCAAGGTAAGGTAAGTAACTAATGATGCGCCATGTTGACAAAG 280
 Db |||||
 QY 221 AAGGCGCCAAACCCAGATTTGCAAGGTAAGGTAAGTAACTAATGATGCGCCATGTTGACAAAG 300
 Db |||||
 QY 241 ATCATCACCAGATCGGCGCAGTAAGGTAAGTAACTAATGATGCGCCATGTTGACAAAG 340
 Db |||||
 QY 281 ATCATCACCAGATCGGCGCAGTAAGGTAAGTAACTAATGATGCGCCATGTTGACAAAG 360
 Db |||||
 QY 301 AACTCCGTAATTTCTCTCACTTCCATAAACCCTGATTAATTTGGTGGAAAGCGACAGCC 400
 Db |||||
 QY 341 AACTCCGTAATTTCTCTCACTTCCATAAACCCTGATTAATTTGGTGGAAAGCGACAGCC 416
 Db |||||
 QY 361 AACCACAAGGTGAGATGTCATCCAC----GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
 Db |||||
 QY 401 AACCACAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
 Db |||||
 QY 417 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGCGATGCGTGAAGATGT 520
 Db |||||
 QY 461 AGAGTTTCTCTCTATATTTCTGTTTCCCGGTTGGAGTCAATGCGATGCGTGAAGATGT 536
 Db |||||
 QY 477 ACATATTTGGTGTAGGGTCCCAATATTTTTCGCGGAGGGTGGTGAACCCGAAAGTTTCTTATA 580
 Db |||||
 QY 521 ACATATTTGGTGTAGGGTCCCAATATTTTTCGCGGAGGGTGGTGAACCCGAAAGTTTCTTATA 596
 Db |||||
 QY 537 TATCGAACCTCCACACATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTTCT 640
 Db |||||
 QY 581 TATCGAACCTCCACACATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTTCT 656
 Db |||||
 QY 597 CTGCTTTTCTTCTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGATGGT 700
 Db |||||
 QY 641 CTGCTTTTCTTCTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGATGGT 700
 Db |||||
 QY 657 T 657
 Db 701 T 701

RESULT 11
 ADW80510
 ID ADW80510 standard; cDNA; 2096 BP.
 XX
 AC ADW80510;
 XX
 XX
 DT 21-APR-2005 (first entry)
 XX
 XX E. grandis caffeic acid O-methyltransferase related cDNA SEQ ID NO:60.
 DE
 XX ss; wood; plant; transcription; caffeic acid O-methyltransferase;
 KW transgenic plant.
 XX
 XX Eucalyptus grandis.
 XX

XX SQ Sequence 534 BP; 151 A; 126 C; 119 G; 138 T; 0 U; 0 Other;
 Query Match 81.3%; Score 534; DB 13; Length 534;
 Best Local Similarity 100.0%; Pred. No. 3.3e-160;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 92 ATGCGCCATGTTGACAAAAGGCTGATTAGTATGATCTTTGGAGTTGTTGGTGCAAAATTTG 151
 DB 1 ATGCGCCATGTTGACAAAAGGCTGATTAGTATGATCTTTGGAGTTGTTGGTGCAAAATTTG 60
 QY 152 CAAGCTGACGATGCCCTCAGGGAATTAAGGCGCCAAACCCAGATTGCAAAAGAGCACA 211
 DB 61 CAAGCTGACGATGCCCTCAGGGAATTAAGGCGCCAAACCCAGATTGCAAAAGAGCACA 120
 QY 212 AGACAGACCCAACTTTCTTAAAGATCATCAGATCGGCGAGTAAGGTTAATA 271
 DB 121 AGACAGACCCAACTTTCTTAAAGATCATCAGATCGGCGAGTAAGGTTAATA 180
 QY 272 TTAATTTAAACAAATAGCTTTGTACCGGAACCTCGTATTCTCTCACTTCCATAAACCC 331
 DB 181 TTAATTTAAACAAATAGCTTTGTACCGGAACCTCGTATTCTCTCACTTCCATAAACCC 240
 QY 332 CTGATTAATTTGGTGGAAAGCGACAGCCAAACCCAAAGGTCAGATGTCATCCACGA 391
 DB 241 CTGATTAATTTGGTGGAAAGCGACAGCCAAACCCAAAGGTCAGATGTCATCCACGA 300
 QY 392 GAG 451
 DB 301 GAG 360
 QY 452 AGTCAATGGCATGCGTGACGAATGTACATATTGGTGTAGGTCCTCAATATTTCGGGAGG 511
 DB 361 AGTCAATGGCATGCGTGACGAATGTACATATTGGTGTAGGTCCTCAATATTTCGGGAGG 420
 QY 512 GTTGGTGAACCGGAAAGTTTCTATATATCGAACCTCCACCACTACCTCACTTCAATCC 571
 DB 421 GTTGGTGAACCGGAAAGTTTCTATATATCGAACCTCCACCACTACCTCACTTCAATCC 480
 QY 572 CCACCATTTACCGTTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 625
 DB 481 CCACCATTTACCGTTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 534
 RESULT 13
 ADQ88320 standard; DNA; 485 BP.
 XX AC ADQ88320;
 XX DT 21-OCT-2004 (first entry)
 XX DE Eucalyptus grandis COMT promoter #2.
 XX KW Transcription; xylogenes; gene expression; transgenic plant; lignin;
 XX KW cellulose; wood; disease resistance;
 XX KW caffeic acid 3-O-methyl transferase promoter; COMT promoter; xylem; ds.
 XX OS Eucalyptus grandis.
 XX PN US2004146904-A1.
 XX PD 29-JUL-2004.
 XX PF 07-NOV-2003; 2003US-00703091.
 XX PR 21-NOV-2002; 2002US-0428087P.
 XX PA (ARBO-) ARBORGEN LLC.
 XX PI Phillips J, Eagleton C;
 XX WP 2004-552666/53.

XX PT New isolated polynucleotide from Eucalyptus grandis that is capable of
 PT initiating and promoting transcription of polynucleotides in plant cells
 PT undergoing xylogenesis, useful in altering lignin content of plants.
 XX PS Claim 1; SEQ ID NO 2; 32pp; English.
 XX CC The invention relates to promoter sequences from Eucalyptus grandis that
 CC is capable of initiating and promoting transcription of polynucleotides
 CC in plant cells undergoing xylogenesis. The invention also provides DNA
 CC construct comprising the promoter and a desired nucleic acid, which can
 CC be used for regulating gene expression in a transgenic plant. The DNA
 CC constructs comprising the promoter sequences of the invention can be used
 CC to regulate the expression of lignin biosynthetic gene and thereby alter
 CC the lignin content in plants, to modify properties such as cellulose
 CC synthesis, wood development, flower development and disease resistance.
 CC The present sequence is Eucalyptus grandis caffeic acid 3-O-methyl
 CC transferase (COMT) promoter that confers xylem-preferred gene expression
 CC in a plant cell.
 XX SQ Sequence 485 BP; 138 A; 120 C; 105 G; 122 T; 0 U; 0 Other;
 Query Match 73.8%; Score 485; DB 13; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.6e-144;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 141 GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCAAACCCAGATTGC 200
 DB 1 GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCAAACCCAGATTGC 60
 QY 201 AAAGAGCACAAG 260
 DB 61 AAAGAGCACAAG 120
 QY 261 TAAGGTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 320
 DB 121 TAAGGTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
 QY 321 TCCATAAACCCTGATTAAATTTGGTGGAAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
 DB 181 TCCATAAACCCTGATTAAATTTGGTGGAAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 381 TCATCCACGAG 440
 DB 241 TCATCCACGAG 300
 QY 441 TCACCGTTGGAGTCAATGGCATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATAT 500
 DB 301 TCACCGTTGGAGTCAATGGCATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATAT 360
 QY 501 TTTGGCGGAGGGTTGGTGAACCGCAAGTTCCCTATATATCGAACCTCCACCACTACCT 560
 DB 361 TTTGGCGGAGGGTTGGTGAACCGCAAGTTCCCTATATATCGAACCTCCACCACTACCT 420
 QY 561 CACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 620
 DB 421 CACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
 QY 621 CGGAA 625
 DB 481 CGGAA 485
 RESULT 14
 ADQ88321
 ID ADQ88321 standard; DNA; 306 BP.
 XX AC ADQ88321;
 XX DT 21-OCT-2004 (first entry)
 XX DE Eucalyptus grandis COMT promoter #3.
 XX WP 2004-552666/53.

Search completed: November 1, 2006, 00:21:19
Job time : 280.948 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:29:19 ; Search time 2135.12 Seconds
(without alignments)
17207.024 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1675

Perfect score: 657

Sequence: 1 ctgagccatttaattcgaga.....aggagagagagaatgggtt 657

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1.*
- 2: gb_est3.*
- 3: gb_est4.*
- 4: gb_est5.*
- 5: gb_est6.*
- 6: gb_est7.*
- 7: gb_est8.*
- 8: gb_est9.*
- 9: gb_est10.*
- 10: gb_est11.*
- 11: gb_est12.*
- 12: gb_est13.*
- 13: gb_est14.*
- 14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47.6	7.2	561	12	CE792380 tigr-gss-
2	47.4	7.2	760	12	BZ731304 OGPBZ50TC
3	46.6	7.1	831	14	AG553107 Mus muscu
4	46.4	7.1	619	10	DT310002 JGI_CAA1
5	45.8	7.0	349	7	BB931786 BB931786
6	45.8	7.0	799	5	CK600115 AGENCOURT
7	45.6	6.9	589	11	AZ829144 2M0106C09
8	45.4	6.9	675	10	DV761691 PchrsEQ00
9	45	6.8	1019	10	DW344263 PP_LEC001
10	44.8	6.8	771	14	AG403694 Mus muscu
11	44.8	6.8	778	10	DT234659 JGI_CAA1
12	44.6	6.8	363	12	BZ708983 OGEAW43TM
13	44.6	6.8	543	11	BZ306338 hx41a10.b
14	44.6	6.8	588	11	BH873693
15	44.6	6.8	669	12	CC693540 OGWFDS96TV
16	44.6	6.8	677	12	CG241281 OGWA391TV
17	44.6	6.8	746	11	AZ360328 IM0103G20
18	44.6	6.8	776	14	CNS01JUK
19	44.6	6.8	927	12	CC671328 OGWCY78TV

c	20	44.4	6.8	499	11	AZ058431
	21	44.4	6.8	550	4	AX250092 BX250092
	22	44.4	6.8	658	11	AZ592362 IM0403A17
	23	44.4	6.8	757	11	BZ076780 lxf74g10.
	24	44.2	6.7	666	1	AV368360 AV368360
	25	44.2	6.7	719	10	DT726802 EST116065
	26	44.2	6.7	759	10	DM103368 CLPZ739.b
	27	44.2	6.7	989	14	CNS05R2J
	28	44	6.7	408	8	CO910517 BJ03007C0
	29	44	6.7	522	11	AZ440830 IM0232P06
	30	43.8	6.7	879	10	DW345288 PP_LEC002
	31	43.8	6.7	897	14	AG844971 Oryza sat
	32	43.6	6.6	232	11	BZ280453 CH230-309
	33	43.6	6.6	440	11	AZ001211 RPCI-23-3
	34	43.6	6.6	442	14	CR192806 Reverse s
	35	43.6	6.6	597	11	AZ460974 IM0266C08
	36	43.6	6.6	717	12	CE081925 tigr-gss-
	37	43.6	6.6	750	14	AG482398 Mus muscu
	38	43.6	6.6	810	8	CN531411 UI-M-HQ0-
	39	43.4	6.6	1044	3	BM800931 AGENCOURT
	40	43.4	6.6	1100	11	BZ117558 CH230-460
	41	43.4	6.6	3304	6	AK079471 Mus muscu
	42	43.2	6.6	508	3	BQ103940 G90575.e
	43	43.2	6.6	600	2	BG803750 0241-38 M
	44	43.2	6.6	738	14	AG562107 Mus muscu
	45	43	6.5	216	11	AZ384008 IM0141D19

ALIGNMENTS

RESULT 1
CE792380/c
LOCUS tigr-gss-dog-17000330896927 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE792380
VERSION CE792380.1 GI:37133144
KEYWORDS GSS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 561)
AUTHORS Kirchner,S.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
Location/Qualifiers
source
1. 561
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BatXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 7.2%; Score 47.6; DB 12; Length 561;
Best Local Similarity 62.7%; Pred. No. 0.015;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

[illegible]

```

VERSION DT310002.1 GI:73650665
KEYWORDS EST.
SOURCE Pinephales promelas
ORGANISM Pinephales promelas
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriiniformes; Cyprinidae; Pinephales.
1 (bases 1 to 619)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Pinephales promelas EST project
Unpublished (2005)
Other ESTs: JGI CAAX1533.fwd
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues
at the beginning of the sequence, this clone was polyadenylated.
The resulting Poly-T sequence has been removed.
Plate: CAAX 0013 row: j column: 24
High quality sequence stop: 348
POLYA=Yes.
FEATURES
source
Location/Qualifiers
1..619
/organism="Pinephales promelas"
/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CAAX1533"
/tissue_type="testis"
/clone_lib="CAAX Pinephales promelas testis 7-8 month
adults, males and females pooled (L)"
/note="Vector: pCMVsp6; The library was made from dr
primed cDNA and cloned into Invitrogen vector pCMVsp6.
Poly A RNA were primed with an oligo dt primer (5'-
GACTAGTCTGATCGGAGCGCGCGCCCTTTTCTTTT-3') ligated
to a SalI adapter (5'- TCGACCCAGCGTCG and 5'-
CGGACGCTGG) and digested with NotI. cDNA was size
selected using 1.1% agarose gel electrophoresis (L
-0.5-1.2k, M -1.2-2.5k, H ~2.5k) then ligated into NotI
and SalI digested pCMVsp6 vector. The work was done at
DOE Joint Genome Institute."
ORIGIN
Query Match 7.1%; Score 46.4; DB 10; Length 619;
Best Local Similarity 70.5%; Pred. No. 0.035;
Matches 62; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 333 TGATTAAATTTGGTGGAAAGCGACGACCAACCCCAAAAGTCTCATGATGTCATCCACGAG 392
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
214 TGTTCAGTTCGGGAAAGACAGACCAACCACTCCAGACCAACCACTCCAGAGAGAG 155
Qy 393 AGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
154 AGAGAGAGAGAGAGAGAGAGAGAGAGAG 127
RESULT 5
LOCUS BB931786 349 bp mRNA linear EST 29-JAN-2006
DEFINITION BB931786 Trifolium pratense three week-old plant SSR-enriched
library Trifolium pratense cDNA clone RCC03640, mRNA sequence.
ACCESSION BB931786
VERSION BB931786.1 GI:86120577

KEYWORDS EST.
SOURCE Trifolium pratense
ORGANISM Trifolium pratense
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Trifolium.
1 (bases 1 to 349)
Sato, S., Isobe, S., Asamizu, E., Nakamura, Y., Ohmido, N., Sakurai, N.,
Klimenko, I., Sasamoto, S., Wada, T., Watanabe, A. and Tabata, S.
Comprehensive structural analysis of the genome of red clover
(Unpublished (2006))
JOURNAL Trifolium pratense
COMMENT The First Laboratory for Plant Gene Research
Contact: Erika Asamizu
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
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Location/Qualifiers
1..349
/organism="Trifolium pratense"
/mol_type="mRNA"
/db_xref="taxon:57577"
/clone="RCC03640"
/dev_stage="three week-old plant"
/clone_lib="Trifolium pratense three week-old plant
SSR-enriched library"
/note="Vector: p7Blue T-Vector; Site_1: EcoRV; variety:
Hokuseki"
ORIGIN
Query Match 7.0%; Score 45.8; DB 7; Length 349;
Best Local Similarity 62.8%; Pred. No. 0.046;
Matches 71; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 347 GGAAGGCGACGACCAACCCCAAAAGTCTCATGATGTCATCCACGAGAGAGAGAGAG 406
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
233 GAAATAGCAACCAACCCCAAAATCTAAACTATTAGCGAGAGAGAGAGAGAGAGAG 292
Qy 407 AGAGAGAGAGAGAGAGTTTCTCTCTATATTCGTTTCCCGGTTGAGTCAATG 459
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
293 AGAGAGAGAGAGTTGTTATTGTTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 345
RESULT 6
LOCUS CK600115 799 bp mRNA linear EST 22-JAN-2004
DEFINITION AGENCOURT 17895063 NIH MGC 234 Rattus norvegicus cDNA clone
IMAGE:7189967 5', mRNA sequence.
ACCESSION CK600115
VERSION CK600115.1 GI:41113272
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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FEATURES

[illegible]

RESULT 11
DT234659/c
LOCUS
DEFINITION
DT234659 778 bp mRNA linear EST 17-AUG-2005
JGI CAAT8286.rev CAAT Pimephales promelas brain 7-8 month adults,
males and females pooled (M) Pimephales promelas cDNA clone
CAAT8286 3', mRNA sequence.
DT234659
DT234659.1 GI:73504794
EST.
Pimephales promelas
Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Pimephales.
1 (bases 1 to 778)
Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Pimephales promelas EST project
Unpublished (2005)
Other ESTs: JGI CAAT8286.fwd
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
CDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues
at the beginning of the sequence, this clone was polyadenylated.
The resulting Poly-T sequence has been removed.
Plate: CAAT 0085 row: K column: 8
High quality sequence stop: 778
POLYA=Yes.

FEATURES
source
1..778
Location/Qualifiers
/organism="Pimephales promelas"
/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CAAT8286"
/tissue type="brain"
/clone_lib="CAAT Pimephales promelas brain 7-8 month
adults, males and females pooled (M)"
/notes="Vector: pCMVsp6; The library was made from dt
primed cDNA and cloned into an invitrogen vector pCMVsp6.
Poly A RNA were primed with an oligo dt primer (5'
GACTAGTCTTAGATCGGCGCGCCCTTTTCTTTTCTTTT -3') ligated
to a SalI adapter (5'-TCGACCCGCGTCCG and 5'-
CGACGCGTGGG) and digested with NotI. cDNA was size
selected using 1.1% agarose gel electrophoresis (L
-0.5-1.2k, M -1.2-2.5k, H -2.5k) then ligated into NotI
and SalI digested pCMVsp6 vector. The work was done at
DOE Joint Genome Institute."

ORIGIN
Query Match 6.8%; Score 44.8; DB 10; Length 778;
Best Local Similarity 64.4%; Pred. No. 0.11; Mismatches 0; Gaps 0;
Matches 67; Conservative 0; Indels 37; Indels 0; Gaps 0;
Qy 345 TGGGAAGCGACAGCCACCAAAAGGTGAGATGTCATCCACGAGAGAGAGAG 404
Db 195 TGAACAGTGAGGTGATGAAGCATAAAGGAAACGTGAGAGAGAGAGAGAGAG 136
Qy 405 AGAGAGAGAGAGAGTTTCTCTATATCTTCGTTACCGGT 448
Db 135 AGAGAGAGAGAGCGGTGGTCTTTGAAGTCTTTGGCCGGT 92

RESULT 12
BZ708983/c
LOCUS
DEFINITION
BZ708983 363 bp DNA linear GSS 19-FEB-2003
OGRAM43TM ZM 0.7-1.5 KB Zea mays genomic clone ZMMBma0220H13,
genomic survey sequence.
ACCESSION
BZ708983
VERSION
BZ708983.1 GI:28429079
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 363)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reanick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGRAM43TC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1..363
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/clone="ZMMBma0220H13"
/clone_lib="ZM 0.7-1.5 KB"
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methylation filtered genomic DNA library"

ORIGIN
Query Match 6.8%; Score 44.6; DB 12; Length 363;
Best Local Similarity 61.7%; Pred. No. 0.1;
Matches 71; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 306 CGTATTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCCAGCCACCC 365
Db 271 CGTTGTGTATGCTTATATATATCTCGTCAAAATATGATGATGAACGCGCTGGCTC 212
Qy 366 ACAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 211 ACGGCACCTTGTATCTGATATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 157

RESULT 13
BZ306338
LOCUS
DEFINITION
BZ306338 543 bp DNA linear GSS 06-NOV-2002
hx41a10.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hx41a10 5', genomic survey sequence.
ACCESSION
BZ306338
VERSION
BZ306338.1 GI:24659045
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 543)
Rabinowicz, P.D., O'Shaughnessy, A.L., Ballija, V., Dedhia, N.,
Karzenburger, F., King, L., Miller, B., Muller, S., Nascimeto, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:25:56 ; Search time 840.519 Seconds
(without alignments)
9604.757 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1675
Perfect score: 657
Sequence: 1 ctgagccatttaattgaga.....aggagaggagagaatgggtt 657

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	657	100.0	3070	6	US-10-137-036-113
2	657	100.0	3070	9	US-10-702-319A-113
3	657	100.0	3070	10	US-10-927-641-113
4	638.2	97.1	661	6	US-10-137-036-12
5	638.2	97.1	661	9	US-10-702-319A-12
6	638.2	97.1	661	10	US-10-927-641-12
7	638.2	97.1	2096	6	US-10-137-036-60
8	638.2	97.1	2096	9	US-10-702-319A-60
9	638.2	97.1	2096	10	US-10-927-641-60
10	534	81.3	534	8	US-10-703-091-1
11	485	73.8	485	8	US-10-703-091-2
12	306	46.6	306	8	US-10-703-091-3
13	293	44.6	293	8	US-10-703-091-4
14	119	18.1	119	8	US-10-703-091-5
15	98	14.9	98	8	US-10-703-091-6
16	75	11.4	1630	7	US-10-174-693-107
17	73.8	11.2	421	7	US-10-174-693-24

18	73.4	11.2	407	7	US-10-174-693-106	Sequence 106, App
19	66	10.0	66	8	US-10-703-091-7	Sequence 7, Appli
20	49.4	7.5	5626	13	US-11-097-143-19390	Sequence 19390, A
21	45.4	6.9	7228	11	US-10-893-483-28	Sequence 28, Appl
22	45	6.8	1951	10	US-10-966-482-18	Sequence 18, Appl
23	43.4	6.6	2000	10	US-10-481-032A-721	Sequence 721, App
24	43.4	6.6	2000	10	US-10-481-032A-721	Sequence 721, App
25	43.4	6.6	2199	10	US-10-481-032A-656	Sequence 656, App
26	42.6	6.5	563	9	US-10-425-115-80646	Sequence 80646, A
27	42.4	6.5	493631	6	US-10-087-192-205	Sequence 205, App
28	41.8	6.4	126132	6	US-10-087-192-1459	Sequence 1459, Ap
29	41.6	6.3	882	6	US-10-027-632-173109	Sequence 173109,
30	41.6	6.3	882	7	US-10-027-632-173109	Sequence 173109,
31	41.6	6.3	53981	6	US-10-087-192-1621	Sequence 1621, Ap
32	41.4	6.3	24080	3	US-09-997-722-79	Sequence 79, Appl
33	41.2	6.3	257	9	US-10-674-124A-21772	Sequence 21772, A
34	41.2	6.3	24879	6	US-10-087-192-307	Sequence 307, App
35	41.2	6.3	176594	8	US-10-322-281-495	Sequence 495, App
36	41	6.2	354	10	US-10-779-543-10544	Sequence 10544, A
37	41	6.2	395	10	US-10-779-543-11769	Sequence 11769, A
38	40.8	6.2	2000	8	US-10-260-238-2334	Sequence 2334, Ap
39	40.8	6.2	43412	7	US-10-085-117-7	Sequence 7, Appli
40	40.8	6.2	100610	11	US-10-330-773-585	Sequence 585, App
41	40.6	6.2	336	9	US-10-674-124A-24865	Sequence 24865, A
42	40.6	6.2	103464	8	US-10-322-281-323	Sequence 323, App
43	40.6	6.2	127567	10	US-10-737-082-47	Sequence 47, Appl
44	40.6	6.2	127567	10	US-10-765-790-47	Sequence 47, Appl
45	40.4	6.1	802	8	US-10-437-963-96920	Sequence 96920, A

ALIGNMENTS

RESULT 1
US-10-137-036-113
; Sequence 113, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Petera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleston, Claire
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-113

Query Match 100.0%; Score 657; DB 6; Length 3070;
Best Local Similarity 100.0%; Pred. No. 9.4e-200;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu Nov 2 13:35:55 2006

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QY 1 CTGAGCATTAAATTCGAGAGCACATCGCCCAAAATTTATTTCTTGTCTGCATAACTGT 60
Db 1019 CTGAGCATTAAATTCGAGAGCACATCGCCCAAAATTTATTTCTTGTCTGCATAACTGT 1078
QY 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 1138
QY 121 GTATGATCTTGGAGTTTGGTGCATTTGCAAGCTGACATGCGCCCTCAGGGAAAT 180
Db 1139 GTATGATCTTGGAGTTTGGTGCATTTGCAAGCTGACATGCGCCCTCAGGGAAAT 1198
QY 181 AAGCGCCCAACCCAGATGTCAAAGAGCACAAAGAGCAGCACCCAACTTTCTTAAACAAG 240
Db 1199 AAGCGCCCAACCCAGATGTCAAAGAGCACAAAGAGCAGCACCCAACTTTCTTAAACAAG 1258
QY 241 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 300
Db 1259 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 1318
QY 301 AACTCCGTATTTCTCTCACTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCAGAGCC 360
Db 1319 AACTCCGTATTTCTCTCACTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCAGAGCC 1378
QY 361 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 1379 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
QY 421 TTTTCTCTATATTTCTGTTTACCGGTTGAGTCAATGGCAGTGGTGAATGTACAT 480
Db 1439 TTTTCTCTATATTTCTGTTTACCGGTTGAGTCAATGGCAGTGGTGAATGTACAT 1498
QY 481 ATTGGTGTAGGTCCTCAATATTTTGGGAGAGGTTGGTGAACCGCAAAAGTTCTTATATC 540
Db 1499 ATTGGTGTAGGTCCTCAATATTTTGGGAGAGGTTGGTGAACCGCAAAAGTTCTTATATC 1558
QY 541 GAACCTCCACCAACCATCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGC 600
Db 1559 GAACCTCCACCAACCATCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGC 1618
QY 601 TTTTCTTTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTT 657
Db 1619 TTTTCTTTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTT 1675
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RESULT 2
US-10-702-319A-113
; Sequence 113, Application US/10702319A
; Publication No. US2005026162A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C5
; CURRENT APPLICATION NUMBER: US/10/702,319A
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: U.S. No. 10/291,447
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 60/425,087
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599
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; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-702-319A-113

Query Match 100.0%; Score 657; DB 9; Length 3070;
Best Local Similarity 100.0%; Pred. No. 9.4e-200;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCATTAAATTCGAGAGCACATCGCCCAAAATTTATTTCTTGTCTGCATAACTGT 60
Db 1019 CTGAGCATTAAATTCGAGAGCACATCGCCCAAAATTTATTTCTTGTCTGCATAACTGT 1078
QY 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 1138
QY 121 GTATGATCTTGGAGTTTGGTGCATTTGCAAGCTGACATGCGCCCTCAGGGAAAT 180
Db 1139 GTATGATCTTGGAGTTTGGTGCATTTGCAAGCTGACATGCGCCCTCAGGGAAAT 1198
QY 181 AAGCGCCCAACCCAGATGTCAAAGAGCACAAAGAGCAGCACCCAACTTTCTTAAACAAG 240
Db 1199 AAGCGCCCAACCCAGATGTCAAAGAGCACAAAGAGCAGCACCCAACTTTCTTAAACAAG 1258
QY 241 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 300
Db 1259 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 1318
QY 301 AACTCCGTATTTCTCTCACTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCAGAGCC 360
Db 1319 AACTCCGTATTTCTCTCACTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCAGAGCC 1378
QY 361 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 1379 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
QY 421 TTTTCTCTATATTTCTGTTTACCGGTTGAGTCAATGGCAGTGGTGAATGTACAT 480
Db 1439 TTTTCTCTATATTTCTGTTTACCGGTTGAGTCAATGGCAGTGGTGAATGTACAT 1498
QY 481 ATTGGTGTAGGTCCTCAATATTTTGGGAGAGGTTGGTGAACCGCAAAAGTTCTTATATC 540
Db 1499 ATTGGTGTAGGTCCTCAATATTTTGGGAGAGGTTGGTGAACCGCAAAAGTTCTTATATC 1558
QY 541 GAACCTCCACCAACCATCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGC 600
Db 1559 GAACCTCCACCAACCATCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGC 1618
QY 601 TTTTCTTTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTT 657
Db 1619 TTTTCTTTGCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTT 1675
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RESULT 3
US-10-927-641-113
; Sequence 113, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C4
; CURRENT APPLICATION NUMBER: US/10/927,641
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; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-113

Query Match      100.0%; Score 657; DB 10; Length 3070;
Best Local Similarity 100.0%; Pred. No. 9.4e-200;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTTCTGCGCATAACTGT 60
Db 1019 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTTCTGCGCATAACTGT 1078

Qy 61 CGAATTTTCTCTTTAGTAAAGTAAACCAATGATCGCCATGTCGACAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGTAAAGTAAACCAATGATCGCCATGTCGACAAAAGGCTGATTA 1138

Qy 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGCCCTCAGGGAAT 180
Db 1139 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGCCCTCAGGGAAT 1198

Qy 181 AAGCGCCCAACCCAGATGTCGAGAGCAAAAGAGCAGACGACCACTTCTTAAACAG 240
Db 1199 AAGCGCCCAACCCAGATGTCGAGAGCAAAAGAGCAGACGACCACTTCTTAAACAG 1258

Qy 241 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 300
Db 1259 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 1318

Qy 301 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 360
Db 1319 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 1378

Qy 361 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 1379 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438

Qy 421 TTTTCTCTATATTTCTGGTTTACGGTTGAGTCAATGGCATGCGTGACCAATGTACAT 480
Db 1439 TTTTCTCTATATTTCTGGTTTACGGTTGAGTCAATGGCATGCGTGACCAATGTACAT 1498

Qy 481 ATTGGTGTAGGGTCCAATATTTTGGGAGGGTTGGTGAAACCGCAAAAGTTCTTATATATC 540
Db 1499 ATTGGTGTAGGGTCCAATATTTTGGGAGGGTTGGTGAAACCGCAAAAGTTCTTATATC 1558

Qy 541 GAACCTCCACCAACATACCTCACTTAATCCCAACCAATTAATTCGTTTATTTCTCTGCG 600
Db 1559 GAACCTCCACCAACATACCTCACTTAATCCCAACCAATTAATTCGTTTATTTCTCTGCG 1618

Qy 601 TTTCTTTGCTCGAGTCTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTT 657
Db 1619 TTTCTTTGCTCGAGTCTCGCGAGAGAGAGAGAGAGAGAGAGAGAGATGGTT 1675
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RESULT 4

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US-10-137-036-12
; Sequence 12, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Bagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-12
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Query Match      97.1%; Score 638.2; DB 6; Length 661;
Best Local Similarity 98.9%; Pred. No. 4.5e-194;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTTCTGCGCATAACTGT 60
Db 1 CTGAGCCATTAAATTCGAGAGACATCGCCCAAAATTAATCTCTTCTGCGCATAACTGT 60

Qy 61 CGAATTTTCTCTTTAGTAAAGTAAACCAATGATCGCCATGTCGACAAAAGGCTGATTA 120
Db 61 CGAATTTTCTCTTTAGTAAAGTAAACCAATGATGTCATGTCGACAAAAGGCTGATTA 120

Qy 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGCCCTCAGGGAAT 180
Db 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGCCCTCAGGGAAT 180

Qy 181 AAGCGCCCAACCCAGATGTCGAGAGCAAAAGAGCAGACGACCACTTCTTAAACAG 240
Db 181 AAGCGCCCAACCCAGATGTCGAGAGCAAAAGAGCAGACGATCCCACTTCTTAAACAG 240

Qy 241 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 300
Db 241 ATCATCACCAGATCGGCCAGTAAGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 300

Qy 301 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 360
Db 301 AACTCCGTATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCC 360

Qy 361 AACCACAAAAGGTCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAG 416
Db 361 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 417 AGAGTTTCTCTCTATATTTCTGGTTTACCGGTTGAGTCAATGGCATGCGTGACCAATGT 476
Db 421 AGAGTTTCTCTCTATATTTCTGGTTTACCGGTTGAGTCAATGGCATGCGTGACCAATGT 480

Qy 477 ACATATTTGGTGTAGGGTCCAATATTTTTCGCGGAGGGTTGGTGAAACCGCAAGTTCTTATA 536
Db 477 ACATATTTGGTGTAGGGTCCAATATTTTTCGCGGAGGGTTGGTGAAACCGCAAGTTCTTATA 536
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Db	481	ACATATTGGTGGTCCCAATATTTTGGGGAGGGTGGTGAAACCGCAAAAGTTCCTATA	540
Qy	537	TATCGAACCTCCACCAACATACCTCACTTCAATCCCACTTATCCGTTTATTTCTCT	596
Db	541	TATCGAACCTCCACCAACATACCTCACTTCAATCCCACTTATCCGTTTATTTCTCT	600
Qy	597	CTGCTTTTCTTCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	656
Db	601	CTGCTTTTCTTCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	660
Qy	657	T 657	
Db	661	T 661	
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US-10-702-319A-12			
; Sequence 12, Application US/10702319A			
; Publication No. US20050026162A1			
; GENERAL INFORMATION:			
; APPLICANT: Perera, Ranjan			
; APPLICANT: Rice, Stephen			
; APPLICANT: Eagleton, Clare			
; TITLE OF INVENTION: Compositions and Methods for the			
; TITLE OF INVENTION: Modification of Gene Expression			
; FILE REFERENCE: 11000.1036C5			
; CURRENT APPLICATION NUMBER: US/10/702,319A			
; PRIOR FILING DATE: 2003-11-06			
; PRIOR APPLICATION NUMBER: U.S. No. 10/291,447			
; PRIOR FILING DATE: 2002-11-08			
; PRIOR APPLICATION NUMBER: U.S. No. 60/425,087			
; PRIOR FILING DATE: 2002-11-08			
; PRIOR APPLICATION NUMBER: U.S. No. 10/137,036			
; PRIOR FILING DATE: 2002-04-30			
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624			
; PRIOR FILING DATE: 2000-11-28			
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401			
; PRIOR FILING DATE: 2000-06-20			
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018			
; PRIOR FILING DATE: 2000-02-24			
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591			
; PRIOR FILING DATE: 1999-07-30			
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599			
; PRIOR FILING DATE: 1999-03-25			
; NUMBER OF SEQ ID NOS: 129			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 12			
; LENGTH: 661			
; TYPE: DNA			
; ORGANISM: Eucalyptus grandis			
US-10-702-319A-12			
Query Match 97.1%; Score 638.2; DB 9; Length 661;			
Best Local Similarity 98.9%; Pred. No. 4.5e-194;			
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;			
Qy	1	CTGAGCCATTAAATTCGAGAGCAGCATCGCCAAAATATTTCTTGTGCGCATAACTGT	60
Db	1	CTGAGCCATTAAATTCGAGAGCAGCATCGCCAAAATATTTCTTGTGCGCATAACTGT	60
Qy	61	CGAATTTTCTTTTAGGTAAGTAACCAATGATGCGCCATGTTGACAAAAGCGTGATTA	120
Db	61	CGAATTTTCTTTTAGGTAAGTAACCAATGATGATCATCATGTTGACAAAAGCGTGATTA	120
Qy	121	GTATGATCTTGGAGTCTTGGTGCAGAAATTTGCAAGCTGAGATGGCCCTCAGGGAAATT	180
Db	121	GTATGATCTTGGAGTCTTGGTGCAGAAATTTGCAAGCTGAGATGGCCCTCAGGGAAATT	180
Qy	181	AAGGGCCCAACCCAGATGCAAGAGCAGCAAAAGAGCAGCCCAACCTTTCTTTTACAAG	240
Db	181	AAGGGCCCAACCCAGATGCAAGAGCAGCAAAAGAGCAGATCCCAACCTTTCTTTACAAG	240
Qy	241	ATCATCACCAGATCGGCCAGTAAAGGGTAAATTAATTAACAATAGCTCTTGTACCGGG	300
Db	241	ATCATCACCAGATCGGCCAGTAAAGGGTAAATTAATTAACAATAGCTCTTGTACCGGG	300
Qy	301	AACTCCCGTATTTCTCTCACTTCCATAAAACCCCTGATTAATTTGGTGGGAAAGCGAGCC	360
Db	301	AACTCCCGTATTTCTCTCACTTCCATAAAACCCCTGATTAATTTGGTGGGAAAGCGAGCC	360
Qy	361	AACCCAAAAGGTGAGATGTCAATCCAC- - -GAGAGAGAGAGAGAGAGAGAGAGAG	416
Db	361	AACCCAAAAGGTGAGATGTCAATCCAC- - -GAGAGAGAGAGAGAGAGAGAGAGAGAG	420
Qy	417	AGAGTTTCTCTCTATATTTCTGGTTTCAACCGTTTGGAGTCAATGGCATGCGTGAATGT	476
Db	421	AGAGTTTCTCTCTATATTTCTGGTTTCAACCGTTTGGAGTCAATGGCATGCGTGAATGT	480
Qy	477	ACATATTGGTGGTCCCAATATTTTGGGGAGGGTGGTGAAACCGCAAAAGTTCCTATA	536
Db	481	ACATATTGGTGGTCCCAATATTTTGGGGAGGGTGGTGAAACCGCAAAAGTTCCTATA	540
Qy	537	TATCGAACCTCCACCAACATACCTCACTTCAATCCCACTTATCCGTTTATTTCTCT	596
Db	541	TATCGAACCTCCACCAACATACCTCACTTCAATCCCACTTATCCGTTTATTTCTCT	600
Qy	597	CTGCTTTTCTTCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	656
Db	601	CTGCTTTTCTTCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	660
Qy	657	T 657	
Db	661	T 661	
RESULT 6			
US-10-927-641-12			
; Sequence 12, Application US/10927641			
; Publication No. US2005024968A1			
; GENERAL INFORMATION:			
; APPLICANT: Perera, Ranjan			
; APPLICANT: Rice, Stephen			
; APPLICANT: Eagleton, Clare			
; APPLICANT: Lasham, Annette			
; APPLICANT: Wood, Marion			
; APPLICANT: Visser, Elizabeth			
; TITLE OF INVENTION: Compositions and Methods for the			
; TITLE OF INVENTION: Modification of Gene Expression			
; FILE REFERENCE: 11000.1036C4			
; CURRENT APPLICATION NUMBER: US/10/927,641			
; CURRENT FILING DATE: 2004-08-27			
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036			
; PRIOR FILING DATE: 2002-04-30			
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115			
; PRIOR FILING DATE: 2001-06-20			
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624			
; PRIOR FILING DATE: 2000-11-28			
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401			
; PRIOR FILING DATE: 2000-06-20			
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018			
; PRIOR FILING DATE: 2000-02-24			
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591			
; PRIOR FILING DATE: 1999-07-30			
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599			
; PRIOR FILING DATE: 1999-03-25			
; NUMBER OF SEQ ID NOS: 143			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 12			
; LENGTH: 661			
; TYPE: DNA			
; ORGANISM: Eucalyptus grandis			
US-10-927-641-12			
Query Match 97.1%; Score 638.2; DB 10; Length 661;			
Best Local Similarity 98.9%; Pred. No. 4.5e-194;			
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;			


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QY 1 CTGAGCCATTAAATTCGAGAGCACATCGCCAAATTAATCTCTTCTGTCGCAATAACTGT 60
DB 1 CTGAGCCATTAAATTCGAGAGCACATCGCCAAATTAATCTCTTCTGTCGCAATAACTGT 60
QY 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA 120
DB 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA 120
QY 121 GTATGATCTTGGAGTGTGTTGTCGCAATTTTCAGCTGACGATGCCCTCAGGGAATTT 180
DB 121 GTATGATCTTGGAGTGTGTTGTCGCAATTTTCAGCTGACGATGCCCTCAGGGAATTT 180
QY 181 AAGCGCCCAACCCAGATTGCAAGAGACCAAGAGCAGCACCAACCTTTCTTTAAACAAG 240
DB 181 AAGCGCCCAACCCAGATTGCAAGAGCAGCACCAAGAGCAGCACCAACCTTTCTTTAAACAAG 240
QY 241 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTAAACAAATAGCTCTTTGACCGGG 300
DB 241 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTAAACAAATAGCTCTTTGACCGGG 300
QY 301 AACTCCGTATTCTCTACATTCCTATTAACCCCTGATTAATTTGGTGGAAAGCGACGCC 360
DB 301 AACTCCGTATTCTCTACATTCCTATTAACCCCTGATTAATTTGGTGGAAAGCGACGCC 360
QY 361 AACCACAAAAGGTCAGATGTCATCCAC --- GAGAGAGAGAGAGAGAGAGAGAGAG 416
DB 361 AACCACAAAAGGTCAGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 417 AGAGTTTTCTCTCTATTAATTTCTGGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 476
DB 421 AGAGTTTTCTCTCTATTAATTTCTGGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 480
QY 477 ACATATTGGTGTAGGTCCTCAATATTTTCGGGAGGTTGGTGAACCGCAAAAGTTCTCTATA 536
DB 481 ACATATTGGTGTAGGTCCTCAATATTTTCGGGAGGTTGGTGAACCGCAAAAGTTCTCTATA 540
QY 537 TATCGAACTCCACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCT 596
DB 541 TATCGAACTCCACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCT 600
QY 597 CTGCTTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 656
DB 601 CTGCTTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGAGATGGGT 660
QY 657 T 657
DB 661 T 661

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RESULT 7

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US-10-137-036-60
; Sequence 60, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018

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; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2096
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; US-10-137-036-60

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Query Match 97.1%; Score 638.2; DB 6; Length 2096;
Best Local Similarity 98.9%; Pred. No. 8.6e-194;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTAATTTCTTCTGTCGCAATAACTGT 60
DB 41 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTAATTTCTTCTGTCGCAATAACTGT 100
QY 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA 120
DB 101 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA 160
QY 121 GTATGATCTTGGAGTGTGTTGTCGCAATTTTGAAGCTTGACGATGCCCTCAGGGAATTT 180
DB 161 GTATGATCTTGGAGTGTGTTGTCGCAATTTTGAAGCTTGACGATGCCCTCAGGGAATTT 220
QY 181 AAGCGCCCAACCCAGATTGCAAGAGACCAAGAGCAGCACCAACCTTTCTTTAAACAAG 240
DB 221 AAGCGCCCAACCCAGATTGCAAGAGCAGCACCAAGAGCAGCACCAACCTTTCTTTAAACAAG 280
QY 241 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTAAACAAATAGCTCTTTGACCGGG 300
DB 281 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTAAACAAATAGCTCTTTGACCGGG 340
QY 301 AACTCCGTATTCTCTACATTCCTCAATTAACCCCTGATTAATTTGGTGGAAAGCGACGCC 360
DB 341 AACTCCGTATTCTCTACATTCCTCAATTAACCCCTGATTAATTTGGTGGAAAGCGACGCC 400
QY 361 AACCACAAAAGGTCAGATGTCATCCAC --- GAGAGAGAGAGAGAGAGAGAGAGAG 416
DB 401 AACCACAAAAGGTCAGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
QY 417 AGAGTTTTCTCTCTATTAATTTCTGGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 476
DB 461 AGAGTTTTCTCTCTATTAATTTCTGGTTTACCGGTTGGAGTCAATGGCATCGTGACGAATGT 520
QY 477 ACATATTGGTGTAGGTCCTCAATATTTTTCGGGAGGTTGGTGAACCGCAAAAGTTCTCTATA 536
DB 521 ACATATTGGTGTAGGTCCTCAATATTTTTCGGGAGGTTGGTGAACCGCAAAAGTTCTCTATA 580
QY 537 TATCGAACTCCACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCT 596
DB 581 TATCGAACTCCACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTCT 640
QY 597 CTGCTTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGATGGGT 656
DB 641 CTGCTTTCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGATGGGT 700
QY 657 T 657
DB 701 T 701

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RESULT 8

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US-10-702-319A-60
; Sequence 60, Application US/10702319A
; Publication No. US20050026162A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen

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APPLICANT: Bagleton, Clare
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.1036c5
CURRENT APPLICATION NUMBER: US/10/702,319A
CURRENT FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: U.S. No. 10/291,447
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: U.S. No. 60/425,087
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: U.S. No. 10/137,036
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 2096
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-10-702-319A-60

Query Match 97.1%; Score 638.2; DB 9; Length 2096;
Best Local Similarity 98.9%; Pred. No. 8.6e-194;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY 1 CTGAGCCATTAAATTCGAGAGACATGCCCAAAATATTCTTCTGTCGCCATAACTGT 60
DB 41 CTGAGCCATTAAATTCGAGAGACATGCCCAAAATATTCTTCTGTCGCCATAACTGT 100
QY 61 CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 120
DB 101 CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 160
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGCCCTCAGGGAATTT 180
DB 161 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGCCCTCAGGGAATTT 220
QY 181 AAGGCGCCAAACCCAGATTGCAAGAGACACAAAGAGCAGACCCACCTTTCTTTAAACAAG 240
DB 221 AAGGCGCCAAACCCAGATTGCAAGAGACACAAAGAGCAGACCTTTCTTTAAACAAG 280
QY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAATTAATTAATTAATTAATTAATTA 300
DB 281 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAATTAATTAATTAATTAATTAATTA 340
QY 301 AACTCGGTAATTTCTCACTTCCATTAACCCCTGATTAATTTGGTGGAAAGCCAGACCC 360
DB 341 AACTCGGTAATTTCTCACTTCCATTAACCCCTGATTAATTTGGTGGAAAGCCAGACCC 400
QY 361 AATCCCAAAAGGTGAGATGTCATCCAC- ---GAGAGAGAGAGAGAGAGAGAGAGAGAG 416
DB 401 AATCCCAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
QY 417 AGAGTTTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGCATGGTGGTACCAATGT 476
DB 461 AGAGTTTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGCATGGTGGTACCAATGT 520
QY 477 ACATATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 536
DB 521 ACATATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 580
QY 537 TATCGAACCTTCCACCACTACCTCACTTCAATFCCCAACATTTATCCGTTTTTATTTCT 596
DB 581 TATCGAACCTTCCACCACTACCTCACTTCAATFCCCAACATTTATCCGTTTTTATTTCT 640

QY 597 CTGCTTTCTTTCTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT 656
DB 641 CTGCTTTCTTTCTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT 700
QY 657 T 657
DB 701 T 701
RESULT 9
US-10-927-641-60
; Sequence 60, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Bagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2096
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-60

Query Match 97.1%; Score 638.2; DB 10; Length 2096;
Best Local Similarity 98.9%; Pred. No. 8.6e-194;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY 1 CTGAGCCATTAAATTCGAGAGACATGCCCAAAATATTCTTCTGTCGCCATAACTGT 60
DB 41 CTGAGCCATTAAATTCGAGAGACATGCCCAAAATATTCTTCTGTCGCCATAACTGT 100
QY 61 CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 120
DB 101 CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 160
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGCCCTCAGGGAATTT 180
DB 161 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGCCCTCAGGGAATTT 220
QY 181 AAGGCGCCAAACCCAGATTGCAAGAGACACAAAGAGCAGACCCACCTTTCTTTAAACAAG 240
DB 221 AAGGCGCCAAACCCAGATTGCAAGAGACACAAAGAGCAGACCTTTCTTTAAACAAG 280
QY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAATTAATTAATTAATTAATTAATTA 300
DB 281 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAATTAATTAATTAATTAATTAATTA 340
QY 301 AACTCGGTAATTTCTCTCACTTCCATTAACCCCTGATTAATTTGGTGGAAAGCCAGACCC 360

Db 341 AACTCCGTAATTTCTCTCACTTCCATAAACCCTGATTAATTTGGTGGGAAAGCGACGCC 400
Qy 361 AACCACAAAAGGTGAGATGTCATCCAC-----GAGAGAGAGAGAGAGAGAGAGAG 416
Db 401 AACCACAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
Qy 417 AGAGTTTTCTCTCTATATTTCTGGTTTCCAGGTTGAGTCAATGGCATCGGTGACGAATGT 476
Db 461 AGAGTTTTCTCTCTATATTTCTGGTTTCCAGGTTGAGTCAATGGCATCGGTGACGAATGT 520
Qy 477 ACATATTTGGTGTAGGGTCCAATATTTTCCGGGAGGGTTGGTCAACCCGCAAAAGTTTCTTATA 536
Db 521 ACATATTTGGTGTAGGGTCCAATATTTTCCGGGAGGGTTGGTCAACCCGCAAAAGTTTCTTATA 580
Qy 537 TATCGAACCTCCACCACTACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCT 596
Db 581 TATCGAACCTCCACCACTACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCT 640
Qy 597 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT 656
Db 641 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT 700
Qy 657 T 657
Db 701 T 701

RESULT 10

US-10-703-091-1
; Sequence 1, Application US/10703091
; Publication No. US20040146904A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE REFERENCE: 044463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/425,087
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-1

Query Match 81.3%; Score 534; DB 8; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.4e-160; Mismatches 0; Indels 0; Gaps 0;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 92 ATGCCCATGTGTGACAAAAGGCTGATTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTG 151
Db 1 ATGCCCATGTGTGACAAAAGGCTGATTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTG 60
Qy 152 CAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCACCCAGATTGCAAAAGAGCAAA 211
Db 61 CAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCACCCAGATTGCAAAAGAGCAAA 120
Qy 212 AGACGACGACCAACCTTTCTTAAACAGATCATCACAGATCGGCCAGTAAGGGTAATA 271
Db 121 AGACGACGACCAACCTTTCTTAAACAGATCATCACAGATCGGCCAGTAAGGGTAATA 180
Qy 272 TTAATTTAAACAATAGCTCTTGTACCGGGAACCTCGGTATTTCTCTCACTTCCATAAAACCC 331
Db 181 TTAATTTAAACAATAGCTCTTGTACCGGGAACCTCGGTATTTCTCTCACTTCCATAAAACCC 240
Qy 332 CTGATTAATTTGGTGGGAAGCGACGCCAACCCACAAAAGGTGAGATGTCATCCACGA 391
Db 241 CTGATTAATTTGGTGGGAAGCGACGCCAACCCACAAAAGGTGAGATGTCATCCACGA 300

Qy 392 GAG 451
Db 301 GAG 360
Qy 452 AGTCAATGGCATGGTGTGACGAATGTACATATTTGGTGTAGGGTCCAATATTTTGGGGAGG 511
Db 361 AGTCAATGGCATGGTGTGACGAATGTACATATTTGGTGTAGGGTCCAATATTTTGGGGAGG 420
Qy 512 GTTGGTGAACCGCAAGTTCCTATATATCGAACCTCCACCACTACCTCACTTCAATCC 571
Db 421 GTTGGTGAACCGCAAGTTCCTATATATCGAACCTCCACCACTACCTCACTTCAATCC 480
Qy 572 CCACATTTATCCGTTTATTTCTCTGCTTTCTTCTGCTGAGTCTCGCGGAA 625
Db 481 CCACATTTATCCGTTTATTTCTCTGCTTTCTTCTGCTGAGTCTCGCGGAA 534

RESULT 11

US-10-703-091-2
; Sequence 2, Application US/10703091
; Publication No. US20040146904A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE REFERENCE: 044463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/425,087
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-2

Query Match 73.8%; Score 485; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 8.1e-145; Mismatches 0; Indels 0; Gaps 0;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCACCCAGATTGC 200
Db 1 GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCACCCAGATTGC 60
Qy 201 AAAGAGCACAAAGAGACGACGCCAACCTTTCTTTAAACAAGATCATCACAGATCGGCAG 260
Db 61 AAAGAGCACAAAGAGACGACGCCAACCTTTCTTTAAACAAGATCATCACAGATCGGCAG 120
Qy 261 TAAGGGTAATTAATTAACAATAGCTCTTGTACCGGGAACCTCGGTATTTCTCTCACT 320
Db 121 TAAGGGTAATTAATTAACAATAGCTCTTGTACCGGGAACCTCGGTATTTCTCTCACT 180
Qy 321 TCATAAACCCCTGATTAAATTTGGTGGGAAAGCGACAGCCAAACCCACAAAAGGTGAGATG 380
Db 181 TCATAAACCCCTGATTAAATTTGGTGGGAAAGCGACAGCCAAACCCACAAAAGGTGAGATG 240
Qy 381 TCATCCCAAG 440
Db 241 TCATCCCAAG 300
Qy 441 TCACCGGTTGGAGTCATGCGTGCAGGATGTAATGTAATGTTAGGGTCCAATAT 500
Db 301 TCACCGGTTGGAGTCATGCGTGCAGGATGTAATGTAATGTTAGGGTCCAATAT 360
Qy 501 TTTGGCGGAGGTTGGTGAACCGCAAAAGTTCTTATATATCGAACCTCCACCACTACCT 560
Db 361 TTTGGCGGAGGTTGGTGAACCGCAAAAGTTCTTATATATCGAACCTCCACCACTACCT 420
Qy 561 CACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGCTTTCTTTGCTGAGTCTCG 620
Db 421 CACTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGCTTTCTTTGCTGAGTCTCG 480

	TYPE: DNA	
	ORGANISM: Eucalyptus grandis	
	US-10-703-091-4	
QY	621 CGGAA 625	
DB	481 CGGAA 485	
RESULT 12		
US-10-703-091-3		
; Sequence 3, Application US/10703091		
; Publication No. US20040146904A1		
; GENERAL INFORMATION:		
; APPLICANT: PHILLIPS, JONATHAN		
; APPLICANT: EAGLETON, CLARE		
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF		
; FILE REFERENCE: 044463-0263		
; CURRENT APPLICATION NUMBER: US/10/703,091		
; CURRENT FILING DATE: 2003-11-07		
; PRIOR APPLICATION NUMBER: 60/425,087		
; PRIOR FILING DATE: 2002-11-08		
; NUMBER OF SEQ ID NOS: 8		
; SOFTWARE: PatentIn Ver. 3.2		
; SEQ ID NO 3		
; LENGTH: 306		
; TYPE: DNA		
; ORGANISM: Eucalyptus grandis		
US-10-703-091-3		
Query Match 46.6%; Score 306; DB 8; Length 306;		
Best Local Similarity 100.0%; Pred. No. 2.7e-87;		
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	320 TTCCATTAACCCCTGATTAAATTTGGTGGGAAGCGACGCCAACCAAAAAGGTGCAGAT 379	
DB	1 TTCCATAAACCCCTGATTAAATTTGGTGGGAAGCGACGCCAACCAAAAAGGTGCAGAT 60	
QY	380 GTCAATCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTTCTCTATATTTCTGG 439	
DB	61 GTCAATCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTTCTCTATATTTCTGG 120	
QY	440 TTCAACCGGTTGGAGTCGAATGGCATGGGTGACGAATGTACATATTTGGTGAGGTCGAATA 499	
DB	121 TTCAACCGGTTGGAGTCGAATGGCATGGGTGACGAATGTACATATTTGGTGAGGTCGAATA 180	
QY	500 TTTTTCGGGGGGTGGTGAACCGCAAGTTCCTATATATCGAACCTCCACCACCATACC 559	
DB	181 TTTTTCGGGGGGTGGTGAACCGCAAGTTCCTATATATCGAACCTCCACCACCATACC 240	
QY	560 TCACCTTCAAATCCCCCACCATTATCCGTTTTATTTCTCTGCTTTCTTTGCTCGAGTCTC 619	
DB	241 TCACCTTCAAATCCCCCACCATTATCCGTTTTATTTCTCTGCTTTCTTTGCTCGAGTCTC 300	
QY	620 CGGAA 625	
DB	301 CGGAA 306	
RESULT 13		
US-10-703-091-4		
; Sequence 4, Application US/10703091		
; Publication No. US20040146904A1		
; GENERAL INFORMATION:		
; APPLICANT: PHILLIPS, JONATHAN		
; APPLICANT: EAGLETON, CLARE		
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF		
; FILE REFERENCE: 044463-0263		
; CURRENT APPLICATION NUMBER: US/10/703,091		
; CURRENT FILING DATE: 2003-11-07		
; PRIOR APPLICATION NUMBER: 60/425,087		
; PRIOR FILING DATE: 2002-11-08		
; NUMBER OF SEQ ID NOS: 8		
; SOFTWARE: PatentIn Ver. 3.2		
; SEQ ID NO 4		

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; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/425,087
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 6
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-6

Query Match      14.9%; Score 98; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      527 AGTTCCTATATCGAACCTCCACCACTACCTCACTTCAATCCCAACCAATTTATCCGT 586
Db      1 AGTTCCTATATCGAACCTCCACCACTACCTCACTTCAATCCCAACCAATTTATCCGT 60

Qy      587 TTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGGA 624
Db      61 TTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGGA 98

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:41:44 ; Search time 122.108 Seconds
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Title: US-10-702-319A-113_COPY_1019_1675

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93555401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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3: /EMC_Celerra_SIDS3/ptodata/2/ina/6/COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/7/COMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	657	100.0	3070	US-09-598-401C-113	Sequence 113, App1
2	638.2	97.1	661	US-09-276-599-12	Sequence 12, App1
3	638.2	97.1	661	US-09-598-401C-12	Sequence 12, App1
4	638.2	97.1	2096	US-09-598-401C-60	Sequence 60, App1
5	75	11.4	1630	US-09-615-192A-107	Sequence 107, App
6	75	11.4	1630	US-09-163-789-107	Sequence 107, App
7	73.8	11.2	421	US-08-975-316-24	Sequence 24, App1
8	73.8	11.2	421	US-09-615-192A-24	Sequence 24, App1
9	73.8	11.2	421	US-09-163-789-24	Sequence 24, App1
10	73.4	11.2	407	US-09-615-192A-106	Sequence 106, App
11	73.4	11.2	407	US-09-163-789-106	Sequence 106, App
12	40.6	6.2	130563	US-09-949-016-12273	Sequence 12273, A
13	40.6	6.2	131379	US-09-949-016-16050	Sequence 16050, A
14	39.6	6.0	458	US-09-270-767-21637	Sequence 21637, A
15	39.6	6.0	1528	US-09-270-767-11960	Sequence 11960, A
16	39.4	6.0	601	US-09-949-016-89176	Sequence 89176, A
17	39.4	6.0	14037	US-09-949-016-17329	Sequence 17329, A
18	39.4	6.0	72604	US-09-268-992-7	Sequence 7, App1
19	39.4	6.0	72604	US-09-657-474-7	Sequence 7, App1
20	39.4	6.0	237510	US-09-949-016-14273	Sequence 14273, A
21	39.2	6.0	36317	US-09-949-016-12697	Sequence 12697, A
22	39.2	6.0	36322	US-09-949-016-14047	Sequence 14047, A
23	39	5.9	2830	US-07-882-292-1	Sequence 1, App1

C 24	39	5.9	2830	2	US-08-331-644-1	Sequence 1, App1
C 25	39	5.9	2830	7	PCT-US93-04102-1	Sequence 1, App1
C 26	38.8	5.9	601	3	US-09-949-016-96409	Sequence 96409, A
C 27	38.8	5.9	601	3	US-09-949-016-96410	Sequence 96410, A
C 28	38.8	5.9	601	3	US-09-949-016-96411	Sequence 96411, A
C 29	38.8	5.9	601	3	US-09-949-016-96675	Sequence 96675, A
C 30	38.8	5.9	601	3	US-09-949-016-96676	Sequence 96676, A
C 31	38.8	5.9	601	3	US-09-949-016-96677	Sequence 96677, A
C 32	38.8	5.9	601	3	US-09-949-016-96941	Sequence 96941, A
C 33	38.8	5.9	601	3	US-09-949-016-96942	Sequence 96942, A
C 34	38.8	5.9	601	3	US-09-949-016-96943	Sequence 96943, A
C 35	38.8	5.9	601	3	US-09-949-016-97207	Sequence 97207, A
C 36	38.8	5.9	601	3	US-09-949-016-97208	Sequence 97208, A
C 37	38.8	5.9	601	3	US-09-949-016-97209	Sequence 97209, A
C 38	38.8	5.9	601	3	US-09-949-016-97473	Sequence 97473, A
C 39	38.8	5.9	601	3	US-09-949-016-97474	Sequence 97474, A
C 40	38.8	5.9	601	3	US-09-949-016-97475	Sequence 97475, A
C 41	38.8	5.9	601	3	US-09-949-016-97739	Sequence 97739, A
C 42	38.8	5.9	601	3	US-09-949-016-97740	Sequence 97740, A
C 43	38.8	5.9	601	3	US-09-949-016-97741	Sequence 97741, A
C 44	38.8	5.9	601	3	US-09-949-016-98005	Sequence 98005, A
C 45	38.8	5.9	601	3	US-09-949-016-98006	Sequence 98006, A

ALIGNMENTS

RESULT 1
US-09-598-401C-113
Sequence 113, Application US/09598401C
Patent No. 6596925
GENERAL INFORMATION:
APPLICANT: Pereira, J. Ranjan
APPLICANT: Eagleton, Clare
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.10362
CURRENT APPLICATION NUMBER: US/09/598, 401C
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 113
LENGTH: 3070
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-598-401C-113
Query Match 100.0%; Score 657; DB 3; Length 3070;
Best Local Similarity 100.0%; Pred. No. 2.2e-209;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTGAGCATTTAATTCGAGACATGCGCCAAATTTCTTCTGTCGATTAAGTGT 60
DB 1019 CTGAGCATTTAATTCGAGACATGCGCCAAATTTCTTCTGTCGATTAAGTGT 1078
OY 61 CGAATTTCTTTTAAAGTAAGTAACCAATGATGCGCATGTTGACAAAAGCTGATTA 120
DB 1079 CGAATTTCTTTTAAAGTAAGTAACCAATGATGCGCATGTTGACAAAAGCTGATTA 1138
OY 121 GTAATGATCTGAGATTTGAGTGAATTTGCAATTTGCAATGATGCGCCCTAGGAAATT 180
DB 1139 GTAATGATCTGAGATTTGAGTGAATTTGCAATTTGCAATGATGCGCCCTAGGAAATT 1198
OY 181 AAGCGCAACCCGATTTGCAAGAGCAAAAGAGCAAGCAACCTTTCTTTAACAAG 240
DB 1199 AAGCGCAACCCGATTTGCAAGAGCAAAAGAGCAAGCAACCTTTCTTTAACAAG 1258

QY	241	ATCATCACCAAGTCCGCCAGTAGAGGGTAAATATTAATTTAAACAATAAGCTTGTACCCGG	300
Db	1259	ATCATCACCAAGTCCGCCAGTAGAGGGTAAATATTAATTTAAACAATAAGCTTGTACCCGG	1318
QY	301	AACTCCGATATTTCTCTCACTTCCATMAACCCCTGATTAATTTGTGGGAAAGCGACAGC	360
Db	1319	AACTCCGATATTTCTCTCACTTCCATMAACCCCTGATTAATTTGTGGGAAAGCGACAGC	1378
QY	361	AAACCACAAAGGTCAAGTGTCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420
Db	1379	AAACCACAAAGGTCAAGTGTCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1438
QY	421	TTTTCTCTATATTCGTGGTCAACGGGTGAGGTGAATGGCATGGCTGACCAATTAAT	480
Db	1439	TTTTCTCTATATTCGTGGTCAACGGGTGAGGTGAATGGCATGGCTGACCAATTAAT	1498
QY	481	ATTGTGTAGGGTCCCAATATTTTGGCGAGGGTGTGAACCGCAAAATTCCTATATATC	540
Db	1499	ATTGTGTAGGGTCCCAATATTTTGGCGAGGGTGTGAACCGCAAAATTCCTATATATC	1558
QY	541	GAACCTCACACCAATACCTCACTTCAATCCCAACATTTATCCGTTTATTTCCCTGCG	600
Db	1559	GAACCTCACACCAATACCTCACTTCAATCCCAACATTTATCCGTTTATTTCCCTGCG	1618
QY	601	TTTCCCTTGGCTCGAGTCTCGCGGAAGAGAGAAAGAGAGAGAGAGAGATGGGTT	657
Db	1619	TTTCCCTTGGCTCGAGTCTCGCGGAAGAGAGAAAGAGAGAGAGAGAGATGGGTT	1675

```

RESULT 2
US-09-276-599-12
Sequence 12, Application US/09276599
Patent No. 6380459
GENERAL INFORMATION:
APPLICANT: Pereira, J. Ranjan
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Composition and methods for the
TITLE OF INVENTION: modification of gene expression
FILE REFERENCE: 11000.1036
CURRENT APPLICATION NUMBER: US/09/276,599
CURRENT FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 661
TYPE: DNA
ORGANISM: Eucalyptus grandis
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)...(654)
NAME/KEY: TATA_signal
LOCATION: (537)...(543)
NAME/KEY: CAAI_signal
LOCATION: (499)...(502)
US-09-276-599-12

```

Query Match	97.1%	Score 638.2;	DB 3;	Length 661;
Best Local Similarity	98.9%;	Pred. No. 1.8e-203;		
Matches 654;	Conservative	0;	Mismatches 3;	Indels 4;
				Gaps 1;

[illegible]

QY	181	AAGGCGCAACCCGAGTTGCAAGAAAGACCAAGACCAAGCCACTTTCTTAAACAG	240
Db	181	AAGGCGCAACCCGAGTTGCAAGAAAGACCAAGACCAAGCCACTTTCTTAAACAG	240
QY	241	ATCATCAACGATGGCCAGTAAGGGTAATTTAAACAAATAGCTCTTGACCGG	300
Db	241	ATCATCAACGATGGCCAGTAAGGGTAATTTAAATTTAAACAAATAGCTCTTGACCGG	300
QY	301	AACCCGTAATTTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAGGACAGCC	360
Db	301	AACCTCGTATTTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAGGACAGCC	360
QY	361	AACCCCAAAAAGTCAGATGTATCCAC---GAGAGAGAGAGAGAGAGAGAGAG	416
Db	361	AACCCCAAAAAGTCAGATGTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAG	420
QY	417	AGAGTTTTCTCTCTAATATTCGAGTTCAACCGTGGAGTCAATGGCAATGCTGACGAATGT	476
Db	421	AGAGTTTTCTCTCTAATATTCGAGTTCAACCGTGGAGTCAATGGCAATGCTGACGAATGT	480
QY	477	ACATATTTGGTGTAGGGTCCCAATATTTTCGGGAGGGTGTGGAAACGCCAAGTTCCTATA	536
Db	481	ACATATTTGGTGTAGGGTCCCAATATTTTCGGGAGGGTGTGGAAACGCCAAGTTCCTATA	540
QY	537	TATCGAAGCTCCACCAACCAATACCTCACTTCAATCCCAACATTTATCCGTTTATTTTCT	596
Db	541	TATCGAAGCTCCACCAACCAATACCTCACTTCAATCCCAACATTTATCCGTTTATTTTCT	600
QY	597	CTGCTTTCTTTGCTCGAGTCTCGCGAAAGAGAGAGAGAGAGAGAGAGATGGGT	656
Db	601	CTGCTTTCTTTGCTCGAGTCTCGCGAAAGAGAGAGAGAGAGAGAGATGGGT	660
QY	657	T 657	
Db	661	T 661	

```

RESULT 3
US-09-598-401C-12
Sequence 12, Application US/09598401C
Patent No. 6596925
GENERAL INFORMATION:
APPLICANT: Perera, J. Ranjan
APPLICANT: Eagleton, Claire
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.1036c2
CURRENT APPLICATION NUMBER: US/09/598,401C
CURRENT FILING DATE: 2000-06-20
PRIORITY APPLICATION NUMBER: U.S. No. 6596925 60/146,592
PRIORITY FILING DATE: 1999-07-30
PRIORITY APPLICATION NUMBER: PCT/NZ00/00018
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: U.S. No. 6596925 09/276,599
PRIORITY FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 661
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-598-401C-12

```

Query Match	97.1%;	Score 638.2;	DB 3;	Length 661;
Best Local Similarity	98.9%;	Pred. No. 1.8e-203;		
Matches 654;	Conservative 0;	Mismatches 3;	Indels 4;	Gaps 1;

Qy 1 CTGAGCCATTATTCGAGAGACATCGCCCAAAATTTATTTCTTTCTGCGCATATCTGT 60

Dy 1 CTGAGCCATTATTCGAGAGACATCGCCCAAAATTTATTTCTTTCTGCGCATATCTGT 60

Qy 61 CGAATTTTCTCTTTTAGGTAAATTAACCAATGANGCGCATGTTGACAAAAAGCGTAGTA 120

Db	CGAATTTTCCTTTAGTGAAGTAACCAATGATGATCTGTGACAAAAGCTGATTA	120
Qy	121	180
Db	121	180
Qy	181	240
Db	181	240
Qy	241	300
Db	241	300
Qy	301	360
Db	301	360
Qy	361	416
Db	361	420
Qy	417	476
Db	421	480
Qy	477	536
Db	481	540
Qy	537	596
Db	541	600
Qy	597	656
Db	601	660
Qy	657	657
Db	661	661

Query Match	Score	DB 3	Length
Best Local Similarity	97.1%;	98.9%;	Pred. No. 3.5e-203;
US-09-598-401C-60	97.1%;	98.9%;	Pred. No. 3.5e-203;
Sequence 60, Application US/09598401C	97.1%;	98.9%;	Pred. No. 3.5e-203;
Patent No. 6596925	97.1%;	98.9%;	Pred. No. 3.5e-203;
GENERAL INFORMATION:	97.1%;	98.9%;	Pred. No. 3.5e-203;
APPLICANT: Perera, J. Rantjan	97.1%;	98.9%;	Pred. No. 3.5e-203;
APPLICANT: Eagleton, Clare	97.1%;	98.9%;	Pred. No. 3.5e-203;
APPLICANT: Rice, Stephen J.	97.1%;	98.9%;	Pred. No. 3.5e-203;
TITLE OF INVENTION: Compositions and Methods for the	97.1%;	98.9%;	Pred. No. 3.5e-203;
TITLE OF INVENTION: Modification of Gene Expression	97.1%;	98.9%;	Pred. No. 3.5e-203;
FILE REFERENCE: 11000.1036C2	97.1%;	98.9%;	Pred. No. 3.5e-203;
CURRENT APPLICATION NUMBER: US/09/598,401C	97.1%;	98.9%;	Pred. No. 3.5e-203;
CURRENT FILING DATE: 2000-06-20	97.1%;	98.9%;	Pred. No. 3.5e-203;
PRIOR APPLICATION NUMBER: U.S. No. 6596925	97.1%;	98.9%;	Pred. No. 3.5e-203;
PRIOR FILING DATE: 1999-07-30	97.1%;	98.9%;	Pred. No. 3.5e-203;
PRIOR APPLICATION NUMBER: PCT/NZ00/00018	97.1%;	98.9%;	Pred. No. 3.5e-203;
PRIOR FILING DATE: 2000-02-24	97.1%;	98.9%;	Pred. No. 3.5e-203;
PRIOR APPLICATION NUMBER: U.S. No. 6596925	97.1%;	98.9%;	Pred. No. 3.5e-203;
PRIOR FILING DATE: 1999-03-25	97.1%;	98.9%;	Pred. No. 3.5e-203;
NUMBER OF SEQ ID NOS: 120	97.1%;	98.9%;	Pred. No. 3.5e-203;
SOFTWARE: FastSeq for Windows Version 4.0	97.1%;	98.9%;	Pred. No. 3.5e-203;
SEQ ID NO 60	97.1%;	98.9%;	Pred. No. 3.5e-203;
LENGTH: 2096	97.1%;	98.9%;	Pred. No. 3.5e-203;
TYPE: DNA	97.1%;	98.9%;	Pred. No. 3.5e-203;
ORGANISM: Eucalyptus grandis	97.1%;	98.9%;	Pred. No. 3.5e-203;
US-09-598-401C-60	97.1%;	98.9%;	Pred. No. 3.5e-203;

```

RESULT 5
; Sequence 107, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630

```

TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-615-192A-107

Query Match 11.4%; Score 75; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 CCGTTTATTTCTCTGCTTCTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAGAGAG 642
DB 1 CCGTTTATTTCTCTGCTTCTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAGAGAG 60

QY 643 AGGAGAGATGGGTT 657
DB 61 AGGAGAGATGGGTT 75

RESULT 6
US-09-169-789-107
Sequence 107, Application US/09169789
Patent No. 6653528
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
FILE REFERENCE: 11000.1003c2
CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: US 08/713,000
NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1630
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-169-789-107

Query Match 11.4%; Score 75; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 CCGTTTATTTCTCTGCTTCTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAGAG 642
DB 1 CCGTTTATTTCTCTGCTTCTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAGAGAG 60

QY 643 AGGAGAGATGGGTT 657
DB 61 AGGAGAGATGGGTT 75

RESULT 7
US-08-975-316-24
Sequence 24, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N., HAYUKKALA, Ilkka
APPLICANT: and GRIERSON, Alascail W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-24

Query Match 11.2%; Score 73.8; DB 2; Length 421;
Best Local Similarity 97.4%; Pred. No. 2.9e-14;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTATTTCTCTGCTTCTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAG 640
DB 13 AGCCGTTTATTTCTCTGCTTCTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAG 72

QY 641 AGGAGAGATGGGTT 657
DB 73 AGGAGAGATGGGTT 89

RESULT 8
US-09-615-192A-24
Sequence 24, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 421
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-615-192A-24

Query Match 11.2%; Score 73.8; DB 3; Length 421;
Best Local Similarity 97.4%; Pred. No. 2.9e-14;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTATTTCTCTGCTTCTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAG 640
DB 13 AGCCGTTTATTTCTCTGATTTCTTGTGCTCGAGTCTCGGAGAGAGAGAGAGAG 72

QY 641 AGAGAGAGATGGTT 657
 |||||
 DB 73 AGAGAGAGATGGTT 89

RESULT 9

US-09-169-789-24
 ; Sequence 24, Application US/09169789
 ; Patent No. 6653528
 ; GENERAL INFORMATION:
 ; APPLICANT: Bloksberg, Leonard N.
 ; APPLICANT: Havukkala, Ilkka
 ; TITLE OF INVENTION: Materials and Methods for the
 ; FILE OF INVENTION: Modification of Plant Lignin Content
 ; FILE REFERENCE: 11000.1003c2
 ; CURRENT APPLICATION NUMBER: US/09/169,789
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 08/975,316
 ; EARLIER FILING DATE: 1997-11-21
 ; EARLIER APPLICATION NUMBER: US 08/713,000
 ; EARLIER FILING DATE: 1996-09-11
 ; NUMBER OF SEQ ID NOS: 185
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 421
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-169-789-24

Query Match 11.2%; Score 73.8; DB 3; Length 421;
 Best Local Similarity 97.4%; Pred. No. 2.9e-14;
 Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTATTTCTCTGCTTTCTTTGCTGAGTCTCGCGAAGAGAGAGAGAG 640
 |||||
 DB 13 AGCGTTTATTTCTCTGATTTCTTTGCTGAGTCTCGCGAAGAGAGAGAGAG 72
 |||||
 QY 641 AGAGAGAGATGGTT 657
 |||||
 DB 73 AGAGAGAGATGGTT 89

RESULT 10

US-09-615-192A-106
 ; Sequence 106, Application US/09615192A
 ; Patent No. 6410718
 ; GENERAL INFORMATION:
 ; APPLICANT: Bloksberg, Leonard N.
 ; APPLICANT: Havukkala, Ilkka
 ; TITLE OF INVENTION: Materials and Methods for the
 ; FILE OF INVENTION: Modification of Plant Lignin Content
 ; FILE REFERENCE: 11000.1003c4U
 ; CURRENT APPLICATION NUMBER: US/09/615,192A
 ; CURRENT FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 08/975,316
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: US 08/713,000
 ; PRIOR FILING DATE: 1996-09-11
 ; PRIOR APPLICATION NUMBER: US 09/169,789
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 405
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 106
 ; LENGTH: 407
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-615-192A-106

Query Match 11.2%; Score 73.4; DB 3; Length 407;
 Best Local Similarity 98.7%; Pred. No. 3.9e-14;
 Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 583 CCGTTTATTTCTCTGCTTTCTTTGCTGAGTCTCGCGAAGAGAGAGAGAG 642

DB 1 CCGTTTATTTCTCTGATTTCTTTGCTGAGTCTCGCGAAGAGAGAGAGAG 60
 |||||
 QY 643 AGAGAGAGATGGTT 657
 |||||
 DB 61 AGAGAGAGATGGTT 75

RESULT 11

US-09-169-789-106
 ; Sequence 106, Application US/09169789
 ; Patent No. 6653528
 ; GENERAL INFORMATION:
 ; APPLICANT: Bloksberg, Leonard N.
 ; APPLICANT: Havukkala, Ilkka
 ; TITLE OF INVENTION: Materials and Methods for the
 ; FILE OF INVENTION: Modification of Plant Lignin Content
 ; FILE REFERENCE: 11000.1003c2
 ; CURRENT APPLICATION NUMBER: US/09/169,789
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 08/975,316
 ; EARLIER FILING DATE: 1997-11-21
 ; EARLIER APPLICATION NUMBER: US 08/713,000
 ; EARLIER FILING DATE: 1996-09-11
 ; NUMBER OF SEQ ID NOS: 185
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 106
 ; LENGTH: 407
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-169-789-106

Query Match 11.2%; Score 73.4; DB 3; Length 407;
 Best Local Similarity 98.7%; Pred. No. 3.9e-14;
 Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 583 CCGTTTATTTCTCTGCTTTCTTTGCTGAGTCTCGCGAAGAGAGAGAGAG 642
 |||||
 DB 1 CCGTTTATTTCTCTGATTTCTTTGCTGAGTCTCGCGAAGAGAGAGAGAG 60
 |||||
 QY 643 AGAGAGAGATGGTT 657
 |||||
 DB 61 AGAGAGAGATGGTT 75

RESULT 12

US-09-949-016-12273/C
 ; Sequence 12273, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12273
 ; LENGTH: 130563
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-12273

Query Match 6.2%; Score 40.6; DB 3; Length 130563;
 Best Local Similarity 73.2%; Pred. No. 0.1;
 Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY	350	AAAGCAGAGCCAAACCCAAAGAGTCAGATGTCATCCACGAGAGAGAGAGAGAGA	409
Db	118294	AAAGGAGAGCCAAACAGAGAAATTCACAGCTGAGAAATGAGAGAGAGAGAGAGAGA	118235
QY	410	GAGAGAGAGAGG	420
Db	118234	GAGAGAGAGAGG	118224

[illegible]

```

RESULT 2
US-11-229-856-80
: Sequence 80, Application US/11229856
: Publication No. US20060130183A1
: GENERAL INFORMATION:
: APPLICANT: FORSTER, RICHARD L.
: APPLICANT: ROTTMANN, WILLIAM H.
: APPLICANT: CONNETT, MARIE B.
: APPLICANT: SANDERS, PAUL
: APPLICANT: ZHANG, GARY
: APPLICANT: FITZGERALD, SANDRA JOANNE
: APPLICANT: EAGLETON, CLARE
: TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
: FILE REFERENCE: 04463-0441
: CURRENT APPLICATION NUMBER: US/11/229,856
: CURRENT FILING DATE: 2005-09-20
: PRIOR APPLICATION NUMBER: 10/946,650
: PRIOR FILING DATE: 2004-09-22
: PRIOR APPLICATION NUMBER: 10/946,644
: PRIOR FILING DATE: 2004-09-22
: NUMBER OF SEQ ID NOS: 86
: SOFTWARE: Patentin Ver. 3.3
: SEQ ID NO 80
: LENGTH: 306
: TYPE: DNA
: ORGANISM: Bucalyptus grandis
US-11-229-856-80

```

Query Match	46.6%	Score 306	DB 8	Length 306
Best Local Similarity	100.0%	Pred. No. 5.9e-89		
Matches 306	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	320	TTCCATTAACCCCTGATTTAATTGGTGGGAAAGCAGACCAACCAAAAAGTTCAGAT	379
Db	1	TTCCATTAACCCCTGATTTAATTGGTGGGAAAGCAGACCAACCAAAAAGTTCAGAT	60
Qy	380	GTCAATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTTCTCTATATTTCGG	438
Db	61	GTCAATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTTCTCTATATTTCGG	120
Qy	440	TTCAACCGGTGGAGTCATATGGCATGTGTCAGACATATGATCATATTGTTGTAAGGTCCATA	499
Db	121	TTCAACCGGTGGAGTCATATGGCATGTGTCAGACATATGATCATATTGTTGTAAGGTCCATA	180
Qy	500	TTTTGGCGGAGGGGTGTGTGAACCGCAAAATTCCTATATATGGAACATCCACACCAATACC	558
Db	181	TTTTGGCGGAGGGGTGTGTGAACCGCAAAATTCCTATATATGGAACATCCACACCAATACC	240
Qy	560	TCACTTCATCCCAACATTAATCGATTTAATTTCCCTGCTTTCCTTGTCTGACAGTCTC	619

Db	241	TCACCTTCATCCCCACACATTATTCGGTTTATTTTCCTCCTGCTTCCCTGTCGAGTTC	300
Qy	620	GGCGAA	625
Db	301	GGCGAA	306

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RESULT 3
US-11-397-533-107
; Sequence 107, Application US/11397533
; Publication No. US2006018385A1
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c6
; CURRENT APPLICATION NUMBER: US/11/397,533
; CURRENT FILING DATE: 2006-04-03
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/143,833
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/615,192
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 10/174,693
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 407
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-107

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Query Match	11.4%	Score 75;	DB 7;	Length 1630;
Best Local Similarity	100.0%;	Pred. No. 1.3e-13;		
Matches 75; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 583 CCGTTTATTTCCTCGCTTCTCTTGGCTCGAGTCTCGCGAAGAGAGAGAAGAGAGAG 64

Db 1 CCGTTTATTTCCTCGCTTCTCTTGGCTCGAGTCTCGCGAAGAGAGAGAAGAGAGAGAG 60

Qy	643	AGGAGAGATGGCTT	65
Db	61	AGGAGAGATGGCTT	75

US-11-397-533-24
Sequence 24, Application US/11397533
Publication No. US20060183895A1
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
Title of Invention: Modification of Plant Lignin Content
FILE REFERENCE: 11000.100366
CURRENT APPLICATION NUMBER: US/11/397,533
CURRENT FILING DATE: 2006-04-03
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 60/143,833
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/615,192

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; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 10/174,693
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 407
; SOFTWARE: FaSTSeq For Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-24

```

Query Match	11.2%	Score 73.8;	DB 7;	Length 421;
Best Local Similarity	97.4%;	Pred. No. 1.6e-13;		
Matches 75; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

OY	581	ATCCGTTTAAATTCCTCTCTCTTCTCTGCTCGAGTCTGCGGAAAGAGAGAAGAGAGG	640
Db	13	AGCCGTTTAAATTCCTCTGATTTCTTCTCTCGAGTCTGCGGAAAGAGAGAAGAGAGG	72
OY	641	AGAGGAGAGAAATGGGTT	657
Db	73	AGAGGAGAGAAATGGGTT	89

RESULT 5
US-11-397-533-106
; Sequence 106, Application US/11397533
; Publication No. US20060183895A1
Journal: INFORMATION

APPLICANT: Bloksberg, Leonard N.
APPLICANT: Haavikala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content

```

FILE REFERENCE: 110007.1003ce
CURRENT APPLICATION NUMBER: US/11/397,533
CURRENT FILING DATE: 2006-04-03
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 60/143,833
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 10/174,693
PRIOR FILING DATE: 2002-06-18
NUMBER OF SEQ ID NOS: 407
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 106
LENGTH: 407
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-11-397-533-106

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Query Match	11.2%	Score 73.4;	DB 7;	Length 407;
Best Local Similarity	98.7%;	Pred. No. 2.1e-13;		
Matches 74;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

0y 583 CCGTTTATTTCTCGACTTCTCTTGTCTCGAGTCTCGGGAAGAGAGAAAGAGAGAG 642
 Db 1 CCGTTTATTTCTCTGATTTCTTGTCTCGAGTCTCGGGAAGAGAGAAAGAGAGAGAG 60

QY	643	AGGAGAGAATCGGTT	657
Db	61	AGGAGAGAATCGGTT	75

RESULT 6
US-11-404-951-96/c
; Sequence 96, Application US/11404951
; Publication No. US20060236421A1

```

; GENERAL INFORMATION:
; APPLICANT: PENNELL, Roger I.
; APPLICANT: DANG, David Vandinh
; APPLICANT: APIYA, Nestor
; TITLE OR INVENTION: Secondary Metabolite Production via Manipulation of
; TITLE OF INVENTION: Genome Methylation
; FILE REFERENCE: 18207-005001
; CURRENT APPLICATION NUMBER: US/11/404,951
; CURRENT FILING DATE: 2006-04-14
; PRIOR APPLICATION NUMBER: 60/671,209
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: 60/753,588
; PRIOR FILING DATE: 2005-11-04
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 96
; LENGTH: 1951
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ..(1951)
; OTHER INFORMATION: Cereas PROMOTER ID no. p524d05
US-11-404-951-96

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Query Match	6.8%	Score 45;	DB 7;	Length 1951;
Best Local Similarity	50.7%;	Pred. No. 0.00076;		
Matches 108;	Conservative 0;	Mismatches 105;	Indels 0;	Gaps 0;

Qy 355 ACAGCCACCCCAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAG 414
Db 768 ACACAGAACAAACAAGCAGAGAAAGTGAAGCAGAGAGAGAGAGAGAGAGAGAG 709

Qy 415 AGAAGTTCCTCTATAATTCGTGCACCGGTTGGAGTCAATGGCATGCCGTACGAAT 474
| | | | |
Db 708 AGAGTGAGACTGCAGTTATTGTGCTTGAGATAGACAAGAAGAACTGAAGGAATGTTGAGA 649

Qy 475 GTACATATTGGTGTAGGGTCCAAATTTTGGCGGAGGGTTGGTGAACCGCAAGTTCTTA 534
Db 648 GAGGGGGTGGTGGTGGTGGTATTGTAGCGCGTGGTGGTGAAGCCCGCGGATCTC 589

Qy	535	TATATCGA	CCTCG	ACCACCA	CATTAC	CTCACT	TCA	567
Db	588	TCTCTCC	CCCTCT	CCCTCCG	CAACAT	TTTA		556

RESULT 7
US-10-449-902-24951/c

Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/449,902
 CURRENT FILING DATE: 2003-05-29
 PRIOR APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: JP 2002-383870
 PRIOR FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: Patentin Ver. 2.1

```

; SEQ ID NO 24951
; LENGTH: 2168
; TYPE: DNA
; ORGANISM: Oryza sativa
; SOURCE: Oryza sativa

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; DATABASE ACCESSION NUMBER: AK100393
 ; DATABASE ENTRY DATE: 2002-08-28
 US-10-449-902-24951


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Query Match      6.3%; Score 41.2; DB 6; Length 176594;
Best Local Similarity 54.7%; Pred. No. 0.13;
Matches 82; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY      271 ATTAAATTAAACAATAAGCTCTGTACCGGAACTCCGATTTCTCTCACTTCCATPAACG 330
      |||||
DB      19504 ATTCAATTAAAGCACTTATTATTGAGAAAGGAAATAGTGCCTTCTCTCACTACCATAGAGGC 19445
      |||||

QY      331 CCTGATTAATTGTGTGGGAAACGACAGCCACCCACAAAAGTCAATGTCATCCACG 390
      |||||
DB      19444 TCCCTGGAGCAATTAATTAAATAATGTATTAATAAGTACAGAGAGAGAGAAAGAGAG 19385
      |||||

QY      391 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
      |||||
DB      19384 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19355
      |||||

RESULT 11
US-11-266-748A-215547
; Sequence 215547, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 215547
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (128)..(132)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (152)..(152)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (160)..(160)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:

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; LOCATION: (211)..(211)
; OTHER INFORMATION: n is a, c, g, or t
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; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
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; LOCATION: (334)..(334)
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; LOCATION: (364)..(364)
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; OTHER INFORMATION: n is a, c, g, or t
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; LOCATION: (398)..(398)
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; NAME/KEY: misc_feature
; LOCATION: (400)..(400)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (407)..(407)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (413)..(413)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (423)..(423)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (428)..(428)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (435)..(435)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature

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Query Match      6.2%  Score 41;  DB 8;  Length 601;
Best local Similarity 73.4%  Pred. No. 0.0083;
Matches 47;  Conservative 0;  Mismatches 17;  Indels 0;  Gaps 0;

QY      390  GAGAGAGAGAGAGAGAGAGAGAGAGAGTTTCTCTCTATATTCGTGGTTCACCGGTT 449
          |||
Db       75   GAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTCTCTCTATATTCGTGGTTCACCGGTT 134

QY      450  GGAG 453
          |
Db      135  NGCG 138

RESULT 12
US-11-266-748A-237674/C
; Sequence 237674, Application US/11266748A
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55615-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 237674
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n is a, c, g, or t

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)_(26)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (32)_(33)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (38)_(38)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (42)_(42)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (44)_(46)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48)_(50)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (55)_(55)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66)_(69)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (84)_(85)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (93)_(93)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (96)_(96)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (105)_(105)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (117)_(117)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (122)_(122)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (127)_(127)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (132)_(132)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (136)_(137)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (144)_(144)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:

NAME/KEY: misc_feature
LOCATION: (149)_(150)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (167)_(167)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (174)_(174)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (179)_(179)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (189)_(189)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (195)_(195)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (204)_(204)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (210)_(210)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (213)_(213)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (234)_(234)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (238)_(238)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (251)_(251)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (268)_(268)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
LOCATION: (273)_(273)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (334)_(334)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (368)_(368)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (381)_(381)

Query Match 6.2%; Score 41; DB 8; Length 601;
Best Local Similarity 73.4%; Pred. No. 0.0083;

us-10-702-319a-113_copy_1019_1675.rnpbn

Matches	47;	Conservative	0;	Mismatches	17;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	-----	--------	----	------	----

QY	450	GGAG	453
Db	467	NGGG	464

RESULT 13
US-10-540-898-585
Sequence 585. Application US/10540898

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/ Sequence 585, Application US/10540898
/ Publication No. US20060166213A1
/
/ GENERAL INFORMATION:
/ APPLICANT: David W. Morris
/ APPLICANT: Marc Malandro
/ TITLE OF INVENTION: Novel Compositions and Methods in Cancer
/ FILE REFERENCE: CH10056-101 (P023367.0003)
/ CURRENT APPLICATION NUMBER: US/10/540,898
/ CURRENT FILING DATE: 2005-06-27
/ PRIOR APPLICATION NUMBER: US 10/330,773
/ PRIOR FILING DATE: 2002-12-27
/ NUMBER OF SEQ ID NOS: 991
/ SOFTWARE: FastSeq for Windows Version 4.0
/
/ SEQ ID NO 585
/ LENGTH: 100610
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/ TYPE: DNA
/ ORGANISM: Mus musculus
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/ FEATURES:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(100610)
/ OTHER INFORMATION: n = A,T,C or G
/
/ US-10-540-898-585

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Query Match	6.2%;	Score 40.8;	DB 6;	Length 100610;
Best Local Similarity	67.9%;	Pred. No. 0.13;		
Matches 57;	Conservative	0;	Mismatches 27;	Indels 0;
			Gaps	0

Oy		390 GAGGAGA GAGA GAGA GAGA GTTTCTCTTAA TTTCTGGTCACCGGT	449
Dβ	35198 GAGAGA GA GAGA GAGA GACA TGCCCTC CTCTGA TTGCATTG AGA GGT	3525	

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QY      450 GGAGTCAATGGCATGCGTGACGAA 473
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Db      35258 AGAGTTATTGTAGCTATGACGGA 35281

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RESULT 14
US-10-539-228-323
Identification MS/10539228

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Publication No. US20060154250A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: CHIR0052-101 (P023370.0003)
CURRENT APPLICATION NUMBER: US/10/539,228
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 323
SEQ ID NO 103464

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1 LENGTH: 103464
2
3 TYPE: DNA
4
5 ORGANISM: Mus musculus
6
7 FEATURE:
8
9 NAME/KEY: misc feature
10 LOCATION: (1)...(103464)
11 OTHER INFORMATION: n = A,T,C or G
12
13 US-10-539-228-323

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74634 CAGAGAGAGAGAGAGAAACGGGCGAAGCACTTGAATACACA CAGAGAGAGAGA 74693

QY		404	GAGAGAGAGAGAGATTTCCTCCTATATCTCGTCCACGC	446
Db		74694	GAGAGAGAGAGAGAGAGAAGAAAAAACCCTATGAATCACCG	74736

RESULT 15
US-10-833-833-77/c
US/10833833

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Publication No. US20060194210A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Malandro, Marc S.
APPLICANT: Lai, Albert
APPLICANT: Tse, Christin
APPLICANT: Patraey, Ali
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 2036-039001
CURRENT APPLICATION NUMBER: US/10/833,833
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 175
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 77
LENGTH: 1320443
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(1320443)
OTHER INFORMATION: n = A, C, G, or T/U
US-10-833-833--77

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Query Match	6.2%	Score 40.6;	DB 6;	Length 1320443;
Best Local Similarity	56.3%;	Pred. No. 0.55;		
Matches	76;	Conservative	0;	Mismatches 59;
			Indels	0;
			Gaps	0;

QY	DB	1252615	1252616	1252617	1252618	1252619	1252620	1252621	1252622	1252623	1252624	1252625	1252626	1252627	1252628	1252629	1252630	1252631	1252632	1252633	1252634	1252635	1252636	1252637	1252638	1252639	1252640	1252641	1252642	1252643	1252644	1252645	1252646	1252647	1252648	1252649	1252650	1252651	1252652	1252653	1252654	1252655	1252656	1252657	1252658	1252659	1252660	1252661	1252662	1252663	1252664	1252665	1252666	1252667	1252668	1252669	1252670	1252671	1252672	1252673	1252674	1252675	1252676	1252677	1252678	1252679	1252680	1252681	1252682	1252683	1252684	1252685	1252686	1252687	1252688	1252689	1252690	1252691	1252692	1252693	1252694	1252695	1252696	1252697	1252698	1252699	1252700	1252701	1252702	1252703	1252704	1252705	1252706	1252707	1252708	1252709	1252710	1252711	1252712	1252713	1252714	1252715	1252716	1252717	1252718	1252719	1252720	1252721	1252722	1252723	1252724	1252725	1252726	1252727	1252728	1252729	1252730	1252731	1252732	1252733	1252734	1252735	1252736	1252737	1252738	1252739	1252740	1252741	1252742	1252743	1252744	1252745	1252746	1252747	1252748	1252749	1252750	1252751	1252752	1252753	1252754	1252755	1252756	1252757	1252758	1252759	1252760	1252761	1252762	1252763	1252764	1252765	1252766	1252767	1252768	1252769	1252770	1252771	1252772	1252773	1252774	1252775	1252776	1252777	1252778	1252779	1252780	1252781	1252782	1252783	1252784	1252785	1252786	1252787	1252788	1252789	1252790	1252791	1252792	1252793	1252794	1252795	1252796	1252797	1252798	1252799	1252800	1252801	1252802	1252803	1252804	1252805	1252806	1252807	1252808	1252809	1252810	1252811	1252812	1252813	1252814	1252815	1252816	1252817	1252818	1252819	1252820	1252821	1252822	1252823	1252824	1252825	1252826	1252827	1252828	1252829	1252830	1252831	1252832	1252833	1252834	1252835	1252836	1252837	1252838	1252839	1252840	1252841	1252842	1252843	1252844	1252845	1252846	1252847	1252848	1252849	1252850	1252851	1252852	1252853	1252854	1252855	1252856	1252857	1252858	1252859	1252860	1252861	1252862	1252863	1252864	1252865	1252866	1252867	1252868	1252869	1252870	1252871	1252872	1252873	1252874	1252875	1252876	1252877	1252878	1252879	1252880	1252881	1252882	1252883	1252884	1252885	1252886	1252887	1252888	1252889	1252890	1252891	1252892	1252893	1252894	1252895	1252896	1252897	1252898	1252899	1252900	1252901	1252902	1252903	1252904	1252905	1252906	1252907	1252908	1252909	1252910	1252911	1252912	1252913	1252914	1252915	1252916	1252917	1252918	1252919	1252920	1252921	1252922	1252923	1252924	1252925	1252926	1252927
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OY		CCCCAAAAGTCTGATGTTCATCCACGAGCAGCACAGACAAGCA 	
D8	363	GGAAAGCGTTTAGGAGGAAGTGCGGAGAAGAGAGAAAAAAGAGAGGA 	125249
Db	125255	GGAAGCGTTTAGGAGGAAGTGCGGAGAAGAGAGAAAAAAGAGAGGA 	125249

QY	423	TTCTCTATATTTCT	437
Db	1252495	GAGTGAGTATAATTT	1252481

Search completed: November 1, 2006, 14:52:54
Job time : 145.489 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:27:09 ; Search time 3570.42 Seconds
(without alignments)
1193.945 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1643
Perfect score: 625
Sequence: 1 ctgagccatttaattcgaga.....tttcctcgcagtcgcgaa 625

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:.*
1: gb_env:.*
2: gb_pat:.*
3: gb_pn:.*
4: gb_pl:.*
5: gb_pr:.*
6: gb_ro:.*
7: gb_sts:.*
8: gb_sy:.*
9: gb_un:.*
10: gb_vl:.*
11: gb_ov:.*
12: gb_hlg:.*
13: gb_in:.*
14: gb_om:.*
15: gb_da:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	3070	2	AR360987 Sequence
2	606.2	97.0	661	2	BD262120 Compositi
3	606.2	97.0	661	2	AR360905 Sequence
4	606.2	97.0	2096	2	BD262168 Compositi
5	606.2	97.0	2096	2	AR360953 Sequence
6	53.2	8.5	249121	12	AC096843 Ratcus no
7	50.2	8.0	198450	12	AC110357 Ratcus no
8	50.2	8.0	218614	12	AC123243 Ratcus no
9	50.2	8.0	252137	12	AC107438 Ratcus no
10	50.2	8.0	193795	12	AC069535 Mus muscu
11	49.4	7.9	5235	12	AC012735 Drosophi1
12	49.4	7.9	5624	2	COS91632 Sequence
13	49.4	7.9	137544	12	AC018487 Drosophi1
14	49.4	7.9	165118	13	AC018488 Drosophi1
15	49.4	7.9	182416	13	AC022345 Drosophi1
16	49.4	7.9	204000	6	AC136645 Ratcus no
17	49.4	7.9	341520	13	AE003498 Drosophi1
18	49.4	7.8	74587	5	HSDJ90205 AL109750 Human DNA

c	19	48.8	7.8	221729	12	AC094575 Ratcus no
c	20	48.8	7.8	248722	12	AC095781 Ratcus no
c	21	48.2	7.7	231530	6	AL671975 Mouse DNA
c	22	48	7.7	230763	12	AC129875 Ratcus no
c	23	48	7.7	244684	12	AC114841 Ratcus no
c	24	48	7.7	298672	12	AC108330 Ratcus no
c	25	47.6	7.6	231	4	AJ865169 Cocos nuc
c	26	47.6	7.6	192583	6	AL671782 Ratcus DNA
c	27	47.6	7.6	306749	12	AL590310 Homo sapi
c	28	47.4	7.6	127293	12	AC026917 Homo sapi
c	29	47.4	7.6	167483	5	AC115540 Homo sapi
c	30	47.4	7.6	183375	12	AC105920 Homo sapi
c	31	47.4	7.6	231007	12	AC141028 Ratcus no
c	32	47.4	7.6	267468	12	AC112812 Ratcus no
c	33	47.2	7.6	166104	6	AC155311 Mus muscu
c	34	47.2	7.6	178590	12	AC132894 Mus muscu
c	35	47	7.5	40987	12	AC175741 Mus muscu
c	36	47	7.5	151930	12	AC161531 Mus muscu
c	37	47	7.5	156084	6	AC166746 Mus muscu
c	38	47	7.5	194657	14	AC124042 Oryctolag
c	39	47	7.5	224378	12	AC145304 Mus muscu
c	40	46.8	7.5	215689	12	AC111687 Ratcus no
c	41	46.8	7.5	220614	12	AC094779 Ratcus no
c	42	46.6	7.5	172527	12	AC181183 Strongylo
c	43	46.6	7.5	175675	12	AC166024 Oryctolag
c	44	46.4	7.4	21686	13	AY578801 Anopheles
c	45	46.4	7.4	215042	12	AC136823 Ratcus no

ALIGNMENTS

RESULT 1	AR360987	Sequence 113 from patent US 6596925.	DNA	linear	PAT 17-AUG-2003
LOCUS	AR360987	3070 bp			
DEFINITION	Sequence 113 from patent US 6596925.				
ACCESSION	AR360987				
VERSION	AR360987.1	GI:33768497			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 3070)				
AUTHORS	Pereira, J.R., Eagleton, C. and Rice, S.J.				
TITLE	Compositions and methods for the modification of gene expression				
JOURNAL	Patent: US 6596925-A 113 22-JUL-2003;				
	Genesis Research & Development Corp. Ltd. and Rubicon Forests				
	Holdings Ltd., Parnell;				
	NZX;				
FEATURES	Location/Qualifiers				
SOURCE	1..3070				
ORIGIN	/organism="unknown"				
	/mol_type="genomic DNA"				
Query Match	100.0%;	Score 625;	DB 2;	Length 3070;	
Best Local Similarity	100.0%;	Pred. No. 1.2e-193;			
Matches	625;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTGAGCCATTTAATTGAGAGACATGCCCAAAATTAATCTCTGTCGCATTAATCTG	60		
Db	1019	CTGAGCCATTTAATTGAGAGACATGCCCAAAATTAATCTCTGTCGCATTAATCTG	1078		
Qy	61	CGAATTTCTCTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAAGCTGATTA	120		
Db	1079	CGAATTTCTCTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAAGCTGATTA	1138		
Qy	121	GTAATGATCTTGAGTGTGTTGTTGTTGCAATTTGCAAGCTGAAGTGGCCCTCAGGAATTT	180		
Db	1139	GTAATGATCTTGAGTGTGTTGTTGTTGCAATTTGCAAGCTGAAGTGGCCCTCAGGAATTT	1198		
Qy	181	AAGGCGCAACCGAATTTGCAAGAGCAAAAGAGCAGCAACCACTTCTTAACAAG	240		

Db	1199	AAGGCGCCAA	CCGAGATTGGCAA	AAGAGACAA	AAGGACGAC	CGACCCAA	CCCTTCTTA	CAACAG	1258
Qy	241	ATCATAC	CCAGATGGCC	AGTAAAGGGT	TATTTATTTAA	CAATAGCTCTT	GTACGGG	300	
Db	1259	ATCATCA	CCAGATGGCC	AGTAAAGGGT	TATTTATTTAA	CAATAGCTCTT	GTACGGG	1318	
Qy	301	AACCCGAT	TTTCTCTCA	CTCACTTCC	ATAAACCCCTG	ATTATTTGGT	GGAAACGAC	360	
Db	1319	AACCTCG	ATTTTCTCTCA	CTCACTTCC	ATAAACCCCTG	ATTATTTGGT	GGAAAGCGAC	1378	
Qy	361	AACCCACA	AAAAGGTCA	GTGTCAT	CCACGAGAGAG	AGAGAGAGAGAG	AGAGAGAG	420	
Db	1379	AACCCACA	AAAAGGTCA	GTGTCAT	CCACGAGAGAG	AGAGAGAGAGAG	AGAGAGAGAG	1438	
Qy	421	TTTTCTCT	CTATATTTCT	GGTTCA	CCGGTTTGA	AGTCAAATGGCAT	GGATGTACAT	480	
Db	1439	TTTTCTCT	CTATATTTCT	GGTTCA	CCGGTTTGA	AGTCAAATGGCAT	GGATGTACAT	1498	
Qy	481	ATTGGTAG	GGGTCC	CAATATTTTGG	CGAGGGTGGT	GTGTAACCGCA	AGTTCTTATATC	540	
Db	1499	ATTGGTAG	GGGTCC	CAATATTTTGG	CGAGGGTGGT	GTGTAACCGCA	AGTTCTTATATC	1558	
Qy	541	GAACCTCA	CCACCAT	CACTCA	CTTCAATCC	CCACCATTTAT	CGTTTATTTCT	600	
Db	1559	GAACCTCA	CCACCAT	CACTCA	CTTCAATCC	CCACCATTTAT	CGTTTATTTCT	1618	
Qy	601	TTTCCTTG	CTCA	GTCTCG	CGGAA	625			
Db	1619	TTTCCTTG	CTCA	GTCTCG	CGGAA	1643			
RESULT 2									
BD262120									
LOCUS	BD262120				661 bp	DNA	linear	PAT 17-JUL-2003	
DEFINITION	Composition and methods for the modification of gene expression.								
ACCESSION	BD262120								
VERSION	BD262120.1				GI:33071888				
KEYWORDS	JP 2002539834-A/12.								
SOURCE	Eucalyptus grandis								
ORGANISM	Eucalyptus grandis								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; Myrtales; Myrtaceae; Eucalyptus.								
REFERENCE	1 (bases 1 to 661)								
AUTHORS	Peterson, R., Rice, S.J. and Eagleton, C.K.								
TITLE	Composition and methods for the modification of gene expression								
JOURNAL	Patent: JP 2002539834-A 12 26-NOV-2002;								
	GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE FORESTS INDUSTRIES LTD								
COMMENT	OS Eucalyptus grandis (flooded gum)								
	PN JP 2002539834-A/12								
	PD 26-NOV-2002								
	PF 24-FEB-2000 JP 2000608755								
	PR 25-MAR-1999 US 09/276599, 30-JUL-1999 US 60/146591								
	RANJAN PERRERA, STEPHEN J RICE, CLARE KATHERINE EAGLETON								
	PC C12N15/09, A01H5/00, C07K14/415, C12N5/10, C12Q1/02, C12Q1/68, PC C12N15/00,								
	PC C12N5/00								
	CC Composition and methods for the modification of gene expression								
FEATURES									
source									
	FH Key				Location/Qualifiers				
	FT 5'UTR				(1)..(654)				
	FT TATA_signal				(537)..(543)				
	FT CANT_signal				(499)..(502).				
					Location/Qualifiers				
					1..661				
					/organism="Eucalyptus grandis"				
					/mol_type="genomic DNA"				
					/db_xref="taxon:71139"				
ORIGIN									
Query Match					97.0%;	Score 606.2;	DB 2;	Length 661;	
Best Local Similarity					98.9%;	Pred. No. 1.1e-187;			

Matches	622/;	Conservative	0;	Mismatches	3;	Indels	4;	Gaps	1
Qy		1	CTGAGGCCATTAA	TTTGAGAGACATGAGCCAAATTAATCTTCTTGCTGCCATAACTGT	60				
Db		1	CTGAGCCATTAA	TTTGCAGAGACATGCCCCAAATTAATCTTCTTGCTGCCATAACTGT	60				
Qy		61	CGAATTTTCTCTTTTAGGTAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA	120					
Db		61	CGAATTTTCTCTTTTAGGTAAGTAACCAATGATGATCATGTTGACAAAAGGCTGATTA	120					
Qy		121	GTATGATCTTGAGTTTGTGTGCAATTTTGCAAGCTGACGATGGCCCCCAGGGAATT	180					
Db		121	GTATGATCTTGAGATTGTGTGTGCAAAATTTTGCAAGCTGACGATGGCCCCCAGGGAATT	180					
Qy		181	AAGCGCGCAACCCAGATTGGCAAAAGAGACAAAGAGACGACCCAACTTTCTTTAACAG	240					
Db		181	AAGCGCGCAACCCAGATTGGCAAAAGAGACAAAGAGACGATCCAACTTTCTTTAACAG	240					
Qy		241	ATCATCAACCAAGTGGCCAGTAAGGGTAATTAATTAACAAATAGCTCTTGTAACGGG	300					
Db		241	ATCATCAACCAAGTGGCCAGTAAGGGTAATTAATTAACAAATAGCTCTTGTAACGGG	300					
Qy		301	AACCTCCGATTTTCTCTCACTTCCATAACCCCGTAAATTTTGGTGGGAAAGCAGACCC	360					
Db		301	AACCTCCGATTTTCTCTCACTTCCATAACCCCGTATTAATTTGGTGGGAAAGGACAGCC	360					
Qy		361	AACCCACAAAAGGTCAATGTCAATCCAC---GAGAGAGAGAGAGAGAGAGAGAG	416					
Db		361	AACCCACAAAAGGTCAATGTCAATCCACGAGAGAGAGAGAGAGAGAGAGAGAG	420					
Qy		417	AGAGTTTCTCTCAATATTCCTGTTTCAACGGTTGAGATGCAATGCGTGAAGCAATGT	476					
Db		421	AGAGTTTCTCTCAATATTCCTGTTTCAACGGTTGAGATGCAATGCGTGAAGCAATGT	480					
Qy		477	ACATATTGTTGTTAGGGTCCAAATATTTTGGCGGAGGGTTGTGAACCGCAAAAGTTCATTA	536					
Db		481	ACATATTGTTGTTAGGGTCCAAATATTTTGGCGGAGGGTTGTGAACCGCAAAAGTTCATTA	540					
Qy		537	TATGGAACCTCCACACCATATCTCTCAATCCCAACCATTTATCGTTTAATTTTCT	596					
Db		541	TATGGAACCTCCACACCATATCTCTCAATCCCAACCATTTATCGTTTAATTTTCT	600					
Qy		597	CTGCTTTCCTTTGCTCGAGTCTCGCGGAA	625					
Db		601	CTGCTTTCCTTTGCTCGAGTCTCGCGGAA	629					
RESULT 3									
		AR360905	661 bp	DNA	linear	PAT 17-AUG-2003			
		LOCUS	AR360905	Sequence 12 from patent US 6596925.					
		DEFINITION	AR360905						
		ACCESSION	AR360905.1	GI:33768415					
		VERSION							
		KEYWORDS							
		SOURCE							
		ORGANISM	Unknown.						
		REFERENCE	1 (bases 1 to 661)						
		AUTHORS	Peterra,J.R., Baglioni,C. and Rice,S.J.						
		TITLE	Compositions and methods for the modification of gene expression						
		JOURNAL	Patent: US 6596925-A 12 22-JUL-2003;						
			Genesis Research & Development Corp. Ltd. and Rubicon Forests						
			Holdings Ltd.; Parnell;						
			NZX;						
		FEATURES	Location/Qualifiers						
		source	1..661						
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		ORIGIN							
		Query Match	97.0%;	Score 606.2;	DB 2;	Length 661;			
		Best Local Similarity	98.9%;	Pred. No. 1.1e-187;					
		Matches 622/;	Conservative 0;	Mismatches 3;	Indels 4;	Gaps 1			

QY 1 CTGAGCCATTAAATCGAGAGACATGCGCCAAATTAATCTTCTGCTGCATTAACGT 60
DB 1 CTGAGCCATTAAATCGAGAGACATGCGCCAAATTAATCTTCTGCTGCATTAACGT 60
QY 61 CGAATTTCTCTTTAGGTAAAGTAACAATGATGCGCCATGTGACAAAGAGCTGATTA 120
DB 61 CGAATTTCTCTTTAGGTAAAGTAACAATGATGCGCCATGTGACAAAGAGCTGATTA 120
QY 121 GTATGATCTTGAAGTTGTTGGTCAAAATTTGCAAGCTGACATGCGCCCTCAGGAAATT 180
DB 121 GTATGATCTTGAAGTTGTTGGTCAAAATTTGCAAGCTGACATGCGCCCTCAGGAAATT 180
QY 181 AAGGCGCCACCCGATGCAAGAGGACAAAGAGCAGACCCCACTTCTCTTAACAG 240
DB 181 AAGGCGCCACCCGATGCAAGAGGACAAAGAGCAGACCCCACTTCTCTTAACAG 240
QY 241 ATCATCAACGATGCGCCAGTAAGGTAATTAATTAACAATAGCTCTTGTACCGGG 300
DB 241 ATCATCAACGATGCGCCAGTAAGGTAATTAATTAACAATAGCTCTTGTACCGGG 300
QY 301 AACTCCGATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCAGCC 360
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QY 361 AACCACAAAGGTCAGATGTCATCCGAC---GAGAGAGAGAGAGAGAGAGAG 416
DB 361 AACCACAAAGGTCAGATGTCATCCGAC---GAGAGAGAGAGAGAGAGAGAGAG 420
QY 417 AGAGTTTCTCTTAATTTCTGTTCAACCGGTTGAGTCAATGCGATCGTACGAAATGT 476
DB 421 AGAGTTTCTCTTAATTTCTGTTCAACCGGTTGAGTCAATGCGATCGTACGAAATGT 480
QY 477 ACATATTGTTGTAAGGTCGAATATTTTGGGAGGTTGTGAACCGCAAGTTCTATA 536
DB 481 ACATATTGTTGTAAGGTCGAATATTTTGGGAGGTTGTGAACCGCAAGTTCTATA 540
QY 537 TATGAACCTCCACACATACCTCACTTCAATCCCACTTAATCCGTTTATTTTCT 596
DB 541 TATGAACCTCCACACATACCTCACTTCAATCCCACTTAATCCGTTTATTTTCT 600
QY 597 CTGCTTCTCTTGTCTGAGTCTCGCGAA 625
DB 601 CTGCTTCTCTTGTCTGAGTCTCGCGAA 629

RESULT 4
BD262168 2096 bp DNA linear PAT 17-JUN-2003
LOCUS Composition and methods for the modification of gene expression.
DEFINITION BD262168
VERSION BD262168.1 GI:33071936
KEYWORDS JP 2002539834-A/60.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 2096)
Perera,R., Rice,S.J. and Eagleton,C.K.
Composition and methods for the modification of gene expression
Patent: JP 2002539834-A 60 26-NOV-2002;
GENESTIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS INDUSTRIES LTD
OS Eucalyptus grandis (flooded gum)
PN JP 2002539834-A/60
PD 26-NOV-2002
RF 24-FEB-2000 JP 2000608755
PR 25-MAR-1999 US 09/276599,30-JUN-1999 US 60/146591 PT
RANJAN PERERA,STEPHEN J RICE,CLARE KATHERINE EAGLETON PC
C12N15/09,A01H5/00,C07K14/415,C12N5/10,C12Q1/02,C12Q1/68, PC
C12N15/00,
PC C12N5/00

CC Composition and methods for the modification of gene CC
expression
FH key Location/Qualifiers
FT source 1..2096
FT location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:71139"

ORIGIN
Query Match 97.0%; Score 606.2; DB 2; Length 2096;
Best Local Similarity 98.9%; Pred. No. 1.6e-187;
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY 1 CTGAGCCATTAAATCGAGAGACATGCGCCAAATTAATCTTCTGCTGCATTAACGT 60
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DB 101 CGAATTTCTCTTTAGGTAAAGTAACAATGATGCGCCATGTGACAAAGAGCTGATTA 160
QY 121 GTATGATCTTGAAGTTGTTGGTCAAAATTTGCAAGCTGACATGCGCCCTCAGGAAATT 180
DB 161 GTATGATCTTGAAGTTGTTGGTCAAAATTTGCAAGCTGACATGCGCCCTCAGGAAATT 220
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DB 341 AACTCCGATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCAGACC 400
QY 361 AACCACAAAGGTCAGATGTCATCCGAC---GAGAGAGAGAGAGAGAGAGAG 416
DB 401 AACCACAAAGGTCAGATGTCATCCGAC---GAGAGAGAGAGAGAGAGAGAG 460
QY 417 AGAGTTTCTCTTAATTTCTGTTCAACCGGTTGAGTCAATGCGATCGTACGAAATGT 476
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QY 537 TATGAACCTCCACACATACCTCACTTCAATCCCACTTAATCCGTTTATTTTCT 596
DB 581 TATGAACCTCCACACATACCTCACTTCAATCCCACTTAATCCGTTTATTTTCT 640
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DB 641 CTGCTTCTCTTGTCTGAGTCTCGCGAA 669

RESULT 5
AR360953 2096 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 60 from patent US 6596925.
DEFINITION AR360953
ACCESSION AR360953
VERSION AR360953.1 GI:33768463
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2096)
Perera,J.R., Eagleton,C. and Rice,S.J.

TITLE Compositions and methods for the modification of gene expression
JOURNAL Patent: US 6596925-A 60 22-JUL-2003;
Genetics Research & Development Corp. Ltd. and Rubicon Forests
Holdings Ltd.; Parnelli;
NZX;

FEATURES
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 97.0%; Score 606.2; DB 2; Length 2096;
Best Local Similarity 98.9%; Pred. No. 1.6e-187;
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

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QY 1 CTGAGCATTAAATTCGAGAGACATGCGCCCAAAATTAATTCCTGCTGCTCAATGCT 60
DB 41 CTGAGCATTAAATTCGAGAGACATGCGCCCAAAATTAATTCCTGCTGCTCAATGCT 100
QY 61 CGAATTTCTCTTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAGCTGATTA 120
DB 101 CGAATTTCTCTTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAGCTGATTA 160
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTCGAGAGACATGCGCCCTCAGGAAAT 180
DB 161 GTATGATCTTGGAGTTGTTGGTCAAAATTCGAGAGACATGCGCCCTCAGGAAAT 220
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QY 361 AACCACAAAAGTGCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
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QY 477 ACATTTGTTGTTGAGGTTCCATTAATTTGGGAGAGGTTGGAGAACCGCAAGTTCCATA 536
DB 521 ACATTTGTTGTTGAGGTTCCATTAATTTGGGAGAGGTTGGAGAACCGCAAGTTCCATA 580
QY 537 TATGCAACCTCCACACCAATACCTCACTTCAATCCCAACATTTATCCGTTTATTTTCT 596
DB 581 TATGCAACCTCCACACCAATACCTCACTTCAATCCCAACATTTATCCGTTTATTTTCT 640
QY 597 CTGCTTTCTTTGCTGAGTCTCGCGGAA 625
DB 641 CTGCTTTCTTTGCTGAGTCTCGCGGAA 669

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RESULT 6 AC096843 249121 bp DNA linear HTG 13-NOV-2002
LOCUS Rattus norvegicus clone CH230-2K10, *** SEQUENCING IN PROGRESS ***,
DEFINITION 4 unordered pieces.

AC096843.4 GI:24941328
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 249121)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarta,J., Benton,J., Bimagne,K., Blankenburg,K., Bonini,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,M., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,J., Dederich,D.A.,
Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Din,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
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Gorelli,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Horn,F., Howard,S., Huber,J., Huliyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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Kratovic,J., Kureishi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
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Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,J., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokwenkwo,S., Ogih,M., Okunolu,G.,
Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Peters,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojibokan,I., Rolfe,S., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoshitari,N., Stinson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansley,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Vallada,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
JOURNAL
TITLE
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 249121)
Worley,K.C.
Direct Submission
Submitted (28-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23195686.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu


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----- Project Information
Center project name: TURZ
Center clone name: CH230-2K10
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 203544 bases at least Q40
Consensus quality: 208066 bases at least Q30
Consensus quality: 210898 bases at least Q20
Estimated insert size: 204933; sum-of-coverage estimation
Quality coverage: 6x in Q20 bases; sum-of-coverage estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html) .
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 244604: contig of 244604 bp in length
* 244605 244704: gap of unknown length
* 244705 245850: contig of 1146 bp in length
* 245851 245950: gap of unknown length
* 245951 247065: contig of 1115 bp in length
* 247066 249121: gap of unknown length
* 249121 249166: contig of 1956 bp in length.
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*     /db_xref="taxon:10116"
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*     end_sequence:BH288263"
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Query Match      8.5%; Score 53.2; DB 12; Length 249121;
Best Local Similarity 54.0%; Pred. No. 7.1e-05;
Matches 109; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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Cy 570 CCCACATTATCCGTTTAT 591
Db 138069 CACAGCATGACAGCATTTT 138090

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LOCUS
DEFINITION
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ACCESSION
AC110357
VERSION
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurgnathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 198450)
Muzny D, Marie M, Metzker M, Lee A, Abramson S, Adams C, Alder J,
Allen C, Allen H, Albrooke S, Amin A, Angiano D,
Anyalebechi V, Aoyagi A, Ayodeji M, Baca E, Baden H,
Baldwin D, Bandaranaike D, Barber M, Barnstead M, Benahmed F,
Biewald K, Blair J, Blankenburg K, Blyth P, Brown M,
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Cardenas V, Carter K, Cavazos I, Caesar H, Center A,
Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J,
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David M, Davis C, Davy-Carroll L, De Anda C, Dederich D,
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Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K,
Egan A, Escotto M, Eugene C, Evans C, Falls T, Fan G,
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Fraser C, Gabisi A, Ganta R, Garcia A, Guerra T, Garza M,
Georgiadis E, Geier K, Gill R, Grady M, Guerra M, Guevara W,
Gunnarsson P, Haaland W, Hamill C, Hamilton C, Hamilton K,
Harvey Y, Havlak P, Hawes A, Henderson N, Hernandez J,
Hernandez R, Hines S, Hladun S, Hodgson A, Hogues M,
Hollins B, Howell S, Huylk S, Hume J, Idlebird D, Jackson A,
Jackson L, Jacob L, Jiang H, Johnson B, Johnson R, Jolivet A,
Karpachy S, Kelly S, Kelly S, Khan Z, King L, Kovar C,
Kowis C, Kraft C, Lebow H, Levan J, Lewis L, Li Z, Liu J,
Liu Y, Liu W, Liu Y, London P, Longacre S, Lopez J,
Lorenshewa L, Loulseged H, Lozano R, Lu X, Ma J,
Maheshwari M, Mahindaratne M, Mahmoud M, Malloy K, Mangum A,
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Mawhinney S, McLeod M, McNeill T, Meenen E,
Milosavljevic A, Miner G, Minja E, Montemayor J, Moore S,
Morgan M, Morris K, Morris S, Munidasa M, Murphy M, Nair L,
Nankervis C, Neal D, Newton N, Nguyen N, Norris S,
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Pasternak S, Paul H, Perez A, Perez L, Plambeck C,
Plopper F, Polinder A, Popovic D, Pirmus E, Pu L,
Piazio M, Quiroz J, Rachlin E, Reeves K, Regier M, Reigh R,
Reilly B, Reilly M, Ren Y, Reuter M, Richards S, Riggs F,
Rivers C, Rodkey T, Rojas A, Rose M, Rose R, Ruiz S,
Sanders W, Savery G, Scherer S, Scott G, Shastman S, Shen H,
Shetty J, Shvartsbeyn A, Sisson I, Sitter C, Smajs D,
Sneed A, Sodergren E, Song X, Sorelle R, Sosa J,
Steinle M, Strong R, Sutton A, Swalek A, Taber J, Taylor C,
Taylor T, Thomas N, Thomas S, Tingey A, Trejos Z, Uemari K,
Valas R, Vera V, Villaseña D, Waldron L, Walker B, Wang J,
Wang Q, Wang S, Warren J, Warren R, Wei X, White F,
Williams G, Willson R, Wlezyk R, Woodson H, Worley K,
Wright D, Wright R, Wu J, Yakub S, Yen J, Yoon L, Yoon V,
Yu P, Zhang J, Zhou J, Zhou X, Zhao S, Dunn D, von
Niederhausen A, Weiss R, Smith D, Holt R, Smith H,
Weinstock G, and Gibbs R. A.
Direct Submission
Unpublished
2 (bases 1 to 198450)
Worley K, C.
Direct Submission
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TITLE      JOURNAL
REFERENCE  AUTHORS
TITLE      JOURNAL
REFERENCE  AUTHORS
TITLE      JOURNAL
REFERENCE  AUTHORS
COMMENT    COMMENT

Velas,R., Vera,V., Villasana,D., Maldron,L., Walker,B., Wang,J.,
Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczky,R., Wooden,H., Wortley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,Y., Zhou,X., Zhao,S., Dunn,D., von
Niedehausen,A., Weiser,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Unpublished
Direct Submission
2 (bases 1 to 252137)
Worley,K.C.
Direct Submission
Submitted (21-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 252137)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:23267955.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly ('contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GMZC
Center clone name: CH230-160A14
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 207940 bases at least Q40
Consensus quality: 210601 bases at least Q30
Consensus quality: 212576 bases at least Q20
Estimated insert size: 216052; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drfc_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*   1 237176: contig of 237176 bp in length
*     1 237276: gap of unknown length
*     * 237277 238346: contig of 1070 bp in length
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	Best Local Similarity	63.9%; Pred. No. 0.00663;	
	Matches	76; Conservative 0; Mismatches 43; Indels 0; Gaps 0.	
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Db	62902 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAATACATGCATGTCTGATGTGTGTA 62902		
Oy	450 GGACTCAATGGCATGCCGTGACGAATGTACATATTTGGTGATGGGTCATATTTGGCGG 508		
Db	62962 AATTATATTCACATGCAAAAGAAATTTGGCAAATAATGCTGTCTGTTTATATTTAACAG 63020		
RESULT 10			
AC069535/c	Mus musculus chromosome 7 clone RP2-453F14, WORKING DRAFT		
LOCUS	AC069535	193795 bp	DNA linear HTG 12-SEP-2001
DEFINITION	Mus musculus chromosome 7 clone RP2-453F14, WORKING DRAFT		
ACCESSION	AC069535		
VERSION	AC069535.15 GI:15559164		
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Mus.		
AUTHORS	1 (bases 1 to 193795) Metzker,M.L., Lewis,L.R., Hume,T., Edwards,C., Harris,C., Dederich,D., Thomas,S., Okumou,J., Carllock,C., Garner,T., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Bunay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Fernandez,C., Ferraguto,D., Forcum-Taney,J., Gill,R., Gorell,J.T.H., Guarnatone,P., Haller,G., Hernandez,J., Hogues,M., Hoak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S., Kovar,C., Liu,X., Liu,W., Louisedge,H., Lorado,R.J., Martin,R., Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S., Neel,D., Nelson,A., Nguyen,R., Nguyen,N., Ogih,M., Parish,B., Perez,L., Relter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstein,G., Worley,K. and Gibbs,R. Direct Submission Unpublished 2 (bases 1 to 193795) Worley,K.C. Direct Submission Submitted (02-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 12, 2001 this sequence version replaced gi:14787158. Genome Center		

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:17:03 ; Search time 264.41 Seconds
(without alignments)
16480.672 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1643
Perfect score: 625
Sequence: 1 ctgagccattcaatcgcaga.....tttgcctcagctcgcgaa 625

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 348612421 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq 8: *
2: geneseqn1980s: *
3: geneseqn1990s: *
4: geneseqn2000s: *
5: geneseqn2001as: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *
15: geneseqn2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	3070	6	ABK17109
2	625	100.0	3070	10	ADH75529
3	625	100.0	3070	14	ADW80563
4	606.2	97.0	661	3	AAC62762
5	606.2	97.0	661	6	ABK17027
6	606.2	97.0	661	10	ADH75428
7	606.2	97.0	661	14	ADW80462
8	606.2	97.0	2096	6	AAC62810
9	606.2	97.0	2096	6	ABK17075
10	606.2	97.0	2096	10	ADH75476
11	606.2	97.0	2096	14	ADW80510
12	534	85.4	534	13	ADQ88319
13	485	77.6	485	13	ADQ88320
14	306	49.0	306	13	ADQ88321
15	293	46.9	293	13	ADQ88322
16	119	19.0	119	13	ADQ88323
17	98	15.7	98	13	ADQ88324
18	66	10.6	66	13	ADQ88325

19	49.4	7.9	5626	4	ABL14766	AD114766 Drosophila
20	45	7.2	1951	14	AD244892	Ad244892 Tissue-sp
21	43.4	6.9	2000	10	ADCO8406	AdCO8406 Rice DNA
22	43.4	6.9	2000	10	ADCO8416	AdCO8416 Rice DNA
23	43.4	6.9	2199	10	ADCO8351	AdCO8351 Rice DNA
24	43	6.9	378	6	ABQ92788	Abq92788 Trilicium
25	43	6.9	1630	3	AAA68014	Aaa68014 Eucalyptu
26	43	6.9	1630	10	ADP41764	Adp41764 O-methyl
27	42.6	6.8	2000	8	ADA71732	Ada71732 Rice gene
28	42.4	6.8	110000	11	ACM43984_3	Conformation (4 of
29	42	6.7	61009	14	AD212537	Ad212537 Murine ca
30	41.8	6.7	385	6	ABQ92741	Abq92741 Trilicium
31	41.8	6.7	421	2	AAV23844	Aav23844 Plant OMT
32	41.8	6.7	421	2	AAZ06845	Aaz06845 Eucalyptu
33	41.8	6.7	421	3	AAA69595	Aaa69595 Eucalyptu
34	41.8	6.7	421	3	AAA67931	Aaa67931 Eucalyptu
35	41.8	6.7	421	10	ADD41681	Add41681 O-methyl
36	41.8	6.7	421	14	AED59781	Aed59781 Eucalyptu
37	41.8	6.7	126192	11	ACN44820	Acn44820 Mouse gen
38	41.8	6.7	132942	14	AD212611	Ad212611 Murine ca
39	41.6	6.7	53981	11	ACM44928	Acn44928 Mouse gen
40	41.4	6.6	407	3	AAA68013	Aaa68013 Eucalyptu
41	41.4	6.6	407	10	ADD41763	Add41763 O-methyl
42	41.4	6.6	24080	9	ADA02813	Ada02813 Mouse Egr
43	41.4	6.6	24080	10	ADB72551	Adb72551 Mouse Egr
44	41.4	6.6	24080	10	ADC85293	Adc85293 Mouse Egr
45	41.4	6.6	24080	12	ADM74408	Adm74408 Murine ca

ALIGNMENTS

RESULT 1
ABK17109
ID ABK17109 standard; cDNA; 3070 BP.
XX
AC ABK17109;
XX
DT 26-MAR-2002 (first entry)
XX
DE Eucalyptus grandis promoter polynucleotide #51.
XX
KW Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;
KW temporally regulated promoter; pinus radiata; Eucalyptus grandis; ss;
KW PCR primer.
XX
OS Eucalyptus grandis.
XX
PN MO200198485-A1.
XX
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-N2000115.
XX
XX 20-JUN-2000; 2000US-00598401.
XX
XX 28-NOV-2000; 2000US-00724624.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
XX
PI Perera R, Rice S, Eagleton C, Lasham A;
XX
XX WPI; 2002-114583/15.
XX
XX Novel polynucleotide promoter sequences from pine and Eucalyptus useful
XX for modifying expression of endogenous and/or heterologous
XX polynucleotides in transgenic plants.
XX
XX Claim 1; Page 103-104; 121pp; English.
XX
XX The invention relates to isolated promoter sequences from pinus radiata
XX and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,
XX flower-, pollen-, bud-, meristem-specific promoters or temporally

CC regulated promoters such as xylogenesis-specific promoters. The promoter
CC polyepitides and their related polynucleotides are useful in the
CC production of genetic constructs, used for modifying gene expression in a
CC target organism, in particular a plant. The method is useful for
CC modifying expression of a polynucleotide that comprises an intron
CC sequence, through removal of the intron sequence. The method is useful
CC for modifying growth and development of plants, and cellular responses to
CC external stimulus, such as environmental factors and disease pathogens.
CC The sequences are useful in genome and physical mapping, in positional
CC cloning of genes, in various assays to determine biological activity, to
CC raise antibodies, to isolate corresponding interacting proteins and other
CC compounds, and to quantitatively determine levels of interacting proteins
CC or other compounds. Sequences ABK17016-ABK17125 represent *Pinus radiata*
CC and *Eucalyptus grandis* polynucleotides and PCR primers used in the method
CC of the invention
CC

SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 625; DB 6; Length 3070;

Best Local Similarity 100.0%; Pred. No. 2.8e-189; Mismatches 0; Gaps 0;

Matches 625; Conservative 0; Indels 0; Gaps 0;

```
QY 1 CTGAGCCATTAAATTCGAGAGACATGCGCCAAATTAATTCCTTGCTGCATTAATCTG 60
DB 1019 CTGAGCCATTAAATTCGAGAGACATGCGCCAAATTAATTCCTTGCTGCATTAATCTG 1078
QY 61 CGAATTTCTCTTTAGGTAAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 120
DB 1079 CGAATTTCTCTTTAGGTAAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 1138
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGTGCATGATGCGCCCTTCAGGAAATT 180
DB 1139 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGTGCATGATGCGCCCTTCAGGAAATT 1198
QY 181 AAGGCGCAACCCGATTCGAAAGAGCAAAAGAGCAGACCACTTCTTAAACAAG 240
DB 1199 AAGGCGCAACCCGATTCGAAAGAGCAAAAGAGCAGACCACTTCTTAAACAAG 1258
QY 241 ATCATCACGATGCGCCAGTAAGGTAATTAATTTAAACAAATAGCTTTGTACCGGG 300
DB 1259 ATCATCACGATGCGCCAGTAAGGTAATTAATTTAAACAAATAGCTTTGTACCGGG 1318
QY 301 AACTCCGTAATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAAGCGACGCC 360
DB 1319 AACTCCGTAATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAAGCGACGCC 1378
QY 361 AACCACAAAGAGTCAGATGTCATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 1379 AACCACAAAGAGTCAGATGTCATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
QY 421 TTTTCTCTTAATTTCTGTTACCGGTTGAGTCAATGCGATGCGATGCAATGTATCAT 480
DB 1439 TTTTCTCTTAATTTCTGTTACCGGTTGAGTCAATGCGATGCGATGCAATGTATCAT 1498
QY 481 ATTGGTGAAGGTCATATTTTGGGGAAGGTTGGTGAACCGCAAGTCTTATATATC 540
DB 1499 ATTGGTGAAGGTCATATTTTGGGGAAGGTTGGTGAACCGCAAGTCTTATATATC 1558
QY 541 GAACCTCCACCACTTACCTCACTTCATCCCAATTTAATCGTTTTATTTCTCTGCG 600
DB 1559 GAACCTCCACCACTTACCTCACTTCATCCCAATTTAATCGTTTTATTTCTCTGCG 1618
QY 601 TTTTCTTGTCTGAAGTCTCGCGGAA 625
DB 1619 TTTTCTTGTCTGAAGTCTCGCGGAA 1643
```

RESULT 2
ADH75529
ID ADH75529 standard; DNA; 3070 BP.

XX ADH75529;
AC
XX

DT 22-APR-2004 (first entry)

XX Eucalyptus grandis superubiquitin related sequence #49.

XX de; Monterey pine; superubiquitin; promoter; gene expression;

KM transgenic plant.

XX Eucalyptus grandis.

XX WO2003093475-A1.

XX 13-NOV-2003.

XX 30-APR-2003; 2003WO-NZ000076.

XX 30-APR-2002; 2002US-00137036.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (RUBI-) RUBICON FORESTS HOLDINGS LTD.

XX Rice SJ, Wood M, Eagleton CK, Visser ES, Perera R;

XX WPI; 2003-903678/82.

XX New polynucleotide of the superubiquitin promoter from *Pinus radiata*,
PT useful in modifying gene expression in a target organism.

XX Disclosure; SEQ ID NO 113; 123bp; English.

CC The invention relates to a new isolated polynucleotide comprising the
CC *Pinus radiata* (Monterey pine) superubiquitin promoter sequence, its
CC complement, reverse sequence or inverted repeat or a
CC sequence having at least 40, 60, 75 or 90% identity with the promoter.
CC The polynucleotide is useful in modifying gene expression in a target
CC organism, especially in transgenic plants. This sequence corresponds to a
CC superubiquitin promoter related sequence.

SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 625; DB 10; Length 3070;

Best Local Similarity 100.0%; Pred. No. 2.8e-189; Mismatches 0; Gaps 0;

Matches 625; Conservative 0; Indels 0; Gaps 0;

```
QY 1 CTGAGCCATTAAATTCGAGAGACATGCGCCAAATTAATTCCTTGCTGCATTAATCTG 60
DB 1019 CTGAGCCATTAAATTCGAGAGACATGCGCCAAATTAATTCCTTGCTGCATTAATCTG 1078
QY 61 CGAATTTCTCTTTAGGTAAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 120
DB 1079 CGAATTTCTCTTTAGGTAAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 1138
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGTGCATGATGCGCCCTTCAGGAAATT 180
DB 1139 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGTGCATGATGCGCCCTTCAGGAAATT 1198
QY 181 AAGGCGCAACCCGATTCGAAAGAGCAAAAGAGCAGACCACTTCTTAAACAAG 240
DB 1199 AAGGCGCAACCCGATTCGAAAGAGCAAAAGAGCAGACCACTTCTTAAACAAG 1258
QY 241 ATCATCACGATGCGCCAGTAAGGTAATTAATTTAACAATAGCTTTGTACCGGG 300
DB 1259 ATCATCACGATGCGCCAGTAAGGTAATTAATTTAACAATAGCTTTGTACCGGG 1318
QY 301 AACTCCGTAATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAAGCGACGCC 360
DB 1319 AACTCCGTAATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAAGCGACGCC 1378
QY 361 AACCACAAAGAGTCAGATGTCATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 1379 AACCACAAAGAGTCAGATGTCATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
QY 421 TTTTCTCTTAATTTCTGTTACCGGTTGAGTCAATGCGATGCGATGCAATGTATCAT 480
```

Db 1439 TTTTCTCTATATTTCTGTTTACCGGTTGGATGCAATGCGTGCATGATGATCAT 1498
 Qy 481 ATTGATGAGGATGCAATTTTGGGAGGTTGGTGAACGGAAGTCTTATATC 540
 Db 1499 ATTGATGAGGATGCAATTTTGGGAGGTTGGTGAACGGAAGTCTTATATC 1558
 Qy 541 GAACCTCACACCATACCTCACTTCAATCCCAACATTTTTCGTTTATTTCTGTC 600
 Db 1559 GAACCTCACACCATACCTCACTTCAATCCCAACATTTTTCGTTTATTTCTGTC 1618
 Qy 601 TTTCCTTTGCTCGAGTCTCGCGAA 625
 Db 1619 TTTCCTTTGCTCGAGTCTCGCGAA 1643

RESULT 3
 ADW80563 standard; cDNA; 3070 BP.
 AC ADM80563;
 XX 21-APR-2005 (first entry)
 DE E. grandis caffeic acid O-methyltransferase cDNA SEQ ID NO:113.
 KW ss: wood; plant; transcription; caffeic acid O-methyltransferase;
 XX transgenic plant.
 OS Eucalyptus grandis.
 FH Key location/Qualifiers
 FT 5'UTR 1..1643
 FT promoter /*tag= a
 FT 1019..1676
 FT /*tag= b

US2005026162-A1.
 03-FEB-2005.
 06-NOV-2003; 2003US-00702319.
 25-MAR-1999; 99US-00276599.
 30-JUL-1999; 99US-0146591P.
 24-FEB-2000; 2000WO-N2000018.
 20-JUN-2000; 2000US-00598401.
 28-NOV-2000; 2000US-00724624.
 09-NOV-2001; 2001US-0345397P.
 30-APR-2002; 2002US-00137036.
 08-NOV-2002; 2002US-00291447.
 08-NOV-2002; 2002US-0425087P.
 (GENE-) GENESIS RES & DEV CORP LTD.
 PA (RUBI-) RUBICON FORESTS HOLDINGS LTD.
 XX
 PI Perera R, Rice SJ, Bagleton CK;
 XX
 DR WPI; 2005-131806/14.
 XX
 PT New isolated polynucleotide sequences comprising a functional vascular
 PT tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase
 PT promoter, useful for modifying gene expression.
 XX
 PS Claim 2; SEQ ID NO 113; 82pp; English.
 XX
 CC The invention relates to a novel isolated polynucleotide sequence
 CC comprising a functional vascular tissue-specific Eucalyptus grandis
 CC caffeic acid O-methyltransferase (cOMT) promoter (ADW80462 or ADW80563).
 CC Also claimed is a genetic construct comprising the above polynucleotide
 CC sequence or a sequence having 2096 base pairs fully defined in the
 CC specification (ADW80510), a host cell comprising the above genetic
 CC construct, a plant comprising the genetic construct, a method for
 CC producing a plant with modified gene expression, and a method for

CC identifying a gene responsible for a desired function or phenotype. The
 CC composition and method are useful for modifying gene expression or for
 CC modifying the transcription of endogenous and/or heterologous
 CC polynucleotides involved in wood formation. The present sequence is used
 CC in the exemplification of the invention.
 XX
 SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;
 Query Match 100.0%; Score 625; DB 14; Length 3070;
 Best Local Similarity 100.0%; Pred. No. 2.8e-189;
 Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTGAGCCATTTAATTCGAGAGCAGATGCGCCAAATATTTCTTCTGCTGCAATACGT 60
 Db 1019 CTGAGCCATTTAATTCGAGAGCAGATGCGCCAAATATTTCTTCTGCTGCAATACGT 1078
 Qy 61 CGAATTTTCTTTTAAAGTAAGTAACCAATGATGCGCCATGTTGACAAAAGCTGATTA 120
 Db 1079 CGAATTTTCTTTTAAAGTAAGTAACCAATGATGCGCCATGTTGACAAAAGCTGATTA 1138
 Qy 121 GTATGATCTTGAAGTTGTTGTTGCAATTTTGAAGTGAAGTGGCCCTCAGGAAAT 180
 Db 1139 GTATGATCTTGAAGTTGTTGTTGCAATTTTGAAGTGAAGTGGCCCTCAGGAAAT 1198
 Qy 181 AAGCGCGCAACCCAGATTGCAAGAGACAAAGAGCAGACCCACTTCTCTTAACAAG 240
 Db 1199 AAGCGCGCAACCCAGATTGCAAGAGACAAAGAGCAGACCCACTTCTCTTAACAAG 1258
 Qy 241 ATCATCACAGATGCGCCAGTAAGGTAATTAATTTAACTTCTTGTACCGGG 300
 Db 1259 ATCATCACAGATGCGCCAGTAAGGTAATTAATTTAACTTCTTGTACCGGG 1318
 Qy 301 AACTCGGTAATTTCTCTACTTCCATAAACCCTGATTAATTTGGTGGAAAGCAGACC 360
 Db 1319 AACTCGGTAATTTCTCTACTTCCATAAACCCTGATTAATTTGGTGGAAAGCAGACC 1378
 Qy 361 AACCACAAAAGTCAGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Db 1379 AACCACAAAAGTCAGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
 Qy 421 TTTTCTCTATATTTCTGTTTACCGGTTGAGTCAATGCGTGAAGATGATCAT 480
 Db 1439 TTTTCTCTATATTTCTGTTTACCGGTTGAGTCAATGCGTGAAGATGATCAT 1498
 Qy 481 ATTGATGAGGATGCAATTTTGGGAGGTTGGTGAACCGGAAGTCTTATATC 540
 Db 1499 ATTGATGAGGATGCAATTTTGGGAGGTTGGTGAACCGGAAGTCTTATATC 1558
 Qy 541 GAACCTCACACCATACCTCACTTCAATCCCAACATTTATCGGTTTATTTCTGTC 600
 Db 1559 GAACCTCACACCATACCTCACTTCAATCCCAACATTTATCGGTTTATTTCTGTC 1618
 Qy 601 TTTCCTTTGCTCGAGTCTCGCGAA 625
 Db 1619 TTTCCTTTGCTCGAGTCTCGCGAA 1643

RESULT 4
 AAC62762 standard; DNA; 661 BP.
 AC AAC62762;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE O-methyl transferase promoter coding sequence #1.
 XX
 KW Promoter; eucalyptus; pine; gene transcription; ds.
 XX
 OS Eucalyptus grandis.
 XX
 PN WO200058474-A1.

PD 05-OCT-2000.
XX 24-FEB-2000; 2000MO-NZ000018.
XX 25-MAR-1999; 99US-00276599.
PR 30-JUL-1999; 99US-0146591P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX Perera R, Rice SJ, Eagleton CK;
PI WPI; 2000-647236/62.
XX
XX Novel promoter sequences useful for modulating transcription of plant DNA
PT sequences of interest and production of polypeptides.
PS Claim 1; Page 48; 93pp; English.
XX
XX The present invention relates to promoter sequences from eucalyptus and
CC pine. The present sequence is one such promoter. This sequence is useful
CC for modulating the transcription of DNA sequences of interest. The
CC sequences may also be used to tag or identify an organism or its
CC reproductive material
XX
SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;
Query Match 97.0%; Score 606.2; DB 3; Length 661;
Best Local Similarity 98.9%; Pred. No. 1.4e-183;
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY 1 CTGAGCCATTAAATTCGAGACACATGCGCCAAATTAATTTCTTGTGCTGCCTAACTGT 60
DB 1 CTGAGCCATTAAATTCGAGACACATGCGCCAAATTAATTTCTTGTGCTGCCTAACTGT 60
QY 61 CGAATTTCTCTTTAGTAGTAAGTAACCAATGATGCGCATTTGACAAAAGGCTGATTA 120
DB 61 CGAATTTCTCTTTAGTAGTAAGTAACCAATGATGCGCATTTGACAAAAGGCTGATTA 120
QY 121 GTATGATCTTGGAGTTGGTGCAAAATTTGCAAGCTGACGATGCGCCCTCAGGAAATT 180
DB 121 GTATGATCTTGGAGTTGGTGCAAAATTTGCAAGCTGACGATGCGCCCTCAGGAAATT 180
QY 181 AAGGCGCAACCCGATTTGCAAAAGCAAAAGGACGACGCCAATCTTCTTAACAG 240
DB 181 AAGGCGCAACCCGATTTGCAAAAGCAAAAGGACGACGCCAATCTTCTTAACAG 240
QY 241 ATCATCCAGATGCGCGCAGTAAGGATTAATTAATTAACAATAGCTCTGTAACGGG 300
DB 241 ATCATCCAGATGCGCGCAGTAAGGATTAATTAATTAACAATAGCTCTGTAACGGG 300
QY 301 AACTCGGATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAAGCAGACC 360
DB 301 AACTCGGATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAAGCAGACC 360
QY 361 AACCACAAAAGGTCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
DB 361 AACCACAAAAGGTCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
QY 417 AGAGTTTCTCTCATATATTTCTGTTACCGGTTGAGCAATGAGCAATGCGGAAATGT 476
DB 421 AGAGTTTCTCTCATATATTTCTGTTACCGGTTGAGCAATGAGCAATGCGGAAATGT 480
QY 477 ACATATTTGTTAGGTCATATATTTTGGGAGGAGGTTGTGAACCGCAAAATTTCTATA 536
DB 481 ACATATTTGTTAGGTCATATATTTTGGGAGGAGGTTGTGAACCGCAAAATTTCTATA 540
QY 537 TATGAAACCTTCACCACTAATCTCACTTCAATCCCAACATTTATCCGTTTATTTCT 596
DB 541 TATGAAACCTTCACCACTAATCTCACTTCAATCCCAACATTTATCCGTTTATTTCT 600
QY 597 CTGCTTCTCTTGTGCTGAGTCTGCGGAA 625
|||||

DB 601 CTGCTTCTCTTGTGCTGAGTCTGCGGAA 629
RESULT 5
ABK17027
ID ABK17027 standard; cDNA; 661 BP.
XX
AC ABK17027;
XX
XX 26-MAR-2002 (first entry)
DE
XX Eucalyptus grandis promoter polynucleotide #6.
XX
XX Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;
KM temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
KM PCR primer.
XX
XX Eucalyptus grandis.
XX
XX NO200198485-A1.
PN
XX 27-DEC-2001.
PD
XX 20-JUN-2001; 2001MO-NZ000115.
PF
XX 20-JUN-2000; 2000US-00598401.
PR 28-NOV-2000; 2000US-00724624.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
XX
PI Perera R, Rice S, Eagleton C, Lasham A;
XX
XX WPI; 2002-114583/15.
DR
XX Novel polynucleotide promoter sequences from pine and Eucalyptus useful
PT for modulating expression of endogenous and/or heterologous
PT polynucleotides in transgenic plants.
XX
PS Claim 1; Page 63-64; 121pp; English.
XX
XX The invention relates to isolated promoter sequences from Pinus radiata
CC and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,
CC flower-, pollen-, bud-, meristem-specific promoters or temporally
CC regulated promoters such as xylogenesis-specific promoters. The promoter
CC polypeptides and their related polynucleotides are useful in the
CC production of genetic constructs, used for modifying gene expression in a
CC target organism, in particular a plant. The method is useful for
CC modifying expression of a polynucleotide that comprises an intron
CC sequence, through removal of the intron sequence. The method is useful
CC for modifying growth and development of plants, and cellular responses to
CC external stimulus, such as environmental factors and disease pathogens.
CC The sequences are useful in genome and physical mapping, in positional
CC cloning of genes, in various assays to determine biological activity, to
CC raise antibodies, to isolate corresponding interacting proteins and other
CC compounds, and to quantitatively determine levels of interacting proteins
CC or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata
CC and Eucalyptus grandis polynucleotides and PCR primers used in the method
CC of the invention
XX
SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;
Query Match 97.0%; Score 606.2; DB 6; Length 661;
Best Local Similarity 98.9%; Pred. No. 1.4e-183;
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY 1 CTGAGCCATTAAATTCGAGACACATGCGCCAAATTAATTTCTTGTGCTGCCTAACTGT 60
DB 1 CTGAGCCATTAAATTCGAGACACATGCGCCAAATTAATTTCTTGTGCTGCCTAACTGT 60
QY 61 CGAATTTCTCTTTAGTAGTAAGTAACCAATGATGCGCATTTGACAAAAGGCTGATTA 120
DB 61 CGAATTTCTCTTTAGTAGTAAGTAACCAATGATGCGCATTTGACAAAAGGCTGATTA 120
|||||

121 GTATGATCTGGAGTGTGTTGGCAAAATTTGCAAGCTGACATGGCCCTCAGGGAATT 180
121 GTATGATCTGGAGTGTGTTGGCAAAATTTGCAAGCTGACATGGCCCTCAGGGAATT 180
181 AAGGCGCAACCCAGATTTGCAAGAGCAAAAGAGCAGACCCACTTTCCTTAACAG 240
181 AAGGCGCAACCCAGATTTGCAAGAGCAAAAGAGCAGACCCACTTTCCTTAACAG 240
241 ATCATCACCAGATCGGCGCAATGAGGTATTAATTTAAACAATAGCTCTTTGACCGG 300
241 ATCATCACCAGATCGGCGCAATGAGGTATTAATTTAAACAATAGCTCTTTGACCGG 300
301 AACTCCGATTTCTCTCACTTCCATTAACCCCTGATTAATTTGTTGGGAAAGCCAGACC 360
301 AACTCCGATTTCTCTCACTTCCATTAACCCCTGATTAATTTGTTGGGAAAGCCAGACC 360
361 AACCCCAAAAGTCCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
361 AACCCCAAAAGTCCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAG 420
417 AGAGTTTCTCTATATTTCTGTTACCGGTTGAGTCAATGCGATCGTGAAGATGT 476
421 AGAGTTTCTCTATATTTCTGTTACCGGTTGAGTCAATGCGATCGTGAAGATGT 480
477 ACATATTGTTGTTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACCGGAAAGTCTATA 536
481 ACATATTGTTGTTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACCGGAAAGTCTATA 540
537 TATCGAACCTCCACACCATACCTCACTTCAATCCCAACATTTATCCGTTTATTTCT 596
541 TATCGAACCTCCACACCATACCTCACTTCAATCCCAACATTTATCCGTTTATTTCT 600
597 CTGCTTCTCTTGTCTGAGTCTCGCGAA 625
601 CTGCTTCTCTTGTCTGAGTCTCGCGAA 629

RESULT 6

ADH75428

ID ADH75428 standard; DNA; 661 BP.

AC ADH75428;

DT 22-APR-2004 (first entry)

DE Eucalyptus grandis superubiquitin related sequence #6.

KW ds; Monterey pine; superubiquitin; promoter; gene expression;

KM transgenic plant.

XX Eucalyptus grandis.

XX WO2003093475-A1.

XX 13-NOV-2003.

XX 30-APR-2003; 2003WO-NZ000076.

XX 30-APR-2002; 2002US-00137036.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (RUBI-) RUBICON FORESTS HOLDINGS LTD.

XX Rice SJ, Wood M, Eagleton CK, Visser ES, Perera R;

XX WPI, 2003-903678/82.

XX New polynucleotide of the superubiquitin promoter from Pinus radiata,

XX useful in modifying gene expression in a target organism.

XX Disclosure; SEQ ID NO 12; 123bp; English.

CC The invention relates to a new isolated polynucleotide comprising the
CC Pinus radiata (Monterey pine) superubiquitin promoter sequence, its
CC complement, reverse complement, reverse sequence or inverted repeat or a
CC sequence having at least 40, 60, 75 or 90% identity with the promoter.
CC The polynucleotide is useful in modifying gene expression in a target
CC organism, especially in transgenic plants. This sequence corresponds to a
CC superubiquitin promoter related sequence.

SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 97.0%; Score 606.2; DB 10; Length 661;

Best Local Similarity 98.9%; Pred. No. 1.4e-183;

Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

1 CTGAGCCATTTAATTCAGAGCAGATGCCCCAAAATTTATCTTGTGTCATACACTGT 60
1 CTGAGCCATTTAATTCAGAGCAGATGCCCCAAAATTTATCTTGTGTCATACACTGT 60
61 CGAATTTTCTCTTTAGGTAAGTAACCAATGATCGCCATGTTGACAAAAGCGTGAATTA 120
61 CGAATTTTCTCTTTAGGTAAGTAACCAATGATCGCCATGTTGACAAAAGCGTGAATTA 120
121 GTATGATCTGGAGTGTGTTGGCAAAATTTGCAAGCTGACATGAGCCCTCAGGGAATT 180
121 GTATGATCTGGAGTGTGTTGGCAAAATTTGCAAGCTGACATGAGCCCTCAGGGAATT 180
181 AAGGCGCAACCCAGATTTGCAAGAGCAAAAGAGCAGACCCACTTTCCTTAACAG 240
181 AAGGCGCAACCCAGATTTGCAAGAGCAAAAGAGCAGACCCACTTTCCTTAACAG 240
241 ATCATCACCAGATGCGCGCAATGAGGTATTAATTTAAACAATAGCTCTTTGACCGG 300
241 ATCATCACCAGATGCGCGCAATGAGGTATTAATTTAAACAATAGCTCTTTGACCGG 300
301 AACTCCGATTTCTCTCACTTCCATTAACCCCTGATTAATTTGTTGGGAAAGCCAGACC 360
301 AACTCCGATTTCTCTCACTTCCATTAACCCCTGATTAATTTGTTGGGAAAGCCAGACC 360
361 AACCCCAAAAGTCCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
361 AACCCCAAAAGTCCAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAG 420
417 AGAGTTTCTCTATATTTCTGTTACCGGTTGAGTCAATGCGATCGTGAAGATGT 476
421 AGAGTTTCTCTATATTTCTGTTACCGGTTGAGTCAATGCGATCGTGAAGATGT 480
477 ACATATTGTTGTTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACCGGAAAGTCTATA 536
481 ACATATTGTTGTTAGGTTCCAAATATTTTGGGAGAGGTTGGTGAACCGGAAAGTCTATA 540
537 TATCGAACCTCCACACCATACCTCACTTCAATCCCAACATTTATCCGTTTATTTCT 596
541 TATCGAACCTCCACACCATACCTCACTTCAATCCCAACATTTATCCGTTTATTTCT 600
597 CTGCTTCTCTTGTCTGAGTCTCGCGAA 625
601 CTGCTTCTCTTGTCTGAGTCTCGCGAA 629

RESULT 7

ADM80462

ID ADM80462 standard; cDNA; 661 BP.

AC ADM80462;

DT 21-APR-2005 (first entry)

DE E. grandis caffeic acid O-methyltransferase promoter SEQ ID NO.12.

KW ss; wood; plant; transcription; caffeic acid O-methyltransferase;

KM transgenic plant.

XX Eucalyptus grandis.

[illegible]

QY	301	AACGCCGATATTTCTCTCACTTCCATAAACCCCGATTAATTTGGTGGAAAGCAGACCC	360					
Db	301	AACGCCGATATTTCTCTCACTTCCATAAACCCCGATTAATTTGGTGGAAAGCAGACCC	360					
QY	361	AACCCACAAAAGGTGAGATGTCATCCAC---GAGAGAGAGAGAGAGAGAGAG	416					
Db	361	AACCCACAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAG	420					
QY	417	AGAGTTTCTCTCATATTTCTGGTTTACCGGTTGGAGTCAATGGCANTGCCGAATGT	476					
Db	421	AGAGTTTCTCTCATATTTCTGGTTTACCGGTTGGAGTCAATGGCANTGCCGAATGT	480					
QY	477	ACATATTTGATGAGGGTCCATATATTTTTCGCGAGAGGTTGGTGAACCGAAAGTTCCTATA	536					
Db	481	ACATATTTGATGAGGGTCCATATATTTTTCGCGAGAGGTTGGTGAACCGAAAGTTCCTATA	540					
QY	537	TATCGAACCCTCCACACCAATACCTCACTTCAATTCGCCACATTTATTCGTTTATTCCT	596					
Db	541	TATCGAACCCTCCACACCAATACCTCACTTCAATTCGCCACATTTATTCGTTTATTCCT	600					
QY	597	CTGCTTTCCTTTGGTGGAGTCTGCGCGAA	625					
Db	601	CTGCTTTCCTTTGGTGGAGTCTGCGCGAA	629					
RESULT 8								
AC	AAC62810	AAC62810 standard; DNA; 2096 BP.						
AC	AAC62810;							
DT	02-FEB-2001	(first entry)						
DE	O-methyl transferase promoter coding sequence #2.							
KM	Promoter; eucalyptus; pine; gene transcription; ds.							
OS	Eucalyptus grandis.							
XX	WO200058474-A1.							
XX	05-OCT-2000.							
PF	24-FEB-2000;	2000WO-NZ000018.						
PR	25-MAR-1999;	99US-00276599.						
PR	30-JUL-1999;	99US-0146591P.						
XX	(GENE-) GENESIS RES & DEV CORP LTD.							
PA	(FLET-) FLETCHER CHALLENGER FORESTS LTD.							
PI	Perera R, Rice SJ, Bagleton CK;							
XX	WPI, 2000-647236/62.							
DR	P-PSDB; AAB28142.							
XX	Novel promoter sequences useful for modulating transcription of plant DNA							
PT	sequences of interest and production of polypeptides.							
XX	Claim 1; Page 61-62; 93pp; English.							
XX	The present invention relates to promoter sequences from eucalyptus and							
CC	pine. The present sequence is one such promoter. This sequence is useful							
CC	for modulating the transcription of DNA sequences of interest. The							
CC	sequences may also be used to tag or identify an organism or its							
CC	reproductive material							
SQ	Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;							
Query Match 97.0%; Score 606.2; DB 3; Length 2096;								
Best Local Similarity 98.9%; Pred. No. 2.5e-183;								
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;								

QY 1 CTGAGCCATTATTCGAGACATGCGCCAAATTAATTCCTGCTGCATTAACGT 60
 DB 41 CTGAGCCATTATTCGAGACATGCGCCAAATTAATTCCTGCTGCATTAACGT 100
 QY 61 CGAATTTCTCTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 120
 DB 101 CGAATTTCTCTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 160
 QY 121 GTATGATCTTGAGTTGTTGTCGAATTTGCAAGCTGACATGCGCCCTGAGGAAATT 180
 DB 161 GTATGATCTTGAGTTGTTGTCGAATTTGCAAGCTGACATGCGCCCTGAGGAAATT 220
 QY 181 AAGGCGCAACCCGATTTGCAAGAGACCAAGAGCAGACCAACCTTCTTAAACAG 240
 DB 221 AAGGCGCAACCCGATTTGCAAGAGACCAAGAGCAGACCAACCTTCTTAAACAG 280
 QY 241 ATCATCACAGATGCGCGAGTAAGGTAATTAATTAACAATAGCTCTTGTACCGGG 300
 DB 281 ATCATCACAGATGCGCGAGTAAGGTAATTAATTAACAATAGCTCTTGTACCGGG 340
 QY 301 AACTCGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGTTGGAAGACGACGCC 360
 DB 341 AACTCGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGTTGGAAGACGACGCC 400
 QY 361 AAGCCCAAAAGGTGATGATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
 DB 401 AAGCCCAAAAGGTGATGATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAG 460
 QY 417 AGAGTTTCTCTATATTTCTGTTCAACCGGTTGAGTCAATGAGCATGCGTAAGTGT 476
 DB 461 AGAGTTTCTCTATATTTCTGTTCAACCGGTTGAGTCAATGAGCATGCGTAAGTGT 520
 QY 477 ACATATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536
 DB 521 ACATATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 580
 QY 537 TATGAGACCTCCACACCATACCTCACTTCAATCCCAACCTTATCCGTTTATTTCCCT 596
 DB 581 TATGAGACCTCCACACCATACCTCACTTCAATCCCAACCTTATCCGTTTATTTCCCT 640
 QY 597 CTGCTTCTCTTGTCTGAGTCTCGCGGAA 625
 DB 641 CTGCTTCTCTTGTCTGAGTCTCGCGGAA 669

RESULT 9
 ABK17075
 ID ABK17075 standard; cDNA; 2096 BP.
 XX AC ABK17075;
 XX DT 26-MAR-2002 (first entry)
 XX DE Eucalyptus grandis promoter polynucleotide #31.
 XX KM Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;
 XX KM temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
 XX KM PCR primer.
 XX OS Eucalyptus grandis.
 XX PN W0200198485-A1.
 XX PD 27-DEC-2001.
 XX PF 20-JUN-2001; 2001WO-NZ000115.
 XX PR 20-JUN-2000; 2000US-00598401.
 XX PR 28-NOV-2000; 2000US-00724624.
 XX PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX PA (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.

XX PI Perera R, Rice S, Eagleton C, Laesham A;
 XX WP1; 2002-114583/15.
 DR P-PSDB; AA080760.
 XX PT Novel polynucleotide promoter sequences from pine and Eucalyptus useful
 PT for modifying expression of endogenous and/or heterologous
 PT polynucleotides in transgenic plants.
 PS Claim 1; Page 78; 121pp; English.
 XX The invention relates to isolated promoter sequences from Pinus radiata
 CC and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,
 CC flower-, pollen-, bud-, meristem-specific promoters or temporally
 CC regulated promoters such as xylogenesis-specific promoters. The promoter
 CC polypeptides and their related polynucleotides are useful in the
 CC production of genetic constructs, used for modifying gene expression in a
 CC target organism, in particular a plant. The method is useful for
 CC modifying expression of a polynucleotide that comprises an intron
 CC sequence, through removal of the intron sequence. The method is useful
 CC for modifying growth and development of plants, and cellular responses to
 CC external stimulus, such as environmental factors and disease pathogens.
 CC The sequences are useful in genome and physical mapping, in positional
 CC cloning of genes, in various assays to determine biological activity, to
 CC raise antibodies, to isolate corresponding interacting proteins and other
 CC compounds, and to quantitatively determine levels of interacting proteins
 CC or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata
 CC and Eucalyptus grandis polynucleotides and PCR primers used in the method
 CC of the invention
 XX SO Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;

Query Match 97.0%; Score 606.2; DB 6; Length 2096;
 Best Local Similarity 98.9%; Pred. No. 2.5e-183;
 Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 CTGAGCCATTATTCGAGACATGCGCCAAATTAATTCCTGCTGCATTAACGT 60
 DB 41 CTGAGCCATTATTCGAGACATGCGCCAAATTAATTCCTGCTGCATTAACGT 100
 QY 61 CGAATTTCTCTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 120
 DB 101 CGAATTTCTCTTTAGTAAGTAACCAATGATGCGCATGTTGACAAAAGGCTGATTA 160
 QY 121 GTATGATCTTGAGTTGTTGTCGAATTTGCAAGCTGACATGCGCCCTGAGGAAATT 180
 DB 161 GTATGATCTTGAGTTGTTGTCGAATTTGCAAGCTGACATGCGCCCTGAGGAAATT 220
 QY 181 AAGGCGCAACCCGATTTGCAAGAGACCAAGAGCAGACCAACCTTCTTAAACAG 240
 DB 221 AAGGCGCAACCCGATTTGCAAGAGACCAAGAGCAGACCAACCTTCTTAAACAG 280
 QY 241 ATCATCACAGATGCGCGAGTAAGGTAATTAATTAACAATAGCTCTTGTACCGGG 300
 DB 281 ATCATCACAGATGCGCGAGTAAGGTAATTAATTAACAATAGCTCTTGTACCGGG 340
 QY 301 AACTCGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGTTGGAAGACGACGCC 360
 DB 341 AACTCGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGTTGGAAGACGACGCC 400
 QY 361 AAGCCCAAAAGGTGATGATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
 DB 401 AAGCCCAAAAGGTGATGATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAG 460
 QY 417 AGAGTTTCTCTATATTTCTGTTCAACCGGTTGAGTCAATGAGCATGCGTAAGTGT 476
 DB 461 AGAGTTTCTCTATATTTCTGTTCAACCGGTTGAGTCAATGAGCATGCGTAAGTGT 520
 QY 477 ACATATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536
 DB 521 ACATATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 580

QY 537 TATCGAAGCTCCACACCATACCTCACTTGAATCCCAACATTTATCGTTTATTTCT 596
DB 581 TATCGAAGCTCCACACCATACCTCACTTGAATCCCAACATTTATCGTTTATTTCT 640
QY 597 CTGCTTCTCTTGTCTGAGTCTGCGGAA 625
DB 641 CTGCTTCTCTTGTCTGAGTCTGCGGAA 669

RESULT 10

ADH75476
ID ADH75476 standard; DNA; 2096 BP.

AC ADH75476;

DT 22-APR-2004 (first entry)

XX Eucalyptus grandis superubiquitin related sequence #31.

DE ds; Monterey pine; superubiquitin; promoter; gene expression;

XX transgenic plant.

XX Eucalyptus grandis.

XX MO2003093475-A1.

XX 13-NOV-2003.

XX 30-APR-2003; 2003WO-NZ000076.

XX 30-APR-2002; 2002US-00137036.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (RUBI-) RUBICON FORESTS HOLDINGS LTD.

XX Rice SJ, Wood M, Bagleton CK, Visser ES, Perera R;

XX WPI; 2003-903678/82.

XX New polynucleotide of the superubiquitin promoter from Pinus radiata,

XX useful in modifying gene expression in a target organism.

XX Disclosure; SEQ ID NO 60; 123bp; English.

XX The invention relates to a new isolated polynucleotide comprising the
CC Pinus radiata (Monterey pine) superubiquitin promoter sequence, its
CC complement, reverse sequence or inverted repeat or a
CC sequence having at least 40, 60, 75 or 90% identity with the promoter.
CC The polynucleotide is useful in modifying gene expression in a target
CC organism, especially in transgenic plants. This sequence corresponds to a
CC superubiquitin promoter related sequence.

XX Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;

XX Query Match 97.0%; Score 606.2; DB 10; Length 2096;

XX Best Local Similarity 98.9%; Pred. No. 2.5e-183;

XX Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 CTGAGCATTAAATTCGAGAGACATGCCCAAAATTTATCTTCTGTCGCAATACTGT 60
DB 41 CTGAGCATTAAATTCGAGAGACATGCCCAAAATTTATCTTCTGTCGCAATACTGT 100
QY 61 CGAATTTTCTCTTTAGTAAGTAACCATGATGCCCATGTTGACAAAAGGCTGATTA 120
DB 101 CGAATTTTCTCTTTAGTAAGTAACCATGATGCCCATGTTGACAAAAGGCTGATTA 160
QY 121 GTATGATCTTGAAGTGTGTGCAATTTGCAAGCTGACGATGCCCTCAGGAAATTT 180
DB 161 GTATGATCTTGAAGTGTGTGCAATTTGCAAGCTGACGATGCCCTCAGGAAATTT 220
QY 181 AAGCGCCAAACCGATTTGCAAGAGACAAAGAGACGACCAACCTTCTTTAAACAG 240
DB 221 AAGCGCCAAACCGATTTGCAAGAGACAAAGAGACGACCAACCTTCTTTAAACAG 280

QY 241 ATCATCAACGATGCGCCAGTAAGGTAATTAATTTAACAAATAGCTCTGTGACCGG 300
DB 281 ATCATCAACGATGCGCCAGTAAGGTAATTAATTTAACAAATAGCTCTGTGACCGG 340
QY 301 AACTCCGATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAGCAGACC 360
DB 341 AACTCCGATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGAAAGCAGACC 400
QY 361 AACCACAAAAGTCAGTGCATCCAC---GAGAGAGAGAGAGAGAGAGAGAG 416
DB 401 AACCACAAAAGTCAGTGCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
QY 417 AGAGTTTCTCTATTAATTTGTTACCGGTTGAGTCAATGCGATGCGGAAATGT 476
DB 461 AGAGTTTCTCTATTAATTTGTTACCGGTTGAGTCAATGCGATGCGGAAATGT 520
QY 477 ACATATGATGAGGATCCAAATATTTGCGGAGGTTGTGAACCGAAAGTTCTATA 536
DB 521 ACATATGATGAGGATCCAAATATTTGCGGAGGTTGTGAACCGAAAGTTCTATA 580
QY 537 TATCGAAGCTCCACACCATACCTCACTTGAATCCCAACATTTATCGTTTATTTCT 596
DB 581 TATCGAAGCTCCACACCATACCTCACTTGAATCCCAACATTTATCGTTTATTTCT 640
QY 597 CTGCTTCTCTTGTCTGAGTCTGCGGAA 625
DB 641 CTGCTTCTCTTGTCTGAGTCTGCGGAA 669

RESULT 11

ADH80510
ID ADH80510 standard; cDNA; 2096 BP.

XX ADH80510;

XX 21-APR-2005 (first entry)

XX E. grandis caffeic acid O-methyltransferase related cDNA SEQ ID NO:60.

XX sb; wood; plant; transcription; caffeic acid O-methyltransferase;

XX transgenic plant.

XX Eucalyptus grandis.

XX US2005026162-A1.

XX 03-FEB-2005.

XX 06-NOV-2003; 2003US-00702319.

XX 25-MAR-1999; 99US-00276599.

XX 30-JUL-1999; 99US-0146591P.

XX 24-FEB-2000; 2000WO-NZ000018.

XX 20-JUN-2000; 2000US-00598401.

XX 28-NOV-2000; 2000US-00724624.

XX 09-NOV-2001; 2001US-0345397P.

XX 30-APR-2002; 2002US-00137036.

XX 08-NOV-2002; 2002US-00291447.

XX 08-NOV-2002; 2002US-0425087P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (RUBI-) RUBICON FORESTS HOLDINGS LTD.

XX Perera R, Rice SJ, Bagleton CK;

XX WPI; 2005-131806/14.

XX New isolated polynucleotide sequences comprising a functional vascular
PT tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase
PT promoter, useful for modifying gene expression.

PS Claim 3; SEQ ID NO 60; 82bp; English.

XX The invention relates to a novel isolated polynucleotide sequence
 CC comprising a functional vascular tissue-specific Eucalyptus grandis
 CC caffeic acid O-methyltransferase (COMT) promoter (ADW80462 or ADW80563).
 CC Also claimed is a genetic construct comprising the above polynucleotide
 CC sequence or a sequence having 2096 base pairs fully defined in the
 CC specification (ADW80510), a host cell comprising the above genetic
 CC construct, a plant comprising the genetic construct, a method for
 CC producing a plant with modified gene expression, and a method for
 CC identifying a gene responsible for a desired function or phenotype. The
 CC composition and methods are useful for modifying gene expression or for
 CC modifying the transcription of endogenous and/or heterologous
 CC polynucleotides involved in wood formation. The present sequence is used
 CC in the exemplification of the invention.

XX Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;

Query Match 97.0%; Score 606.2; DB 14; Length 2096;
 Best Local Similarity 98.9%; Pred. No. 2.5e-183;
 Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 1 CTGAGCCATTAAATTCGAGACACATGCCCAAAATTAATTTCTTCTGCTGCATTAATCTGT 60
 Db 41 CTGAGCCATTAAATTCGAGACACATGCCCAAAATTAATTTCTTCTGCTGCATTAATCTGT 100
 Qy 61 CGAATTTTCTTTTAAAGTAAACCAATGATGCGCATTTGACAAAAGGCTGATTA 120
 Db 101 CGAATTTTCTTTTAAAGTAAACCAATGATGCGCATTTGACAAAAGGCTGATTA 160
 Qy 121 GTATGATCTTGAAGTGTGTGTCMAATTTGCAAGCTGACATGAGCCCTTCAGGAAATTT 180
 Db 161 GTATGATCTTGAAGTGTGTGTCMAATTTGCAAGCTGACATGAGCCCTTCAGGAAATTT 220
 Qy 181 AAGGCGCCAAACCAAGTTGCAAGACAAAGACAGACCACTTTCTTTAACAG 240
 Db 221 AAGGCGCCAAACCAAGTTGCAAGACAAAGACAGACCACTTTCTTTAACAG 280
 Qy 241 ATCATCACCAATGCGCGAGTAAGGTAATTAATTAACAATAGCTCTTGAACGGG 300
 Db 281 ATCATCACCAATGCGCGAGTAAGGTAATTAATTAACAATAGCTCTTGAACGGG 340
 Qy 301 AACTCCGATTTCTCTCACTTCCATTAACCCCTGATTAATTTGGTGGAAAGCGACGCC 360
 Db 341 AACTCCGATTTCTCTCACTTCCATTAACCCCTGATTAATTTGGTGGAAAGCGACGCC 400
 Qy 361 AACCACAAAGATGATGATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
 Db 401 AACCACAAAGATGATGATCCAC---GAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
 Qy 417 AGAGTTTCTCTTAATTTCTGTTTACCGGTTGAGTCAATGGCATGCGTGAAGATGT 476
 Db 461 AGAGTTTCTCTTAATTTCTGTTTACCGGTTGAGTCAATGGCATGCGTGAAGATGT 520
 Qy 477 ACATATTTGATGAGGATCAATATTTTGGGAGGGGTTGTGAACCGCAAGTTCTCTATA 536
 Db 521 ACATATTTGATGAGGATCAATATTTTGGGAGGGGTTGTGAACCGCAAGTTCTCTATA 580
 Qy 537 TATGCAACCTCCACCACTCACTTCAATCCCAACATTTATCCGTTTATTTTCT 596
 Db 581 TATGCAACCTCCACCACTCACTTCAATCCCAACATTTATCCGTTTATTTTCT 640
 Qy 597 CTGCTTTCTTTTCTGAGTCTCGCGAA 625
 Db 641 CTGCTTTCTTTTCTGAGTCTCGCGAA 669

RESULT 12

ADQ88319 ID ADQ88319 standard; DNA; 534 BP.

XX AC ADQ88319;

XX DT 21-OCT-2004 (first entry)

XX Eucalyptus grandis COMT promoter #1.
 DE Transcription; xylogenesis; gene expression; transgenic plant; lignin;
 XX cellulose; wood; disease resistance;
 KM caffeic acid 3-O-methyl transferase promoter; COMT promoter; xylem; ds.
 OS Eucalyptus grandis.
 XX US2004146904-A1.
 XX 29-JUN-2004.
 XX 07-NOV-2003; 2003US-00703091.
 XX 21-NOV-2002; 2002US-0428087P.
 XX (ARBO-) ARBORGEM LLC.
 XX Phillips J, Eagleton C;
 XX WPI; 2004-552666/53.
 XX
 XX New isolated polynucleotide from Eucalyptus grandis that is capable of
 PT initiating and promoting transcription of polynucleotides in plant cells
 PT undergoing xylogenesis, useful in altering lignin content of plants.
 PS Claim 1; SEQ ID NO 1; 32pp; English.
 XX

XX The invention relates to promoter sequences from Eucalyptus grandis that
 CC is capable of initiating and promoting transcription of polynucleotides
 CC in plant cells undergoing xylogenesis. The invention also provides DNA
 CC construct comprising the promoter and a desired nucleic acid, which can
 CC be used for regulating gene expression in a transgenic plant. The DNA
 CC constructs comprising the promoter sequences of the invention can be used
 CC to regulate the expression of lignin biosynthetic gene and thereby alter
 CC the lignin content in plants, to modify properties such as cellulose
 CC synthesis, wood development, flower development and disease resistance.
 CC The present sequence is Eucalyptus grandis caffeic acid 3-O-methyl
 CC transferase (COMT) promoter that confers xylem-preferred gene expression
 CC in a plant cell.

SQ Sequence 534 BP; 151 A; 126 C; 119 G; 138 T; 0 U; 0 Other;

Query Match 85.4%; Score 534; DB 13; Length 534;
 Best Local Similarity 100.0%; Pred. No. 1.9e-160;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 ATGGCGCATGTTGCAAAAAGGCTGATTAATGATCTTGAAGTGTGTCMAATTTTG 151
 Db 1 ATGGCGCATGTTGCAAAAAGGCTGATTAATGATCTTGAAGTGTGTCMAATTTTG 60
 Qy 152 CAAGCTGACATGCGCCCTCAGGAAATTAAGGCCCAACCAAGTTGCAAGACAA 211
 Db 61 CAAGCTGACATGCGCCCTCAGGAAATTAAGGCCCAACCAAGTTGCAAGACAA 120
 Qy 212 AGAGCAGACCCAACTTTCTTAACAAGATCATACCAATGCGCGAGTAAGGTAATA 271
 Db 121 AGAGCAGACCCAACTTTCTTAACAAGATCATACCAATGCGCGAGTAAGGTAATA 180
 Qy 272 TTAATTAACAATAGCTCTTGTACCGGGAACCTCGATTTCTCTCACTTCCATTAACCC 331
 Db 181 TTAATTAACAATAGCTCTTGTACCGGGAACCTCGATTTCTCTCACTTCCATTAACCC 240
 Qy 332 CTGATTAATTTGTTGGAAAGCGACAGCCCAACCAAAAAGTGCATGTCACGA 391
 Db 241 CTGATTAATTTGTTGGAAAGCGACAGCCCAACCAAAAAGTGCATGTCACGA 300
 Qy 392 GAG 451
 Db 301 GAG 360
 Qy 452 AGTCATAGGATGCGTACGAATGTACATATTGGTGAAGGTCCAAATTTTGGCGGAG 511

CC to regulate the expression of lignin biosynthetic gene and thereby alter
CC the lignin content in plants, to modify properties such as cellulose
CC synthesis, wood development, flower development and disease resistance.
CC The present sequence is Eucalyptus grandis caffeic acid 3-O-methyl
CC transferase (COMT) promoter that confers xylem-preferred gene expression
CC in a plant cell.

SO Sequence 306 BP; 80 A; 73 C; 70 G; 83 T; 0 U; 0 Other;

Query Match 49.0%; Score 306; DB 13; Length 306;

Best Local Similarity 100.0%; Pred. No. 2,2e-87;

Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 320 TTCCATTAACCCCGATTATTTGGTGGAAAGGAGAGCCACCCACAAAAGTCAAT 379
DB 1 TTCAATTAACCCCGATTATTTGGTGGAAAGGAGAGCCACCCACAAAAGTCAAT 60
OY 380 GTCAATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 439
DB 61 GTCAATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
OY 440 TTCAACCGGTGAGTCAATGCGATGCGTGAAGATGTCATATTGGTGTAGGGTCAATA 499
DB 121 TTCAACCGGTGAGTCAATGCGATGCGTGAAGATGTCATATTGGTGTAGGGTCAATA 180
OY 500 TTTTGGCGGAGAGGTTGGTGAACCGCAAGTTCCTATATATGAAACCTCCACACCATACC 559
DB 181 TTTTGGCGGAGAGGTTGGTGAACCGCAAGTTCCTATATATGAAACCTCCACACCATACC 240
OY 560 TCACCTCAATCCCAACCATTTATCCGTTTATTTCTCTGCTTCCTTGCAGAGTCTC 619
DB 241 TCACCTCAATCCCAACCATTTATCCGTTTATTTCTCTGCTTCCTTGCAGAGTCTC 300
OY 620 GCGGAA 625
DB 301 GCGGAA 306
```

RESULT 15

ADQ88322

ID ADQ88322 standard; DNA; 293 BP.

AC ADQ88322;

DT 21-OCT-2004 (first entry)

DE Eucalyptus grandis COMT promoter #4.

KW Transcription; xylogenesis; gene expression; transgenic plant; lignin;

KW cellulose; wood; disease resistance;

KW caffeic acid 3-O-methyl transferase promoter; COMT promoter; xylem; ds.

XX Eucalyptus grandis.

OS US2004146904-A1.

PN 29-JUL-2004.

PD 07-NOV-2003; 2003US-00703091.

PF 21-NOV-2002; 2002US-0428087P.

PR (ARBO-) ARBORGEN LLC.

PA Phillips J, Eagleton C;

PI WPI; 2004-55266/53.

DR New isolated polynucleotide from Eucalyptus grandis that is capable of

PT initiating and promoting transcription of polynucleotides in plant cells

PT undergoing xylogenesis, useful in altering lignin content of plants.

PS Claim 1; SEQ ID NO 4; 32pp; English.

XX The invention relates to promoter sequences from Eucalyptus grandis that
CC is capable of initiating and promoting transcription of polynucleotides
CC in plant cells undergoing xylogenesis. The invention also provides DNA
CC construct comprising the promoter and a desired nucleic acid, which can
CC be used for regulating gene expression in a transgenic plant. The DNA
CC constructs comprising the promoter sequences of the invention can be used
CC to regulate the expression of lignin biosynthetic gene and thereby alter
CC the lignin content in plants, to modify properties such as cellulose
CC synthesis, wood development, flower development and disease resistance.
CC The present sequence is Eucalyptus grandis caffeic acid 3-O-methyl
CC transferase (COMT) promoter that confers xylem-preferred gene expression
CC in a plant cell.

SO Sequence 293 BP; 76 A; 67 C; 70 G; 80 T; 0 U; 0 Other;

Query Match 46.9%; Score 293; DB 13; Length 293;

Best Local Similarity 100.0%; Pred. No. 3,2e-83;

Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 333 TGATTAATTTGGTGGAAAGCGACAGCCACCAACCAAAAGTCAAGTCAATCCACAGAG 392
DB 1 TGATTAATTTGGTGGAAAGCGACAGCCACCAACCAAAAGTCAAGTCAATCCACAGAG 60
OY 393 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 452
DB 61 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
OY 453 GTCAATGGCATGCGTGAAGATGTCATATTGGTGTAGGGTCCAAATTTTGGCGGAGGG 512
DB 121 GTCAATGGCATGCGTGAAGATGTCATATTGGTGTAGGGTCCAAATTTTGGCGGAGGG 180
OY 513 TTGGTGAACCGCAAGTTCCTATATATCGAAACCTCCGACCAACATCTCAATCCC 572
DB 181 TTGGTGAACCGCAAGTTCCTATATATCGAAACCTCCGACCAACATCTCAATCCC 240
OY 573 CACCAATTAATCCGTTTATTTCTCTGCTTCTTCTGCTGAGTCTGCGGAA 625
DB 241 CACCAATTAATCCGTTTATTTCTCTGCTTCTTCTGCTGAGTCTGCGGAA 293
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Search completed: November 1, 2006, 00:21:20

Job time : 265.41 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:29:19 ; Search time 2031.12 Seconds
(without alignment)
17207.024 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1643

Perfect score: 625

Sequence: 1 ctgagcattcaatcgcgaga.....tttgctgcgagtcgcgga 625

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	47.6	7.6	561	12	CE792380 tigr-gss-
2	47.4	7.6	760	12	BZ731304 OGFZ50TC
3	46.6	7.5	831	14	AG559107 Mus muscu
C 4	46.4	7.4	619	10	DT310002 JGI CAAX1
5	45.8	7.3	349	7	BB931786 BB931786
C 6	45.8	7.3	799	5	CK600115 AGENCOURT
C 7	45.6	7.3	589	11	AZ829144 ZM0106C09
8	45.4	7.3	675	10	DV761691 PchHSE000
9	45	7.2	1019	10	DW344263 PP_LEC001
10	44.8	7.2	771	14	AG403694 Mus muscu
C 11	44.8	7.2	778	10	DT34659 JGI CAAT8
C 12	44.6	7.1	363	12	BZ708983 OGFZ50TC
13	44.6	7.1	588	11	BZ306338 h4x1a10.b
C 14	44.6	7.1	588	11	BH873693 hp46c12.9
15	44.6	7.1	669	12	CC693540 OGFZ50TC
16	44.6	7.1	677	12	CG241281 OGFZ50TC
17	44.6	7.1	746	11	AZ360328 IM0103G20
18	44.6	7.1	927	12	CC671328 OGFZ50TC
C 19	44.4	7.1	499	11	AZ058431 RPT-23-4

20	44.4	7.1	550	4	BX250092
21	44.4	7.1	658	11	AZ592362 IM0403A17
C 22	44.4	7.1	757	11	BZ076780
C 23	44.2	7.1	666	1	AV368360
C 24	44.2	7.1	719	10	DT726802
C 25	44.2	7.1	759	10	DW103368
C 26	44.2	7.1	776	14	CNS01JUK
C 27	44.2	7.1	989	14	CNS05RZJ
28	44	7.0	899	14	CO910517
29	44	7.0	522	11	AZ440830
C 30	43.8	7.0	879	10	DW345288
C 31	43.8	7.0	897	14	AG844971
C 32	43.6	7.0	232	11	BZ280453
C 33	43.6	7.0	440	11	AZ001211
C 34	43.6	7.0	442	14	CR192806
C 35	43.6	7.0	597	11	AZ460974
C 36	43.6	7.0	717	12	CE081925
C 37	43.6	7.0	750	14	AG482398
C 38	43.6	7.0	810	8	CNS31411
39	43.4	6.9	1044	3	BM800931
40	43.4	6.9	1100	11	BZ17558
41	43.4	6.9	3304	6	AK079471
42	43.2	6.9	508	3	BQ103940
43	43.2	6.9	600	2	BG803750
C 44	43.2	6.9	738	14	AG562107
C 45	43	6.9	216	11	AZ384008

ALIGNMENTS

RESULT 1
LOCUS CE792380/c 561 bp DNA linear GSS 30-SEP-2003
DEFINITION tigr-gss-dog-17000330896927 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE792380
VERSION CE792380.1 GI:37133144
KEYWORDS GSS:
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (Baese 1 to 561)
AUTHORS Kirkness,B.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
Ruch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
FEATURES
source location/Qualifiers
1..561
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="DOG Library"
/note="Site 1: BactX; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match 7.6%; Score 47.6; DB 12; Length 561;
Best Local Similarity 62.7%; Pred. No. 0.014;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY	303	CTCCGATATTTCTCTCACTTCCATPAACCCCTGATTAATTTGGTGGAAAGCAGACGCCAA	362
Db	364	CTCTCTCTCTCTCGCTTCCATCAATGAATAAATAAATCTTTAAAAAAGATCATPA	305
QY	363	CCCAACAAAGTCAGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420
Db	304	TTAACAAAGATTTTATTTATTTATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAG	247
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LOCUS	B2731304	760 bp	DNA
DEFINITION	OGFBZ507C_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0249u04,	linear	GSS 03-MAR-2003
ACCESSION	B2731304		
VERSION	B2731304		
KEYWORDS	genomic survey sequence.		
SOURCE	B2731304.1	GI:28705008	
ORGANISM	Zea mays		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD		
	clade; Panicoideae; Andropogoneae; Zea.		
	1 (bases 1 to 760)		
	Whitelaw,C.A., Rackenbush,J., Van Aken,S., Uteback,T.,		
	Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,		
	Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.		
	Consortium for Maize Genomics		
	Unpublished (2002)		
	Other GSSs: OGFBZ507M		
	Contact: Cathy Whitelaw		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA		
	Tel: 301-838-5843		
	Fax: 301-838-0208		
	Email: whitelaw@tigr.org		
	Seq primer: TP		
	Class: methylation filtered.		
FEATURES			
source	location/Qualifiers		
	1..760		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/strain="B73"		
	/db_xref="taxon:4577"		
	/clone="ZMMBma0249u04"		
	/clone_1lb="ZM_0.7_1.5_KB"		
	/note="Vector: pBCSK-1 Site 1: HincII; 0.7-1.5 kb		
	methylation filtered genomic DNA library"		
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Best Local Similarity	62.0%;	Pred. No. 0.017;	46;
Matches	75;	Conservative	0;
	Mismatches	46;	Indels
	Gaps	0;	
QY	300	GAATCCGATATTTCTCTCACTTCCATPAACCCCTGATTAATTTGGTGGAAAGCAGAC	359
Db	4	GAGGTCGGTGTGTGATGCTTATATATCTGCTGCAATATGATGATGAACAGCGC	63
QY	360	CAACCCACAAAGCTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAG	419
Db	64	TGGCTACGGCACTTGATTCGATATGTCGAGAGAGAGAGAGAGAGAGAGAGAGA	123
QY	420	G 420	
Db	124	G 124	
RESULT 3			
LOCUS	AG559107	831 bp	DNA
DEFINITION	Mus musculus molossinus DNA, clone:MSNg01-477N16.T7, genomic survey	linear	GSS 23-DEC-2004
ACCESSION	AG559107		
	sequence.		

VERSION	AGS9107.1	GI:48319805
KEYWORDS	GSS.	Mus musculus molossinus (Japanese wild mouse)
SOURCE	Mus musculus molossinus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.	
REFERENCE AUTHORS	1 Abe,K., Noguchi,H., Tagawa,K., Yuzurika,M., Toyoda,A., Kojima,T., Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriawaki,K. and Shiroishi,T.	
TITLE	Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis	
JOURNAL	Genome Res. 14 (12), 2439-2447	(2004)
PUBMED	15574823	
REFERENCE	2 (bases 1 to 831)	
AUTHORS	Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-Chou,Tsurumi-Ku Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)	
COMMENT	Clones are derived from the mouse BAC library MSM01. For BAC library availability, please contact Kunyua Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center. The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp	
PRIMERS	Sequencing : T7 LIBRARY : pBAC3.6 Vector : EcoRI R.site 1 : EcoRI R.site 2 : EcoRI.	
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source	1..831	
	/organism="Mus musculus molossinus"	
	/mol_type="genomic DNA"	
	/sub_species="molossinus"	
	/db_xref="taxon:57486"	
	/clone="MSM01-477N16.T7"	
	/sex="male"	
	/tissue-type="mixture of kidney and spleen"	
	/clone_lib="MSM01 Mouse Male BAC Library"	
ORIGIN		
Query Match	7.5%; Score 46.6; DB 14; Length 831;	
Best Local Similarity	58.9%; Pred.No.0.03; Indels 53; Gaps 0;	
Matches	76; Conservative 0; Mismatches 53; Gaps 0;	
DQ	390 GAGAGAAGAGAAGAGAAGAGAAGAGATTCTCTCATATTTGTGGTCAACCGCT 449	
DQ	279 GAGAGGAGAGAGGAGAGGAGAGAGGAGAGNTTTTTTTTTTTTTTTTTNNNTTT 338	
DQ	450 GGAGTCATGCATCCGTCGACGAATGTATCATATTTGGTAGGTCACAATATTTTGCGGA 509	
DQ	339 GTGTTTGTGGGTGGGTGGGTGTGTGTTTGTGTTTGTGTCGTGTGTGTGGGG 398	
DQ	510 GGGTTGGTG 518	
DQ	399 GGGGTGGTG 407	
RESULT 4		
LOCUS	DT310002/c	619 bp mRNA linear EST 19-AUG-2005
DEFINITION	JGI_CAAI533.rev CAAX Pimphales promelas testis 7-8 month adults, males and females pooled (L) Pimphales promelas cDNA clone	
ACCESSION	CAA1533 3'	mRNA sequence.
	DT310002	

KEYWORDS EST.
SOURCE Trifolium pratense
ORGANISM Trifolium pratense
AUTHORS Bukarjota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trifolium.
REFERENCE 1 (bases 1 to 349)
Sato,S., Isobe,S., Asamizu,E., Nakamura,Y., Ohmido,N., Sakurai,N., Klimentko,I., Saamotoko,S., Wada,T., Watanabe,A. and Tabata,S.
TITLE Comprehensive structural analysis of the genome of red clover (Trifolium pratense)
JOURNAL Unpublished (2006)
COMMENT Contact: Erika Asamizu
The First Laboratory For Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
source
1..349
location/Qualifiers
1..349
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SSR-enriched library"
/note="Vector: pTBlue T-Vector; Site_1: EcoRV; variety:
Hokuseki"
ORIGIN
Query Match 7.3%; Score 45.8; DB 7; Length 349;
Best Local Similarity 62.8%; Pred. No. 0.042;
Matches 71; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 347 GGAAAGGAGAGAGCCACCAAAAGGTGCATGTCTCCACGAGAGAGAGAGAGAG 406
DB 233 GAAATATGCAAAACCAACCAAAATCTTAAACTTTAGCCGAGAGAGAGAGAGAGAG 292
QY 407 AGAGAGAGAGAGAGTTTCTCTATATATTCGTTCACCGGTGAGTCAATG 459
DB 293 AGAGAGAGAGAGGTGTATTGTCTTCTCTCTCTCTCTCTCTCTCTCTGTTGAATG 345
RESULT 6
CK600115/c 799 bp mRNA linear EST 22-JAN-2004
LOCUS AGNCOCURT 17895063 NIH MGC_234 Rattus norvegicus cDNA clone
DEFINITION IMAGE:7189967 5', mRNA sequence.
ACCESSION CK600115
VERSION CK600115.1 GI:4113272
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
AUTHORS Bukarjota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 799)
NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcgaps-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov

RESULT 11
DT234659/c
LOCUS
DEFINITION
ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

DT234659 778 bp mRNA linear EST 17-AUG-2005
JGI CMA78286.rev CMA7 Pimephales promelas brain 7-8 month adults,
males and females pooled (M) Pimephales promelas cDNA clone
CMA78286 3', mRNA sequence.
DT234659
DT234659.1 GI:73504794
EST.
Pimephales promelas
Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Pimephales.
1 (bases 1 to 778)
Richardson, P., Lucas, S., Rohrsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Pimephales promelas EST project
Unpublished (2005)
Other ESTs: JGI CMA78286.Fwd
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
CDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix 'rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues
at the beginning of the sequence, this clone was polyadenylated.
The resulting Poly-T sequence has been removed.
Plate: CMA7 0085 row: k column: 8
High quality sequence stop: 778
POLYA=yes.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CMA78286"
/tissue_type="brain"
/clone_id="CMA7 Pimephales promelas brain 7-8 month
adults, males and females pooled (M)"
/note="Vector: pCMVSPORT6; The library was made from dt
primed cDNA and cloned into Invitrogen vector pCMVSPORT6.
Poly A RNA were primed with an oligo dt primer (5'-
GACTAGTTCTAGATCGGAGCGCGCTTTTCTTTTCTTTT-3') ligated
to a SalI adapter (5'- TCGACCCAGCGGTCG and 5'-
CGGACGCTGGG) and digested with NotI. cDNA was size
selected using 1.1% agarose gel electrophoresis (L
~0.5-1.2k, M ~1.2-2.5k, H ~2.5k) then ligated into NotI
and SalI digested pCMVSPORT6 vector. The work was done at
DOE Joint Genome Institute."

ORIGIN

Query Match 7.2%; Score 44.8; DB 10; Length 778;
Best Local Similarity 64.4%; Pred. No. 0.1; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 37;
QY 345 TGGGAAAGCGACGACCAACCAAGGTCAGATGATCCGAGAGAGAGAGAG 404
DB 195 TGAAGAGTGAAGAGTAAAGCACTAAAGGAAACGAGAGAGAGAGAGAGAG 136
QY 405 AGAGAGAGAGAGAGAGTTTCTCTCTAATATTTGCTTACCGGT 448
DB 135 AGAGAGAGAGAGAGCGGTGCTTGAAGTCTTTGCGCGGT 92

RESULT 12
B2708983/c
LOCUS
DEFINITION
ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B2708983 363 bp DNA linear GSS 19-FEB-2003
OCEBAM43TM_ZM_0_7_1.5 KB Zea mays genomic clone ZMMBMA0220H13,
genomic survey sequence.
B2708983
B2708983.1 GI:28429079
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 363)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uteerback, T.,
Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OCEBAM43TC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers

FEATURES
source

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Best Local Similarity 61.7%; Pred. No. 0.097; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 44;
QY 306 CGTATTTCTCTCACTTCCATTAACCCCTGATTAATTGTTGGGAAAGCGACGCCACCC 365
DB 271 CGTTGTTGATGCTTATATATCTCGTCAATATATGATGATGAACGACGGCTGGCTC 212
QY 366 ACAAGAGTCAGATGATATCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 211 ACGGACACCTTGATCTGATATGCGGAGAGAGAGAGAGAGAGAGAGAGAG 157
RESULT 13
B2306338
LOCUS
DEFINITION
ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

B2306338 543 bp DNA linear GSS 06-NOV-2002
hxA1a10.b1 WGS-Zmaysf (JM107 adapted methyl filtered) Zea mays
genomic clone hxA1a10 5', genomic survey sequence.
B2306338
B2306338.1 GI:24659045
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 543)
Rabinowitz, P.D., O'Shaughnessy, A.L., Ballia, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, B., Miller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)

Thu Nov 2 13:35:54 2006

us-10-702-319a-113_copy_1019_1643.rst

Best Local Similarity 61.7%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 306 CGTATTTCTCTCACTTCCATTAACCCCTGATTATTTGTTGGGAAAGCGACGCCAACC 365
DB 451 CGTTGTTGTAATGCTTATATATACTCGTGCMAATAATGATGTATGACGACGCTGCTC 510
QY 366 ACAAAGGTCAATGTCATCCCAAGAGAGAGAGAGAGAGAGAGAG 420
DB 511 ACGGACCTTGATCTGATATGCTGAAGAGAGAGAGAGAGAGAGAG 565

Search completed: November 1, 2006, 07:01:22
Job time : 2032.12 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:41:44 ; Search time 116.161 Seconds
(without alignments)
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Title: US-10-702-319a-113_COPY_1019_1643
Perfect score: 625
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93555401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /EMC Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC Celerra_SIDS3/ptodata/2/ina/8B COMB.seq:*
- 5: /EMC Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
- 8: /EMC Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	606.2	97.0	661	3	US-09-276-599-12
3	606.2	97.0	661	3	US-09-598-401C-12
4	606.2	97.0	2096	3	US-09-598-401C-60
5	43	6.9	1630	3	US-09-615-192A-107
6	43	6.9	1630	3	US-09-169-789-107
7	41.8	6.7	421	2	US-08-975-316-24
8	41.8	6.7	421	3	US-09-615-192A-24
9	41.8	6.7	421	3	US-09-169-789-24
10	41.4	6.6	407	3	US-09-615-192A-106
11	41.4	6.6	407	3	US-09-169-789-106
12	40.6	6.5	130563	3	US-09-949-016-12273
13	40.6	6.5	131379	3	US-09-949-016-16050
14	39.6	6.3	458	3	US-09-270-767-27637
15	39.6	6.3	1528	3	US-09-270-767-11960
16	39.4	6.3	601	3	US-09-949-016-89176
17	39.4	6.3	14037	3	US-09-949-016-17329
18	39.4	6.3	72604	3	US-09-268-992-7
19	39.4	6.3	72604	3	US-09-657-474-7
20	39.4	6.3	237510	3	US-09-949-016-14273
21	39.2	6.3	36317	3	US-09-949-016-12697
22	39.2	6.3	36322	3	US-09-949-016-14047
23	39	6.2	2830	2	US-07-882-292-1

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c	28	38.8	6.2	601	3	US-09-949-016-96411	Sequence 96411, A
c	29	38.8	6.2	601	3	US-09-949-016-96675	Sequence 96675, A
c	30	38.8	6.2	601	3	US-09-949-016-96676	Sequence 96676, A
c	31	38.8	6.2	601	3	US-09-949-016-96677	Sequence 96677, A
c	32	38.8	6.2	601	3	US-09-949-016-96941	Sequence 96941, A
c	33	38.8	6.2	601	3	US-09-949-016-96942	Sequence 96942, A
c	34	38.8	6.2	601	3	US-09-949-016-96943	Sequence 96943, A
c	35	38.8	6.2	601	3	US-09-949-016-97207	Sequence 97207, A
c	36	38.8	6.2	601	3	US-09-949-016-97208	Sequence 97208, A
c	37	38.8	6.2	601	3	US-09-949-016-97209	Sequence 97209, A
c	38	38.8	6.2	601	3	US-09-949-016-97473	Sequence 97473, A
c	39	38.8	6.2	601	3	US-09-949-016-97474	Sequence 97474, A
c	40	38.8	6.2	601	3	US-09-949-016-97739	Sequence 97739, A
c	41	38.8	6.2	601	3	US-09-949-016-97740	Sequence 97740, A
c	42	38.8	6.2	601	3	US-09-949-016-97741	Sequence 97741, A
c	43	38.8	6.2	601	3	US-09-949-016-98005	Sequence 98005, A
c	44	38.8	6.2	601	3	US-09-949-016-98006	Sequence 98006, A
c	45	38.8	6.2	601	3	US-09-949-016-98006	Sequence 98006, A

ALIGNMENTS

RESULT 1

US-09-598-401C-113
; Sequence 113, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Petera, J. Ranjan
; APPLICANT: Bagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1036C2
; CURRENT APPLICATION NUMBER: US/09/598,401C
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-113

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Best Local Similarity 100.0%; Pred. No. 4,7e-198;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	CGAATTTCTCTTTTAGTAAAGTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA	120
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 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGCTCTTGACCGGG 300
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 477 ACATATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 536
 481 ACATATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 540
 537 TATCGAACCTCCACCAACCATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCT 596
 541 TATCGAACCTCCACCAACCATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCT 600
 597 CTGCTTTCTCTGCTCGAGTCTCGCGAA 625
 601 CTGCTTTCTCTGCTCGAGTCTCGCGAA 629

RESULT 3

US-09-598-401C-12
 ; Sequence 12, Application US/09598401C
 ; Patent No. 6596925
 ; GENERAL INFORMATION:
 ; APPLICANT: Perera, J. Ranjan
 ; APPLICANT: Eagleton, Clare
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; FILE REFERENCE: 11000.1036C2
 ; CURRENT FILING DATE: 2000-06-20
 ; CURRENT APPLICATION NUMBER: US/09/598,401C
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
 ; PRIOR FILING DATE: 1999-03-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 661
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 ; US-09-598-401C-12

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 541 GAACCTCCACCAACCATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTG 600
 1559 GAACCTCCACCAACCATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTG 1618
 601 TTTCTCTGCTCGAGTCTCGCGAA 625
 1619 TTTCTCTGCTCGAGTCTCGCGAA 1643

RESULT 2

US-09-276-599-12
 ; Sequence 12, Application US/09276599
 ; Patent No. 6380459
 ; GENERAL INFORMATION:
 ; APPLICANT: Perera, J. Ranjan
 ; APPLICANT: Rice, Stephen J.
 ; TITLE OF INVENTION: Composition and methods for the
 ; FILE REFERENCE: 11000.1036
 ; CURRENT FILING DATE: 1999-03-25
 ; CURRENT APPLICATION NUMBER: US/09/276,599
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Fast-Seq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 661
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 ; NAME/KEY: 5'UTR
 ; LOCATION: (1)...(654)
 ; NAME/KEY: TATA signal
 ; LOCATION: (537)...(543)
 ; NAME/KEY: CAAT signal
 ; LOCATION: (499)...(502)
 ; US-09-276-599-12

Query Match 97.0%; Score 606.2; DB 3; Length 661;
 Best Local Similarity 98.9%; Pred. No. 3.9e-192;
 Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
 1 CTGAGCCATTTAATTCGAGACACATCGCCCAAAATTTCTTTCTTGCTGCCATAACTGT 60
 1 CTGAGCCATTTAATTCGAGACACATCGCCCAAAATTTCTTTCTTGCTGCCATAACTGT 60
 61 CGAATTTCTCTTTTAGTAAAGTAAACCAATGATCGGCATGTTGACAAAAGCTGATTA 120
 61 CGAATTTCTCTTTTAGTAAAGTAAACCAATGATGATCATGTTGACAAAAGCTGATTA 120
 121 GTATGATCTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGGAAAT 180
 121 GTATGATCTTGGAGTTGTTGGTGCATAATTTGCAAGCTGACGATGGCCCTCAGGAAAT 180

Thu Nov 2 13:35:53 2006

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; LENGTH: 421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-975-316-24

Query Match      6.7%; Score 41.8; DB 2; Length 421;
Best Local Similarity 95.6%; Pred. No. 0.0016;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTATTTCCTCTGCTTCCTTTGCTCGAGTCTCGCGGAA 625
Db 13 AGCCGTTTATTTCCTCTGCTTCCTTTGCTCGAGTCTCGCGGAA 57

RESULT 8
US-09-615-192A-24
; Sequence 24, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-24

Query Match      6.7%; Score 41.8; DB 3; Length 421;
Best Local Similarity 95.6%; Pred. No. 0.0016;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTATTTCCTCTGCTTCCTTTGCTCGAGTCTCGCGGAA 625
Db 13 AGCCGTTTATTTCCTCTGCTTCCTTTGCTCGAGTCTCGCGGAA 57

RESULT 9
US-09-169-789-24
; Sequence 24, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: US 08/713,000
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-24

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RESULT 6
US-09-169-789-107
; Sequence 107, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: US 08/713,000
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-107

Query Match      6.9%; Score 43; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 CCGTTTATTTCCTCTGCTTCCTTTGCTCGAGTCTCGCGGAA 625
Db 1 CCGTTTATTTCCTCTGCTTCCTTTGCTCGAGTCTCGCGGAA 43

RESULT 7
US-08-975-316-24
; Sequence 24, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:

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Query Match 6.7%; Score 41.8; DB 3; Length 421;
Best Local Similarity 95.6%; Pred. No. 0.0016;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 581 ATCCGTTTATTTCTCTGCTTCTTTGCTCGAGTCTCGCGAA 625
Db 13 AGCCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAA 57

RESULT 10

US-09-615-192A-106
; Sequence 106, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-106

Query Match 6.6%; Score 41.4; DB 3; Length 407;
Best Local Similarity 97.7%; Pred. No. 0.0021;
Matches 42; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 583 CCGTTTATTTCTCTGCTTCTTTGCTCGAGTCTCGCGAA 625
Db 1 CCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAA 43

RESULT 11

US-09-169-789-106
; Sequence 106, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: US 08/713,000
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-106

Query Match 6.6%; Score 41.4; DB 3; Length 407;
Best Local Similarity 97.7%; Pred. No. 0.0021;
Matches 42; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 583 CCGTTTATTTCTCTGCTTCTTTGCTCGAGTCTCGCGAA 625
Db 1 CCGTTTATTTCTCTGATTTCTTTGCTCGAGTCTCGCGAA 43

RESULT 12

US-09-949-016-12273/c
; Sequence 12273, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12273
; LENGTH: 130563
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12273

Query Match 6.5%; Score 40.6; DB 3; Length 130563;
Best Local Similarity 73.2%; Pred. No. 0.095;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 350 AAGCGACAGCCACCCACAAAGGTCAGATGTATCCACGAGAGAGAGAGAGA 409
Db 118294 AAAAGGAAGCCAAACACAGAGAAAATCAGCTGAGAAATCGAGAGAGAGAGAGA 118235

Qy 410 GAGAGAGAGAG 420

Db 118234 GAGAGAGAGAG 118224

RESULT 13

US-09-949-016-16050/c
; Sequence 16050, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16050
; LENGTH: 131379
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16050

Query Match 6.5%; Score 40.6; DB 3; Length 131379;
Best Local Similarity 73.2%; Pred. No. 0.096;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 350 AAGCGACAGCCACCCACAAAGGTCAGATGTATCCACGAGAGAGAGAGAGA 409

Search completed: November 1, 2006, 11:48:34
Job time : 116.161 secs

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:25:56 ; Search time 799.58 Seconds
(without alignments)
9604.757 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1643

Perfect score: 625

Sequence: 1 ctgagccattatttgaga.....tttctgctgagctctgcggaa 625

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	3070	6	US-10-137-036-113
2	625	100.0	3070	9	US-10-702-319A-113
3	625	100.0	3070	10	US-10-927-641-113
4	606.2	97.0	661	6	US-10-137-036-12
5	606.2	97.0	661	9	US-10-702-319A-12
6	606.2	97.0	661	10	US-10-927-641-12
7	606.2	97.0	2096	6	US-10-137-036-60
8	606.2	97.0	2096	9	US-10-702-319A-60
9	606.2	97.0	2096	10	US-10-927-641-60
10	534	85.4	534	8	US-10-703-091-1
11	485	77.6	485	8	US-10-703-091-2
12	306	49.0	306	8	US-10-703-091-3
13	293	46.9	293	8	US-10-703-091-4
14	119	19.0	119	8	US-10-703-091-5
15	98	15.7	98	8	US-10-703-091-6
16	66	10.6	66	8	US-10-703-091-7
17	49.4	7.9	5626	13	US-11-097-143-19390

C 18	45.4	7.3	7228	11	US-10-893-483-28	Sequence 28, Appl
C 19	45	7.2	1951	10	US-10-966-482-18	Sequence 18, Appl
C 20	43.4	6.9	2000	10	US-10-481-032A-711	Sequence 711, App
C 21	43.4	6.9	2000	10	US-10-481-032A-721	Sequence 721, App
C 22	43.4	6.9	2199	10	US-10-481-032A-656	Sequence 656, App
C 23	43	6.9	1630	7	US-10-174-693-107	Sequence 107, App
C 24	42.6	6.8	563	9	US-10-425-115-80646	Sequence 80646, A
C 25	42.4	6.8	493631	6	US-10-087-192-205	Sequence 205, App
C 26	41.8	6.7	421	7	US-10-174-693-24	Sequence 24, Appl
C 27	41.8	6.7	126192	6	US-10-087-192-1459	Sequence 1459, Ap
C 28	41.6	6.7	882	6	US-10-027-632-173109	Sequence 173109,
C 29	41.6	6.7	53981	6	US-10-087-192-1621	Sequence 1621, Ap
C 30	41.6	6.6	407	7	US-10-174-693-106	Sequence 106, App
C 31	41.4	6.6	24080	3	US-09-997-722-79	Sequence 79, Appl
C 32	41.2	6.6	257	9	US-10-674-124A-21772	Sequence 21772, A
C 33	41.2	6.6	24879	6	US-10-087-192-307	Sequence 307, App
C 34	41.2	6.6	176594	8	US-10-322-281-495	Sequence 495, App
C 35	41.2	6.6	354	10	US-10-779-543-10544	Sequence 10544, A
C 36	41	6.6	395	10	US-10-779-543-11769	Sequence 11769, A
C 37	41	6.6	395	10	US-10-360-238-2334	Sequence 2334, Ap
C 38	40.8	6.5	2000	8	US-10-085-117-7	Sequence 7, Appli
C 39	40.8	6.5	43412	7	US-10-330-773-585	Sequence 585, App
C 40	40.8	6.5	100610	11	US-10-674-124A-24865	Sequence 24865, A
C 41	40.6	6.5	336	9	US-10-322-281-323	Sequence 323, App
C 42	40.6	6.5	103464	8	US-10-737-082-47	Sequence 47, Appl
C 43	40.6	6.5	127567	10	US-10-765-790-47	Sequence 96920, A
C 44	40.6	6.5	127567	10	US-10-765-790-47	
C 45	40.4	6.5	802	8	US-10-437-963-96920	

ALIGNMENTS

RESULT 1

US-10-137-036-113
; Sequence 113, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Petera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Bagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2001-06-20
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-20
; PRIOR FILING DATE: 2000-06-20
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-07-30
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-113

Query Match 100.0%; Score 625; DB 6; Length 3070;
Best Local Similarity 100.0%; Pred. No. 9.7e-188;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu Nov 2 13:35:54 2006

QY 1 CTGAGCATTAAATTCGAGACACATCGCCCAAAATTAATCTTCTGTCGCATAACTGT 60
Db 1019 CTGAGCATTAAATTCGAGACACATCGCCCAAAATTAATCTTCTGTCGCATAACTGT 1078
QY 61 CGAATTTTCTCTTTAGGTAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGGTAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 1138
QY 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCGCCCTCAGGGAATTT 180
Db 1139 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCGCCCTCAGGGAATTT 1198
QY 181 AAGCGGCCAACCCAGATTGCAAGAGCAAAAGAGCAGCAACCTTTCTTAAACAAG 240
Db 1199 AAGCGGCCAACCCAGATTGCAAGAGCAGCAACCTTTCTTAAACAAG 1258
QY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAACAATAGCTCTTGTACCGGG 300
Db 1259 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAACAATAGCTCTTGTACCGGG 1318
QY 301 AACTCCGTAATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGC 360
Db 1319 AACTCCGTAATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGC 1378
QY 361 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 1379 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
QY 421 TTTTCTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGATCGGTGACGAATGTACAT 480
Db 1439 TTTTCTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGATCGGTGACGAATGTACAT 1498
QY 481 ATTGGTGTAGGTCGCAATATTTTGGGAGGGTTGGTGAAACCGCAAGTTTCTTATATC 540
Db 1499 ATTGGTGTAGGTCGCAATATTTTGGGAGGGTTGGTGAAACCGCAAGTTTCTTATATC 1558
QY 541 GAACCTCCACCACTACCTCACTTCAATCCCAATTAATTCGTTTATTTCTCTGCG 600
Db 1559 GAACCTCCACCACTACCTCACTTCAATCCCAATTAATTCGTTTATTTCTCTGCG 1618
QY 601 TTTTCTTTGCTCGAGTCTCGCGAA 625
Db 1619 TTTTCTTTGCTCGAGTCTCGCGAA 1643

RESULT 2
US-10-702-319A-113
; Sequence 113, Application US/10702319A
; Publication No. US20050026162A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c5
; CURRENT APPLICATION NUMBER: US/10702.319A
; PRIOR FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: U.S. No. 10/291,447
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 60/425,087
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599

; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-702-319A-113
Query Match 100.0%; Score 625; DB 9; Length 3070;
Best Local Similarity 100.0%; Pred. No. 9.7e-188; Indels 0; Gaps 0;
Matches 625; Conservative 0; Mismatches 0;
QY 1 CTGAGCATTAAATTCGAGACACATCGCCCAAAATTAATCTTCTGTCGCATAACTGT 60
Db 1019 CTGAGCATTAAATTCGAGACACATCGCCCAAAATTAATCTTCTGTCGCATAACTGT 1078
QY 61 CGAATTTTCTCTTTAGGTAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGGTAAGTAACCAATGATGCGCCATGTTGACAAAAGGCTGATTA 1138
QY 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCGCCCTCAGGGAATTT 180
Db 1139 GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCGCCCTCAGGGAATTT 1198
QY 181 AAGCGGCCAACCCAGATTGCAAGAGCAGCAACCTTTCTTAAACAAG 240
Db 1199 AAGCGGCCAACCCAGATTGCAAGAGCAGCAACCTTTCTTAAACAAG 1258
QY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAACAATAGCTCTTGTACCGGG 300
Db 1259 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTAACAATAGCTCTTGTACCGGG 1318
QY 301 AACTCCGTAATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGC 360
Db 1319 AACTCCGTAATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGC 1378
QY 361 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 1379 AACCACAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
QY 421 TTTTCTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGATCGGTGACGAATGTACAT 480
Db 1439 TTTTCTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGATCGGTGACGAATGTACAT 1498
QY 481 ATTGGTGTAGGTCGCAATATTTTGGGAGGGTTGGTGAAACCGCAAGTTTCTTATATC 540
Db 1499 ATTGGTGTAGGTCGCAATATTTTGGGAGGGTTGGTGAAACCGCAAGTTTCTTATATC 1558
QY 541 GAACCTCCACCACTACCTCACTTCAATCCCAATTAATTCGTTTATTTCTCTGCG 600
Db 1559 GAACCTCCACCACTACCTCACTTCAATCCCAATTAATTCGTTTATTTCTCTGCG 1618
QY 601 TTTTCTTTGCTCGAGTCTCGCGAA 625
Db 1619 TTTTCTTTGCTCGAGTCTCGCGAA 1643

RESULT 3
US-10-927-641-113
; Sequence 113, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10927.641

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; CURRENT FILING DATE: 2004-08-27
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-113

Query Match 100.0%; Score 625; DB 10; Length 3070;
Best Local Similarity 100.0%; Pred. No. 9.7e-188;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGCCATTAAATTCGAGAGCAGCATCGCCCAAAATTTATCTTCTGCTGCCATACTGT 60
Db 1019 CTGAGCCATTAAATTCGAGAGCAGCATCGCCCAAAATTTATCTTCTGCTGCCATACTGT 1078

Qy 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCATGTTGACAAAAAGGCTGATTA 120
Db 1079 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCATGTTGACAAAAAGGCTGATTA 1138

Qy 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGGCCCTCAGGGAAT 180
Db 1139 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGGCCCTCAGGGAAT 1198

Qy 181 AAGCGCCCAACCCAGATTGCAAGAGCACAAGAGCAGACCCACCTTTCTTCAACAAG 240
Db 1199 AAGCGCCCAACCCAGATTGCAAGAGCACAAGAGCAGACCCACCTTTCTTCAACAAG 1258

Qy 241 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTTAAACAATAGCTCTGTACCGGG 300
Db 1259 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTTAAACAATAGCTCTGTACCGGG 1318

Qy 301 AACTCCGATTTCTCTCACTTTCCATAAACCCCTGATTAATTTTGGTGGGAAAGCGACAGCC 360
Db 1319 AACTCCGATTTCTCTCACTTTCCATAAACCCCTGATTAATTTTGGTGGGAAAGCGACAGCC 1378

Qy 361 AACCCCAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 1379 AACCCCAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438

Qy 421 TTTTCTCTATATTTCTGTTTCAACCGGTCGAGTCATGCAATGCATCGCTGAGCAATGTACAT 480
Db 1439 TTTTCTCTATATTTCTGTTTCAACCGGTCGAGTCATGCAATGCATCGCTGAGCAATGTACAT 1498

Qy 481 ATTGGGTAGGGTCCAAATATTTTGGCGGAGGGTTGGTGAACCGCAAAAGTTTCTTATATATC 540
Db 1499 ATTGGGTAGGGTCCAAATATTTTGGCGGAGGGTTGGTGAACCGCAAAAGTTTCTTATATC 1558

Qy 541 GAACCTCCACCAATACCTACCTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGTC 600
Db 1559 GAACCTCCACCAATACCTACCTTCAATCCCAACCAATTTATCCGTTTATTTCTCTGTC 1618

Qy 601 TTTTCTTTGCTCGAGTCTCGGGA 625
Db 1619 TTTTCTTTGCTCGAGTCTCGGGA 1643

RESULT 4
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US-10-137-036-12
; Sequence 12; Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eashleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C4
; CURRENT APPLICATION NUMBER: US/10/137,036
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-12

Query Match 97.0%; Score 606.2; DB 6; Length 661;
Best Local Similarity 98.9%; Pred. No. 4.2e-182;
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 1 CTGAGCCATTAAATTCGAGAGCAGCATCGCCCAAAATTTATCTTCTGCTGCCATACTGT 60
Db 1 CTGAGCCATTAAATTCGAGAGCAGCATCGCCCAAAATTTATCTTCTGCTGCCATACTGT 60

Qy 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCATGTTGACAAAAAGGCTGATTA 120
Db 61 CGAATTTTCTCTTTAGTAAAGTAACCAATGATGCGCATGTTGACAAAAAGGCTGATTA 120

Qy 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGGCCCTCAGGGAAT 180
Db 121 GTATGATCTTGGAGTTGTTGGTGCAAAATTTTCAAGCTGACGATGGCCCTCAGGGAAT 180

Qy 181 AAGCGCCCAACCCAGATTGCAAGAGCACAAGAGCAGACCCACCTTTCTTCAACAAG 240
Db 181 AAGCGCCCAACCCAGATTGCAAGAGCACAAGAGCAGACCCACCTTTCTTCAACAAG 240

Qy 241 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTTAAACAATAGCTCTGTACCGGG 300
Db 241 ATCATCACAGATCGGCCAGTAAGGTAATTAATTTTAAACAATAGCTCTGTACCGGG 300

Qy 301 AACTCCGATTTCTCTCACTTTCCATAAACCCCTGATTAATTTTGGTGGGAAAGCGACAGCC 360
Db 301 AACTCCGATTTCTCTCACTTTCCATAAACCCCTGATTAATTTTGGTGGGAAAGCGACAGCC 360

Qy 361 AACCCCAAAAGGTCAGATGTCATCCAC-----GAGAGAGAGAGAGAGAGAGAGAGAG 416
Db 361 AACCCCAAAAGGTCAGATGTCATCCACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 417 AGAGTTTCTCTCTATATTTCTGTTTCAACCGGTTGGAGTCAATGGCATGCGTACGATGT 476
Db 421 AGAGTTTCTCTCTATATTTCTGTTTCAACCGGTTGGAGTCAATGGCATGCGTACGATGT 480

Qy 477 ACATATTTGGTGGAGGTCCTCAATATTTTGGGGAGGGTTGGTGAACCGCAAAAGTTTCTTATA 536
Db 477 ACATATTTGGTGGAGGTCCTCAATATTTTGGGGAGGGTTGGTGAACCGCAAAAGTTTCTTATA 536
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481	ACATATTGGTGTA	GGGTC	CAATATTTT	CGGGAGGGT	TGCTGA	ACCGCAAGTT	CTCTATA	540
537	TATCGAACTCC	ACACCA	CATACCT	CAC	TTC	CAATCCCA	CCCATTTATTCCT	596
541	TATCGAACTCC	ACACCA	CATACCT	CAC	TTC	CAATCCCA	CCCATTTATTCCT	600
597	CTGCTTTCTTT	GGCTCG	AGTCT	CGGGAA	625			
601	CTGCTTTCTTT	GGCTCG	AGTCT	CGGGAA	629			

RESULT 5
US-10-702-319A-12
; Sequence 12, Application US/10702319A
; Publication No. US20050026162A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression

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; CURRENT APPLICATION NUMBER: 2003-11-06
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: U.S. No. 10/291,447
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 60/425,087
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-702-319A-12

Query Match          97.0%;   Score 606.2;   DB 9;   Length 661;
Best Local Similarity 98.9%;   Pred. No. 4.2e-182;   Indels 4;   Gaps 1;
Matches 622;   Conservative

QY      1   CTGAGCGCATTTAAATTCGAGAGCACATCGCCCAAAATTTCTTCTGTGCGCAATACTGT 60
Dd      1   CTGAGCGCATTTAAATTCGAGAGCACATCGCCCAAAATTTCTTCTGTGCGCAATACTGT 60

QY      61  CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATGCCCATGTGTGACAAAAGGCTGATTA 120
Dd      61  CGAATTTTCTCTTTTAGTAAAGTAAACCAATGATGCCCATGTGTGACAAAAGGCTGATTA 120

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Qy	121	GTATGATCTTGGAGTGTGTGGTCAAAATTGCAAGCTGACGATGCGGAAATT	180
Db	121	GTATGATCTTGGAGTGTGTGGTCAAAATTGCAAGCTGACGATGCGGAAATT	180
Qy	181	AAGCGCCAAACCCAGATTGCAAGAGCACAAGAGCAGCACCAACTTCTTAAACAAG	240
Db	181	AAGCGCCAAACCCAGATTGCAAGAGCACAAGAGCAGCATCCAACTTTCTTAAACAAG	240
Qy	241	ATCATCACGATCGGCCAGTAGGGTAATTAAATTTAAACAATAGCTCTTGTACCGGG	300
Db	241	ATCATCACGATCGGCCAGTAAGGGTAATTAAATTTAAACAATAGCTCTTGTACCGGG	300

Thu Nov 2 13:35:54 2006

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; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2096
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; US-10-702-319A-60

Query Match      97.0%; Score 606.2; DB 9; Length 2096;
Best Local Similarity 98.9%; Pred. No. 7.9e-182;
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTTCTTCTGCTGCCATAACTGT 60
Db 41 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTTCTTCTGCTGCCATAACTGT 100
QY 61 CGAATTTCTCTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 120
Db 101 CGAATTTCTCTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 160
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 180
Db 161 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 220
QY 181 AAGGCGCCAAACCCAGATTGCAAGAGCACAAAGAGCACGCCCAACCTTTCTTAAACAAG 240
Db 221 AAGGCGCCAAACCCAGATTGCAAGAGCACAAAGAGCACGCCCAACCTTTCTTAAACAAG 280
QY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGCTCTGTACCGGG 300
Db 281 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGCTCTGTACCGGG 340
QY 301 AACTCGGTATTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGCC 360
Db 341 AACTCGGTATTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGCC 400
QY 361 AACCCCAAAAGGTGAGATGTCATCCAC-----GAGAGAGAGAGAGAGAGAGAG 416
Db 401 AACCCCAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
QY 417 AGAGTTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGAAATGT 476
Db 461 AGAGTTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGAAATGT 520
QY 477 ACATATTGGTGTAGGGTCCAATATTTTGGGGAGGGTGGTGAACCGGAAAGTTCCTATA 536
Db 521 ACATATTGGTGTAGGGTCCAATATTTTGGGGAGGGTGGTGAACCGGAAAGTTCCTATA 580
QY 537 TATCGAACCTCCACACATACCTCAATCCCAACCTCAATTTATTCCTTTTATTCCT 596
Db 581 TATCGAACCTCCACACATACCTCAATCCCAACCTCAATTTATTCCTTTTATTCCT 640
QY 597 CTGCTTTCTTTGCTCGAGTCTCGGGAA 625
Db 641 CTGCTTTCTTTGCTCGAGTCTCGGGAA 669
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RESULT 9
US-10-927-641-60
; Sequence 60, Application US/10927641
; Publication No. US2005024968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Bagleton, Claire
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
;
```

```

; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2096
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; US-10-927-641-60

Query Match      97.0%; Score 606.2; DB 10; Length 2096;
Best Local Similarity 98.9%; Pred. No. 7.9e-182;
Matches 622; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTTCTTCTGCTGCCATAACTGT 60
Db 41 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTTCTTCTGCTGCCATAACTGT 100
QY 61 CGAATTTCTCTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 120
Db 101 CGAATTTCTCTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 160
QY 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 180
Db 161 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 220
QY 181 AAGGCGCCAAACCCAGATTGCAAGAGCACAAAGAGCACGCCCAACCTTTCTTAAACAAG 240
Db 221 AAGGCGCCAAACCCAGATTGCAAGAGCACAAAGAGCACGCCCAACCTTTCTTAAACAAG 280
QY 241 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGCTCTGTACCGGG 300
Db 281 ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGCTCTGTACCGGG 340
QY 301 AACTCGGTATTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGCC 360
Db 341 AACTCGGTATTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGCC 400
QY 361 AACCCCAAAAGGTGAGATGTCATCCAC-----GAGAGAGAGAGAGAGAGAGAGAG 416
Db 401 AACCCCAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
QY 417 AGAGTTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGAAATGT 476
Db 461 AGAGTTTCTCTATATTTCTGTTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGAAATGT 520
QY 477 ACATATTGGTGTAGGGTCCAATATTTTGGGGAGGGTGGTGAACCGGAAAGTTCCTATA 536
Db 521 ACATATTGGTGTAGGGTCCAATATTTTGGGGAGGGTGGTGAACCGGAAAGTTCCTATA 580
QY 537 TATCGAACCTCCACACATACCTCAATCCCAACCTCAATTTATTCCTTTTATTCCT 596
Db 581 TATCGAACCTCCACACATACCTCAATCCCAACCTCAATTTATTCCTTTTATTCCT 640
QY 597 CTGCTTTCTTTGCTCGAGTCTCGGGAA 625
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; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE REFERENCE: 044463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; CURRENT FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-1

Query Match      85.4%; Score 534; DB 8; Length 534;
Best Local Similarity 100.0%; Pred. No. 4.1e-159; Indels 0; Gaps 0;
Matches 534; Conservative 0; Mismatches 0;

Qy 92 ATGCCCATGTTGCAAAAGCGCTGATATGATGATCTTGGAGTGTGGTGCATAATTTG 151
Db 1 ATGCCCATGTTGCAAAAGCGCTGATATGATGATCTTGGAGTGTGGTGCATAATTTG 60

Qy 152 CAAGCTGACGATGCGCCCTCAGGGAATTAAGGCGCCCAACCCAGATTGCAAGAGCAAA 211
Db 61 CAAGCTGACGATGCGCCCTCAGGGAATTAAGGCGCCCAACCCAGATTGCAAGAGCAAA 120

Qy 212 AGACGACGACCAACCTTTCTTAAAGAGATCATCACCAGATCGCCAGTAAGGTTAATA 271
Db 121 AGACGACGACCAACCTTTCTTAAAGAGATCATCACCAGATCGCCAGTAAGGTTAATA 180

Qy 272 TTAATTTAAACAAATAGCTTTGTACCGGGAACCTCGTATTTCTCTCACTTCCATAAACCC 331
Db 181 TTAATTTAAACAAATAGCTTTGTACCGGGAACCTCGTATTTCTCTCACTTCCATAAACCC 240

Qy 332 CTGATTAATTTGGTGGGAAGCGACAGCCAAACCCACAAAGGTGAGATGTCATCCACGA 391
Db 241 CTGATTAATTTGGTGGGAAGCGACAGCCAAACCCACAAAGGTGAGATGTCATCCACGA 300

Qy 392 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451
Db 301 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

Qy 452 AGTCAATGGCATGCGTACAGGAATGTACATATTTGGTGGTGGTGGTGGTGGTGGTGG 511
Db 361 AGTCAATGGCATGCGTACAGGAATGTACATATTTGGTGGTGGTGGTGGTGGTGGTGG 420

Qy 512 GTTGGTGAACCGGAAGTTCTTATATATCGAACTCCACCACTCACTCACTCACTCACT 571
Db 421 GTTGGTGAACCGGAAGTTCTTATATATCGAACTCCACCACTCACTCACTCACTCACT 480

Qy 572 CCACCATTTATCCGTTTATTTCTCTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 625
Db 481 CCACCATTTATCCGTTTATTTCTCTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 534

RESULT 11
US-10-703-091-2
; Sequence 2, Application US/10703091
; Publication No. US20040146904A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE REFERENCE: 044463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; CURRENT FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-2

Query Match      77.6%; Score 485; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-143; Indels 0; Gaps 0;
Matches 485; Conservative 0; Mismatches 0;

Qy 141 GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCCAACCCAGATTGC 200
Db 1 GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGGCGCCCAACCCAGATTGC 60

Qy 201 AAAGAGCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 260
Db 61 AAAGAGCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120

Qy 261 TAAGGGTAATTAATTAATTTAAACAAATAGCTCTGTACCGGGAACCTCGTATTTCTCTCACT 320
Db 121 TAAGGGTAATTAATTAATTTAAACAAATAGCTCTGTACCGGGAACCTCGTATTTCTCTCACT 180

Qy 321 TCCATAAACCCCTGATTAAATTTGGTGGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
Db 181 TCCATAAACCCCTGATTAAATTTGGTGGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

Qy 381 TCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440
Db 241 TCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

Qy 441 TCACCGGTTGGAGTCAATGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
Db 301 TCACCGGTTGGAGTCAATGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

Qy 501 TTTGCGGAGGGTGGTGAACCGCAAGTTCCCTATATATCGAACTCCACCACTACCT 560
Db 361 TTTGCGGAGGGTGGTGAACCGCAAGTTCCCTATATATCGAACTCCACCACTACCT 420

Qy 561 CACTTCAATCCCAACCAATTTACGTTTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
Db 421 CACTTCAATCCCAACCAATTTATCGTTTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Qy 621 CGGAA 625
Db 481 CGGAA 485

RESULT 12
US-10-703-091-3
; Sequence 3, Application US/10703091
; Publication No. US20040146904A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE REFERENCE: 044463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; CURRENT FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-3

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Search completed: November 1, 2006, 14:26:07
Job time : 800.58 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:48:44 ; Search time 135.549 Seconds
(without alignment)
8946.617 Million cell updates/sec

Title: US-10-702-319A-113_COPY_1019_1643

Perfect score: 625

Sequence: 1 ctgagccatttaattcagaga.....tttctcgtcagctcgcgga 625

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2461376 seqs, 970166171 residues

Total number of hits satisfying chosen parameters: ... 4922752

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

- 1: /EMC Celleria_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC Celleria_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC Celleria_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC Celleria_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC Celleria_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC Celleria_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC Celleria_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC Celleria_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.1*
- 9: /EMC Celleria_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.2*
- 10: /EMC Celleria_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	485	77.6	485	US-11-229-856-78	Sequence 78, Appl
2	306	49.0	306	US-11-229-856-80	Sequence 80, Appl
3	45	7.2	1951	US-11-404-951-96	Sequence 96, Appl
4	43	6.9	1630	US-11-397-533-107	Sequence 107, Appl
5	42.6	6.8	2168	US-10-449-902-24951	Sequence 24951, A
6	42	6.7	61009	US-10-669-920-57	Sequence 57, Appl
7	41.8	6.7	421	US-11-397-533-24	Sequence 24, Appl
8	41.4	6.6	407	US-11-397-533-106	Sequence 106, Appl
9	41.4	6.6	176594	US-10-539-228-495	Sequence 495, Appl
10	41.2	6.6	601	US-11-266-748A-215547	Sequence 215547, A
11	41	6.6	601	US-11-266-748A-237674	Sequence 237674, A
12	41	6.6	100610	US-10-540-898-585	Sequence 585, Appl
13	40.8	6.5	103464	US-10-539-228-323	Sequence 323, Appl
14	40.6	6.5	1320443	US-10-833-833-77	Sequence 77, Appl
15	40.6	6.5	2175	US-10-449-902-20101	Sequence 20101, A
16	40.4	6.5	2175	US-10-539-228-395	Sequence 395, Appl
17	40	6.4	54037	US-10-540-898-511	Sequence 511, Appl
18	39.8	6.4	58687	US-10-449-902-25043	Sequence 25043, A
19	39.6	6.3	2651	US-10-090-997-421	Sequence 421, Appl
20	39.6	6.3	4794	US-11-330-726-103	Sequence 103, Appl
21	39.6	6.3	96597	US-10-669-920-720	Sequence 720, Appl
22	39.6	6.3	124233		
23	39.6	6.3	124233		

ALIGNMENTS

RESULT 1

US-11-229-856-78

; Sequence 78, Application US/11229856

; Publication No. US20060130183A1

; GENERAL INFORMATION:

; APPLICANT: FORSTER, RICHARD L.

; APPLICANT: ROTHMANN, WILLIAM H.

; APPLICANT: CONNETT, MARIE B.

; APPLICANT: SANDERS, PAUL

; APPLICANT: ZHANG, GARY

; APPLICANT: FITZGERALD, SANDRA JOANNE

; APPLICANT: EAGLETON, CLARE

; TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT

; FILE REFERENCE: 04463-0441

; CURRENT APPLICATION NUMBER: US/11/229,856

; PRIOR FILING DATE: 2005-09-20

; PRIOR FILING DATE: 10/946,650

; PRIOR FILING DATE: 2004-09-22

; PRIOR FILING DATE: 10/946,644

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 78

; LENGTH: 485

; TYPE: DNA

; ORGANISM: Eucalyptus grandis

US-11-229-856-78

Query Match 77.6%; Score 485; DB 8; Length 485;

Best Local Similarity 100.0%; Pred. No. 4.3e-148; Indels 0; Gaps 0;

Matches 485; Conservative 0; Mismatches 0

Qy	141	GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATAATTAAGCGCCCAACCCAGATTGC	200
Db	1	GTGCAAAATTTGCAAGCTGACGATGGCCCTCAGGGAATAATTAAGCGCCCAACCCAGATTGC	60
Qy	201	AAAGAGCAAAAGACGACGCCAACCTTTCTTAAACAAGATCATACAGATCGGCCAG	260
Db	61	AAAGAGCAAAAGACGACGCCAACCTTTCTTAAACAAGATCATACAGATCGGCCAG	120
Qy	261	TAAGGGTAATTAATTAATTAACAATAGCTCTGTACCGGAACTCCGTAATTTCTCTCACT	320
Db	121	TAAGGGTAATTAATTAATTAACAATAGCTCTGTACCGGAACTCCGTAATTTCTCTCACT	180
Qy	321	TCCATAAACCCCTGATTAAATTTGTGGGAAAGACACAGCCCAACCCAGATG	380

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[illegible]

	Query Match	49.0%; Score 306; DB 8; Length 306;	
	Best Local Similarity	100.0%; Pred. NO. 1.le-89;	
Matches	Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	320	TTCCTAAACCCCTGATTAATTGGTGGGAAGCGCAGACCAACCACA AAAAGGTGCAGAT	379
DB	1	TTCCTAAACCCCTGATTAATTGGTGGGAAGCGCAGACCAACCACA AAAAGGTGCAGAT	60
QY	380	GTCATCCCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTTCTCTATAATTTCTGG	439
DB	61	GTCATCCCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTTCTCTATAATTTCTGG	120
QY	440	TTCACCGTTGGAGTCAATGGCATCGCTGCAGATGTACATATTTGGTGTAGGTTCCAATA	499
DB	121	TTCACCGTTGGAGTCAATGGCATCGCTGCAGAATGTACATATTTGGTGTAGGTTCCAATA	180
QY	500	TTTTTGGCGGAGGTGGTCAAACCGAAAAGTTTCCTATATATCGAACCTCCACCACCATACC	559
DB	181	TTTTTGGCGGAGGGTGGTGAAACGCCNAAGTTTCCTATATATCGAACCTCCACCACCATACC	240
QY	560	TCACTTCMAATCCCACCAATTAFCGGTTTTTATTTTCCTCTGCTTTCCTTTGCTCGAGTCTC	619

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Db      241 TCACITTCATCCCACTTATCGTTTATTTCCTGCTTCCTCCTGCCTGGAGATC 308
Qy      620 GCGGAA 625
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Db      301 GCGGAA 306

RESULT 3
US-11-404-951-96/c
; Sequence 96, Application US/11404951
; Publication No. US20060236421A1
; GENERAL INFORMATION:
; APPLICANT: DANG, David Vandinh
; APPLICANT: PENNELL, Roger I.
; APPLICANT: APIYA, Nestor
; TITLE OF INVENTION: Secondary Metabolite Production via Manipulation of
; TITLE OF INVENTION: Genome Methylation
; FILE REFERENCE: 18207-005001
; CURRENT APPLICATION NUMBER: US/11/404,951
; CURRENT FILING DATE: 2006-04-14
; PRIOR APPLICATION NUMBER: 60/671,209
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: 60/733,588
; PRIOR FILING DATE: 2005-11-04
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 96
; LENGTH: 1951
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1951)
; OTHER INFORMATION: Ceres PROMOTER ID no. p524d05
US-11-404-951-96

Query Match           7.2%; Score 45; DB 7; Length 1951;
Best Local Similarity 50.7%; Pred. No. 0.0006;         0; Gaps
Matches 108; Conservative 0; Mismatches 105; Indels 0;

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[illegible]

RESULT 6
US-10-669-920-57/c
; Sequence 57, Application US/10669920
; Publication No. US20060194265A1

RESULT 7
US-11-397-533-24
Sequence 24, Application US/11397533
Publication No. US20060183895A1
GENERAL INFORMATION:
APPLICANT: Blockberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c6
CURRENT APPLICATION NUMBER: US/11/397,533
CURRENT FILING DATE: 2006-04-03
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 60/143,833
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 10/174,693
PRIOR FILING DATE: 2002-06-18
NUMBER OF SEQ ID NOS: 407

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-24

Query Match      6.7%; Score 41.8; DB 7; Length 421;
Best Local Similarity 95.6%; Pred. No. 0.0031;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 ATCCGTTTTATTTCCTCCTTCTCCTTTCTCCTCGAGTCTCGCGAA 625
Db 13 AGCCGTTTTATTTCCTCCTGATTTCTTCTCCTCGAGTCTCGCGAA 57

RESULT 8
US-10-669-920-131/c
; Sequence 131, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 132942
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(132942)
; OTHER INFORMATION: n = A,T,C or G
US-10-669-920-131

Query Match      6.7%; Score 41.8; DB 6; Length 132942;
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Matches 58; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Db 111610 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGATATTGTCTATCTACCAGATACACTGT 111551

QY 450 GGAGTCAATGCCATCGTGACGAAT 474
Db 111550 GAAGTACAGAGATGTATGACCAC 111526

RESULT 9
US-11-397-533-106
; Sequence 106, Application US/11397533
; Publication No. US20060183895A1
; GENERAL INFORMATION:

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[illegible]

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	Best Local Similarity	62.1%;	Pred. No. 0.12;		
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QY	404	GAGAGAGAGAGAGAGGTTTTCTCTCTATATTCTGGTTCCCG	446		
Db	74694	GAGAGAGAGAGAGAGAGAAAGAAAACATTATGAATCCCG	74736		

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:27:09 ; Search time 17537.9 Seconds
(without alignments)
11193.945 Million cell updates/sec

Title: US-10-702-319A-113

Perfect score: 3070

Sequence: 1 agcaccatcagcaaaaaata.....acttcgaacaaaaaaa 3070

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3070	100.0	3070	2	AR360987 Sequence
2	2020.4	65.8	2096	2	BD262168 Compositi
3	2020.4	65.8	2096	2	AR360953 Sequence
4	1429.6	46.6	1630	2	BD224383 Materials
5	1429.6	46.6	1630	2	AR216433 Sequence
6	1429.6	46.6	1630	2	AR432835 Sequence
7	1314	42.8	1452	4	EGOWTRN
8	676.6	22.0	1300	4	AF006009
9	676	22.0	1876	2	AX773024
10	676	22.0	1876	4	AF220491
11	675.8	22.0	1098	2	AX773026
12	671.6	21.9	1408	4	DQ001169
13	664	21.6	1393	4	AB086104
14	663.2	21.6	1339	4	AF439740
15	651.8	21.2	1268	4	PACOMT1
16	638.2	20.8	661	2	BD262120
17	638.2	20.8	661	2	AR360905
18	631	20.6	1503	2	AR637756 Sequence

19	631	20.6	1503	4	PTLECA
20	621.6	20.2	1080	4	AF237777
21	618.2	20.1	1368	2	A26484
22	618.2	20.1	1368	2	AR076850
23	618.2	20.1	1375	4	POFOME
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25	605.4	19.7	1331	4	SSNCAFMEH
26	603.8	19.7	1370	2	AR366728
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32	577.6	18.8	1187	4	AF154918
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35	564.8	18.4	1157	4	AY081565
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ALIGNMENTS

RESULT 1
AR360987
LOCUS AR360987 3070 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 113 from patent US 6596925.
ACCESSION AR360987
VERSION AR360987.1 GI:33768497

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3070)

AUTHORS Perera,J.R., Bagleton,C. and Rice,S.J.

TITLE Compositions and methods for the modification of gene expression

JOURNAL Patent: US 6596925-A 113 22-JUN-2003;

Genesis Research & Development Corp. Ltd. and Rubicon Forests

Holdings Ltd.; Parnell;

NZX;

FEATURES Location/Qualifiers

source 1..3070

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match	100.0%;	Score 3070;	DB 2;	Length 3070;
Best Local Similarity	100.0%;	Pred. No. 0;		
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DB	1	AGCACCATCAGCAAAAAATAGATGGATAGAGTGGGACACCACTGTTTCAGTTTGATTC	60	
QY	61	CTTGAGATGACCTACAGTGTAGTGTAGTAATAGATGGGATTAATAGATTCACACGAG	120	
DB	61	CTTGAGATGACCTACAGTGTAGTGTAGTAATAGATGGGATTAATAGATTCACACGAG	120	
QY	121	GATATAAAGCTAGGAGATAGGGATCTCCCGTCTGTATGCTCGGTTAGTTGAAAAATA	180	
DB	121	GATATAAAGCTAGGAGATAGGGATCTCCCGTCTGTATGCTCGGTTAGTTGAAAAATA	180	
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 361 ACATTTCTGACTTTAAATTTGATGTAGAACCTCTTAGACTATTAATAATTTGCTGTAAT 420
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DEFINITION Composition and methods for the modification of gene expression.
ACCESSION BD262168
VERSION BD262168.1 GI:33071936
KEYWORDS JP 2002539834-A/60.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 2096)
REFERENCE
AUTHORS Perera,R., Rice,S.J. and Bagleton,C.K.
TITLE Composition and methods for the modification of gene expression
JOURNAL Patent: JP 2002539834-A 60 26-NOV-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS INDUSTRIES LTD
OS Eucalyptus grandis (flooded gum)
PN JP 2002539834-A/60
PD 26-NOV-2002
PF 24-FEB-2000 JP 2000608755
PR 25-MAR-1999 US 09/276599, 30-JUL-1999 US 60/146591 PI
RANJAN PERERA, STEPHEN J RICE, CLARE KATHERINE BAGLETON PC

C12N15/09, A01H5/00, C07K14/415, C12N5/10, C12Q1/02, C12Q1/68, PC
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;
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Qy	1915	CGGCTGTGGCGAGCTACTCCGTGCTCAGGTGACCCCTCCGCGACCTCCCGATGGCAAG	1974
Db	941	CGGCTGTGGCGAGCTACTCCGTGCTCAGGTGACCCCTCCGCGACCTCCCGATGGCAAG	1000
Qy	1975	GTGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGACGGG	2034
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Db	1241	GATCACTCCACCATTAATGAGAAGATATCTGMAACATACAAAGGGCTTCGAGGGCCCT	1300
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Qy	2575	TGTACCCAGACACGACCTTAGCGACCAAGATGTGATCCATCGACTGCATCATGTTGG	2634
Db	1601	TGTACCCAGACACGACCTTAGCGACCAAGATGTGATCCATCGACTGCATCATGTTGG	1660
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Qy	2995	ATGGATGCGCTGAATGATGAAATTTGTGATATTTCTCTTTTTCAGTAAATCACTT	3054
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LOCUS	AR360953	2096 bp	DNA
DEFINITION	Sequence 60 from patent US 6596925.	linear	PAT 17-AUG-2003
ACCESSION	AR360953		
VERSION	AR360953.1	GI:33768463	
KEYWORDS	Unknown.		
SOURCE	ORGANISM		
REFERENCE	1 (bases 1 to 2096)		
AUTHORS	Perera, J.R., Bagleton, C. and Rice, S.J.		
TITLE	Compositions and methods for the modification of gene expression		
JOURNAL	Patent: US 6596925-A 60 22-JUL-2003;		
	Genesis Research & Development Corp. Ltd. and Rubicon Forests		
	Holdings Ltd.; Parnell;		
	NZX;		
ORIGIN	Query Match	65.8%;	Score 2020.4; DB 2; Length 2096;
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	Matches 2041;	Conservative 0;	Mismatches 11; Indels 4; Gaps 1;
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Qy	1139	GTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCTGACGATGCCCTCAGGGAATTT	1198
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Qy	1319	AACCTCGGATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAACGACGACC	1378
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Db	461	AGAGTTTCTCTCTCTATATTTCTGGTTTCCCGTTGGAGTCAATGGCATGCGTGACGAATGT	520

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VERSION AR432835.1 GI:40195438
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Blokeberg, L.N. and Havukkala, I.
TITLE Pinus radiata nucleic acids encoding O-methyl transferase and methods for the modification of plant lignin content therewith
JOURNAL Patent: US 6653528-A 107 25-NOV-2003; Genesis Research & Development Corporation Limited and Rubican Forests Industries Limited; Parnell; NZX;

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DB 181 AGGCGCCCATCGAGCTCGACCTCTCGAGATCATGCGCAAGGACGCGCGCGCTTC 240
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• RESULT 7

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Myrtales; Onagraceae; Clarkia.
REFERENCE
AUTHORS
TITLE
Wang, J. and Pichersky, E.
Nucleotide Sequence of S-Adenosyl-L-Methionine:Caffeic Acid
3-O-Methyltransferase from Clarkia breweri (Accession No. AF006009)
(PGR97-104)
JOURNAL
Plant Physiol. 114, 1567 (1997)
REFERENCE
AUTHORS
TITLE
Wang, J. and Pichersky, E.
Characterization of (iso)eugeneol O-methyltransferase Involved in
Floral Scent Production in Clarkia breweri
Unpublished
JOURNAL
3 (bases 1 to 1300)
AUTHORS
Wang, J. and Pichersky, E.
TITLE
Direct Submission
JOURNAL
Submitted (29-MAY-1997) Biology, University of Michigan, 830 North
University Avenue, Ann Arbor, MI 48109, USA

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VERSION
KEYWORDS
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REFERENCE
1 Schwab, W., Kaldenhoff, R. and Wein, M.
Multifunctional caffeic acid o-methyltransferase
Patent: WO 03046163-A 1 05-JUN-2003;
Bayerische Julius-Maximilians-Universitaet Wuerzburg (DE)

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Query Match 22.0%; Score 676; DB 2; Length 1876;
Best Local Similarity 77.0%; Pred. No. 5.9e-172;
Matches 850; Conservative 0; Mismatches 250; Indels 4; Gaps 2;

Qy 1666 AGAATGGGTTCCGACGGGCTCCGAGACCCAGATGACCCGACCCCAAGTCTCGGACGACGAG 1725

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Qy 1726 GCGAACCTCTTCGCCATGACAGCTGGCGAGCGCTCCGTCCTCCCATGCTCTTAAAGGCC 1785

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Qy 1786 GCCATCGAGATCGACTCTCGAGATCATGGCAAGGACCGGCGCGGCTCTTCTCTCC 1845

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Db 280 CCTAGTGATCTAGCTCTCAGCTTCGACCAAGAACCCCGAAGCTCCGGTCATGCTCCAC 339

Qy 1906 CGGATCTTCGGCTGCTGGCAGCTACTCCGTCGTCAGTGCACCTCCGACCTCCGACCTCC 1965

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Db 460 GAAGATGGGCTCTCTATTGCTCTCTGCTCTCTGATGACCAAGGACCAAGGCTCTTCA 519

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Db 580 GGCATGACTGCAATTTGATTTACCATGCAAGGCTGATTTCAACAGGCTCTTCAACAG 639

Qy 2206 GGAATGCTGATCACTCCACCATTAATGAAAGATTAATGAAAGATTAATGAAAGATTA 2265

Db 640 GGAATGCTGATCACTCCACCATTAATGAAAGATTAATGAAAGATTAATGAAAGATTA 699

Qy 2266 GAGGCGCTCGAGACCGTGTGTCGATGTCGAGGCGGCACTGGGCGCGCTGCTGCTGCTG 2325

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 QY 2625 ATCATGTGGCCCAACCCAGCGGAAAGAGAGGACACAGAGGATTCGAGGCAATG 2684
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RESULT 10

AF220491 LOCUS 1876 bp mRNA linear PLN 27-JAN-2000
 DEFINITION Fragaria x ananassa O-methyltransferase (omt1) mRNA, complete cds.
 ACCESSION AF220491
 VERSION AF220491.1 GI:6760442
 KEYWORDS
 SOURCE
 ORGANISM
 Fragaria x ananassa
 Fragaria x ananassa
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Fragaria.
 1 (bases 1 to 1876)
 Kaldenhoff, R., Wein, M. and Schwab, W.
 Isolation and characterization of a O-methyltransferase from
 strawberry
 Unpublished
 2 (bases 1 to 1876)
 Kaldenhoff, R., Wein, M. and Schwab, W.
 Direct Submission
 Submitted (03-JAN-2000) Botanik I, Julius-von-Sachs-Institut fuer
 Blowsensschaften, Julius-von-Sachs-Platz 2, Wuerzburg 97082,
 Germany

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ORIGIN

Query Match 22.0%; Score 676; DB 4; Length 1876;
 Best Local Similarity 77.0%; Pred. No. 5.9e-172;
 Matches 850; Conservative 0; Mismatches 250; Indels 4; Gaps 2;
 QY 1666 AGAATGGTTCGACCGGCTCCGAGACCCAGATGACCCCGACCCAAAGTCTCGAGCGAGAG 1725
 DB 103 AAAATGGTTCACCGG--CGAGACTCAGATGACTCCGACCCCATGTCTCCGACGAGAA 159
 QY 1726' GCCAACTCTTCGCCATGAGCTGGCGAGCGCTCCGTCCTCCCATGGTCTTAAAGGCC 1785
 DB 160 GCCAACTCTTCGCCATGCAACTCGCAGCGCTCCGTCCTCCCATGGTCTTCAAGGCC 219
 QY 1786 GCCATCGAGATCGACCTCTCGAGATCATGCGCAAGAGACGGGCGCGGCTTCCTCTCC 1845
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 DB 460 GAAGATGGCGTCTCTATTGCTGCTCTCTGCTCATGAACCCAGGACAAAGTCTCTCGTCGAG 519
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Db	1000	ATTCTTCCTGTTGCCACACAGACTAGCTTGCCACCAAGGAGTTGTCCATATGGATGTG	1059
QY	2625	ATCATGTTGGCCACAAACCCAGCGGGAAAGAGAGGACACAGAGGAGTTGAGGCATTG	2684
Db	1060	ATCATGTTGGCGCACAACTCGCGCAAGAGAGAGCGGACGAGAAATTTGAAGCCCTG	1119
QY	2685	GCCAAAGGGCCGGANTTCAGGGCTTCCAAAGTCATGTGCTGGCTTTTCGGCACTCACGTC	2744
Db	1120	GCTAAGGGTTCTGGATTCCAAAGGCATTCGCGTCTGCTGTGATGCTTTCAACACCTATGTC	1179
QY	2745	ATGGAGTTCTGAAGACCGCTTGA	2768
Db	1180	ATTGAGTTCTTAAGAAGATCTGA	1203
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LOCUS	AX773026	Sequence 3 from Patent WO03046163.	
ACCESSION	AX773026		
VERSION	AX773026.1	GI:32485194	
KEYWORDS			
SOURCE		Fragaria x ananassa	
ORGANISM		Fragaria x ananassa	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	
		rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Fragaria.	
REFERENCE			
AUTHORS		Schwab, W., Kaldenhoff, R. and Wein, M.	
TITLE		Multifunctional caffeic acid o-methyltransferase	
JOURNAL		Patent: WO 03046163-A 3 05-JUN-2003;	
		Bayerische Julius-Maximilians-Universitaet Wuerzburg (DE)	
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QY	1739	CCATGACGTGGCGAGCGCTCGGTCTCCCATGGTCTTAAGCGCGCCATCGAGATCG	1798
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QY	1799	ACCTCTCGAGATCATGCGGACGAGCGCGCGGCGGTTCCTCTCCACGGGGAAATCG	1858
Db	128	ACCTCTTGGAGATCATGCGGACGAGCGCGGACCCGGCTCTTCTCTCCCTAGTGATCTAG	187
QY	1859	CGGCACAGCTCCCGAACCCAGAACCCCGAGGACCCCGTCAATGCTGACCGGATCTCCGCG	1918
Db	188	CCTCTCAGCTTCGACCAAGAACCCCGAGTCCGGTCAATGCTCGACCGTATGCTTCGCG	247
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Db	248	TTCTGGCCAGCTACTCCATTTCTAACTGCTCATGTGGTAGCTTCGCGCGGCAAGTTG	307
QY	1979	AGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTTGGTCAAGAACGAGGACGGGTTCT	2038
Db	308	AGAGGCTCTACTGTTTGGACCTGTGTGTAAGTTCTTGACCAAGAAATGAAGATGGCGTCT	367
QY	2039	CCATGCGCGCATCTCAATTTGATGTAACAGGACCAAAATCTCATGGAAGCTGTATTACC	2098
Db	368	CTATTGCTGCTCTCTGCGCTCATGAACCAAGGACCAAGGTCCTCGTCGAGAGCTGTATCAT	427

QY	2099	TGAAGATGCGGTCTCTGAAGCGGAATCCCATTTCAACAAGCGGTACGGGATGACCGGT	2158
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QY	2159	TCCAGTATCATGGCACCGCCGCAATTCACAAGATCTTTAAACCGGGAATGCTGATC	2218
Db	488	TTGATTTACCATGGAATGACCTAGATTCAAACAGGTCTTCAACAGGGAATGGCTGACC	547
QY	2219	ACTCCACCAATTACTGAAGAAGATACCTGAACACATACAAGGGCTTCGAGGGCCTCGAGA	2278
Db	548	ACTCCACCAATTACTGAAGAAGAAATCTCTTGAGACTTACAAAGGCTTCGAGGGCCTCAAT	607
QY	2279	CCGTGTCGATGTCGAGCGGCACCTGGGGCCGCTCAGCATGATGCTGTGTCGCAATACC	2338
Db	608	CCATCGTTGATGTCGGTGGCGCACCGAGCTGTGGTGAACATGATCGTTCCAGATACC	667
QY	2339	CATCAATGAAGGATCAACTTCGAC - CGCCCCAAGGATTGAAGACGCCCAACCCCTTC	2397
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LOCUS	DQ001169	Acacia mangium x Acacia auriculiformis caffeic acid	
DEFINITION		O-methyltransferase mRNA, complete cds.	
ACCESSION	DQ001169		
VERSION	DQ001169.1	GI:68159361	
KEYWORDS			
SOURCE		Acacia mangium x Acacia auriculiformis	
ORGANISM		Acacia mangium x Acacia auriculiformis	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	
		rosids; eurosids 1; Fabales; Fabaceae; Mimosoideae; Acacieae;	
		Acacia.	
REFERENCE			
AUTHORS		1 (bases 1 to 1408)	
TITLE		Sukganah, A., Wickneswari, R. and Choong, C.Y.	
		Full length of Acacia mangium x Acacia auriculiformis hybrid cDNA	
		clones encoding cinnamoyl-CoA reductase (CCR) and caffeic acid	
		O-methyltransferase (COMT)	
JOURNAL		Unpublished	
REFERENCE			
AUTHORS		2 (bases 1 to 1408)	
TITLE		Choong, C.Y., Wickneswari, R. and Sukganah, A.	
		Direct Submission	
JOURNAL		Submitted (07-APR-2005) School of Environmental and Natural	

Resource Sciences, Universiti Kebangsaan Malaysia, Faculty of Science and Technology, Bangi, Selangor 43600, Malaysia	
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QY	1919 TGCTGCGCAGCTACTCGTCTCACGTGCACCTCCGCGACCTCCCGCATGGCAAGTCG 1978
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QY	1979 AGCGGCTCTACGGCTTAGCGCGCGGTGTGCAAGTTCTTTGGTCAAGAACGAGACGGGGTCT 2038
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QY	2279 CCGTGTTCGATGTCGAGGCGGCACATGGGGCGGTGCTCAGCATGATGCTTGCCAAATACC 2338
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QY	2339 CATCAATGAAGGATCACTTCGACC-GCCCCAAGGATTGAAGACGCCCCACCCCTTC 2397
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QY	2698 GATTTGAGGGCTTCCAGTCAATGCTGCTGCTTTCGGCACTCACGTCATGGAGTTCTGA 2757
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QY	2758 AGACCGCTTGAATCTGCTCTCTGCTGCTGATGTTTC 2791
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Best Local Similarity		74.8%; Pred. No. 1.1e-168;	
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Qy	1726	GCGAATCTCTTCGCCATGCGAGCTGGCGAGCGCTCGTCTGCCATGCTCCCAATGCTCTTAAAGGCC	1785
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Db	313	CGGATGCTTCGCTTCTGGCCAGCTACTCCATTCTAACCTACTCTCTTGCGTACACTCCG	372
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Db	373	GACGCAAGTTGAGAGGCTCTACGGTTTGGGACCTGTGTGTAATCTTTGACCAAGAAC	432
Qy	2026	GAGGACGGGCTCCATCGCGGCACTCACTTGATGAACAGGACAAATCTCTCATGGAA	2085
Db	433	GAAGATGGTGCTCCATGTCGCTCTCTGCTCATGAACCAAGAGGCTCTCGTCGAG	492
Qy	2086	AGCTGGTATTACCTGAAGAATGCGGCTCTTGAAGCGGAATCCCATTCACACGGGCTAC	2145
Db	493	AGCTGTATCATCTAAAGGATGCACTCTTGATGGTGGGATTCATTTAAACAGGCGCTAT	552
Qy	2146	GGGATGACGGGTTGAGTATCATGTCACGACCGGATTCACCAAGATCTTTAAACGG	2205
Db	553	GGAATGACTGCTTTGATTTACCATGGAATGACCTTAGATTCAACAGGCTCTCAACAAG	612
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Db	673	GAGGGCTCACATCCATCCATGTTATGTCGAGGCGGCACTGGGCGCGTCTCAGCATGATC	732
Qy	2326	GTTCGCAAAATACCATCAATGAAGGATCACTTCGAC - CGCCCAACGAGATGAAGAC	2384
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Db	793	GCTCTCAATATCTCTGGTGTCAACATGTTGGAGGGGACATGTTTGTAGTGTACCGAA	852
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RCH439740			
LOCUS			
DEFINITION			
Rosa chinensis mRNA for caffeic acid O-methyltransferase (comt1 gene).			
ACCESSION			
AJ439740.1 GI:27527919			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.			
REFERENCE			
AUTHORS			
1 (bases 1 to 1339)			
Scalliet,G., Journot,N., Jullien,P.F., Baudino,S., Magnard,J.L., Channelliere,S., Verne,P., Dumas,C., Bendahmane,M., Cock,M. and Hugueney,P.			
Biosynthesis of the major scent components 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene by novel rose O-methyltransferases			
FEBS Lett. 523 (1-3), 113-118 (2002)			
PUBMED			
12123815			
REFERENCE			
2 (bases 1 to 1339)			
Cock,J. Mark.			
Direct Submission			
TITLE			
Submitted (25-MAR-2002) RDP, ENSL, 46, allée d'Italie, Lyon cedex 07 69364, France			
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ORIGIN

Query Match	21.6%;	Score 663.2;	DB 4;	Length 1339;	
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Qy	2266	GAGGCGCTCGAGACGCTGGTGTGATGTCGAGGCGGACTGGGCGGCTCGAGATGATC	2325		
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Qy	2326	GTTCGCAAAATACCATCAATGAAGAGGATCACTTTCGAC--CGCCCCAACGATTTGAAGAC	2384		
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Qy	2385	GCCCCACCCCTCTCTGTTGTCAAGCAGCTCGAGGCGGACATGTTGTCGAGGTTCCAAAG	2444		
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Qy	2625	ATCATGTTGGCCCAACACCCAGCGGAAAGAGAGACAGACAGAGGAGTTCGAGGCATTG	2684		
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Qy	2685	GCCAAAGGGCCCGGATTTTCAGGCTTTCCAAAGTCATGTCGCTTTCGCGCATTCAGTC	2744		
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RESULT 15

PACOMT1 1268 bp mRNA linear PLN 18-APR-2005
DEFINITION P.amygdalus mRNA for caffeic O-methyltransferase.

ACCESSION X83217
VERSION X83217.1 GI:602587
KEYWORDS caffeic acid O-methyltransferase.
SOURCE Prunus dulcis (almond)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

REFERENCE

1 Garcia-Mas,J., Messegue,R., Arus,P. and Puigdomenech,P.
The Electronic Plant Gene Register
Plant Physiol. 108 (3), 1341-1343 (1995)
1228545

REFERENCE

2 (bases 1 to 1268)
Puigdomenech,P.
Direct Submission
Submitted (05-DEC-1994) P. Puigdomenech, Dept. Genetica Molecular
CID-CSIC, Jordi Girona 18-26, 08034 Barcelona, SPAIN
Location/Qualifiers

FEATURES

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gene

CDS

ORIGIN

Query Match 21.2%; Score 651.8; DB 4; Length 1268;
Best Local Similarity 75.7%; Pred. No. 2.4e-165;
Matches 820; Conservative 0; Mismatches 262; Indels 1; Gaps 1;

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Db 1113 TGA 1115

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 Job time : 17542.9 secs

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 1807 GAGATCATGGCCAAAGAGCGGCGCGGTCCTCTCCACGGGGGAAATCGCGGCACAG 1866
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 2766 TGA 2768
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2006, 23:17:03 ; Search time 1298.78 Seconds
(without alignments)
16480.672 Million cell updates/sec

Title: US-10-702-319A-113

Perfect score: 3070

Sequence: 1 agcaccatcagcaaaaata.....acttcgaacaaaaaaaaa 3070

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Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
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Maximum Match 100%
Listing first 45 summaries

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- 12: geneseqn2004as:
- 13: geneseqn2004bs:
- 14: geneseqn2005a:
- 15: geneseqn2005b:
- 16: geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
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2	3070	100.0	3070	10	ADH75529	Adh75529 Eucalyptu
3	3070	100.0	3070	14	ADW80563	Adw80563 E. grandi
4	2020.4	65.8	2096	3	AAc62810	Aac62810 O-methyl
5	2020.4	65.8	2096	6	ABK17075	ABK17075 Eucalyptu
6	2020.4	65.8	2096	10	ADH75476	Adh75476 Eucalyptu
7	2020.4	65.8	2096	14	ADW80510	Adw80510 E. grandi
8	1429.6	46.6	1630	3	AAa68014	Aaa68014 Eucalyptu
9	1429.6	46.6	1630	10	ADd41764	Add41764 O-methyl
10	676	22.0	1876	9	AAI60735	Aai60735 Strawberry
11	638.2	20.8	661	3	AAc62762	Aac62762 O-methyl
12	638.2	20.8	661	6	ABK17027	ABK17027 Eucalyptu
13	638.2	20.8	661	10	ADH75428	Adh75428 Eucalyptu
14	638.2	20.8	661	14	ADW80462	Adw80462 E. grandi
15	631	20.6	1501	6	ABK48067	ABK48067 CDNA enco
16	631	20.6	1503	10	ADD93899	Add93899 Quaking a
17	629.4	20.5	1503	2	AAx26295	Aax26295 Aspen bis
18	618.2	20.1	1368	2	AAQ38448	Aaq38448 pPLC4 cod

CC regulated promoters such as xylogenesis-specific promoters. The promoter
CC polypeptides and their related polynucleotides are useful in the
CC production of genetic constructs, used for modifying gene expression in a
CC target organism, in particular a plant. The method is useful for
CC modifying expression of a polynucleotide that comprises an intron
CC sequence, through removal of the intron sequence. The method is useful
CC for modifying growth and development of plants, and cellular responses to
CC external stimulus, such as environmental factors and disease pathogens.
CC The sequences are useful in genome and physical mapping, in positional
CC cloning of genes, in various assays to determine biological activity, to
CC raise antibodies, to isolate corresponding interacting proteins and other
CC compounds, and to quantitatively determine levels of interacting proteins
CC or other compounds. Sequences AK17016-ABK17125 represent Pinus radiata
CC and Eucalyptus grandis polynucleotides and PCR primers used in the method
CC of the invention
XX
SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;
Query Match 100.0%; Score 3070; DB 6; Length 3070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1621 TCCTTTGCTCGAGTCTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTTCGACC 1680
QY 1681 GGCTCCGAGACCCAGATGACCCCGACCCAGATCTCGGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 GGCTCCGAGACCCAGATGACCCCGACCCAGATCTCGGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 ATGAGCTGGGAGCGCTCGGTCTCCCATGCTTAAAGCCCGCAATCGAGATCGAC 1800
DB 1741 ATGAGCTGGGAGCGCTCGGTCTCCCATGCTTAAAGCCCGCAATCGAGATCGAC 1800
QY 1801 CTCCTTCGAGATCATGGCCCAAGGACGCGGCGCGGCTCTCTCCACGGGGGAAATCGCG 1860
DB 1801 CTCCTTCGAGATCATGGCCCAAGGACGCGGCGCGGCTCTCTCCACGGGGGAAATCGCG 1860

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Qy 1861 GCACAGCTCCCGACCCGAGGACACCCGTCATGCTCGACCGGATCTTCGGCTG 1920
Db 1861 GCACAGCTCCCGACCCGAGGACACCCGTCATGCTCGACCGGATCTTCGGCTG 1920
Qy 1921 CTGCCAGCTACTCCGTGCTCAGTGCACCTCCGCGACCTCCCGATGGCAAGTTCGAG 1980
Db 1921 CTGCCAGCTACTCCGTGCTCAGTGCACCTCCGCGACCTCCCGATGGCAAGTTCGAG 1980
Qy 1981 CGGCTCTACGGCTTAGCGCGGTGCAAGTCTTGGTCAAGAACGAGGACGGGTCTCC 2040
Db 1981 CGGCTCTACGGCTTAGCGCGGTGCAAGTCTTGGTCAAGAACGAGGACGGGTCTCC 2040
Qy 2041 ATCCCGCAGCTCAACTTTGATGAACAGGACCAAAATCTCATGGAAGCTGTATTACCTG 2100
Db 2041 ATCCCGCAGCTCAACTTTGATGAACAGGACCAAAATCTCATGGAAGCTGTATTACCTG 2100
Qy 2101 AAAGATCGGTCTTTGAAGCGGGAATCCCATTTCAACAAAGGCTACGGGATGACCGGCTC 2160
Db 2101 AAAGATCGGTCTTTGAAGCGGGAATCCCATTTCAACAAAGGCTACGGGATGACCGGCTC 2160
Qy 2161 GAGTATCATGCGACCGGACCTCAACAAAGATCTTAAACCGGGGAATGCTGTATCAC 2220
Db 2161 GAGTATCATGCGACCGGACCTCAACAAAGATCTTAAACCGGGGAATGCTGTATCAC 2220
Qy 2221 TCCACCATTTACTGAAGAAGATCTCGAAACATACAAAGGCTTCGAGGGCTTCGAGACC 2280
Db 2221 TCCACCATTTACTGAAGAAGATCTCGAAACATACAAAGGCTTCGAGGGCTTCGAGACC 2280
Qy 2281 GTGTGCGATGTCGAGCGGCACTGGGGCCGTGCTCAGCATGATCGTTGCCAAATACCCA 2340
Db 2281 GTGTGCGATGTCGAGCGGCACTGGGGCCGTGCTCAGCATGATCGTTGCCAAATACCCA 2340
Qy 2341 TCAATGAAGGGAATCAACTTCGACCGGCCCCAACGGATTGAGACGCCCCCTTCCTG 2400
Db 2341 TCAATGAAGGGAATCAACTTCGACCGGCCCCAACGGATTGAGACGCCCCCTTCCTG 2400
Qy 2401 GTGTCAAGCAGCTCGAGGGGACATGTTGTCGACGCTTCCAAAGGGAGATGCCATTTTCA 2460
Db 2401 GTGTCAAGCAGCTCGAGGGGACATGTTGTCGACGCTTCCAAAGGGAGATGCCATTTTCA 2460
Qy 2461 TGAAGTGGATATGCCATGACTGAGTGAAGCAACATTCGCGAAGTTCCTCAAGAACTGCT 2520
Db 2461 TGAAGTGGATATGCCATGACTGAGTGAAGCAACATTCGCGAAGTTCCTCAAGAACTGCT 2520
Qy 2521 ACGATGCGCTTCCCAACATGAAGGATGATCGTTCGAGAGTGCCTCCCTGTGACC 2580
Db 2521 ACGATGCGCTTCCCAACATGAAGGATGATCGTTCGAGAGTGCCTCCCTGTGACC 2580
Qy 2581 CAGACAGAGCTAGCGACCAAGAAATGTGATCCACATCGACTCATGTTGGCCCA 2640
Db 2581 CAGACAGAGCTAGCGACCAAGAAATGTGATCCACATCGACTCATGTTGGCCCA 2640
Qy 2641 ACCAGGCGGGAAGAGAGGACACAGAGGAGTTCGAGGCAATTCGCCAAAGGGCCGGAT 2700
Db 2641 ACCAGGCGGGAAGAGAGGACACAGAGGAGTTCGAGGCAATTCGCCAAAGGGCCGGAT 2700
Qy 2701 TTCAGGCTTCCAAAGTCAATGCTGCGCTTCGCGACTCAGCTCATGAGTTCCTGAAGA 2760
Db 2701 TTCAGGCTTCCAAAGTCAATGCTGCGCTTCGCGACTCAGCTCATGAGTTCCTGAAGA 2760
Qy 2761 CCGCTTGATCTGCTCCTCTGTTGGTGTGTTTCATGTTCTTGGATTGAAAGTTCGTGAAG 2820
Db 2761 CCGCTTGATCTGCTCCTCTGTTGGTGTGTTTCATGTTCTTGGATTGAAAGTTCGTGAAG 2820
Qy 2821 GAGCCCTTTTCTCAGTGTGCTTCGCGATACCAAGTTCCTCTCATAAAGGAAACAATA 2880
Db 2821 GAGCCCTTTTCTCAGTGTGCTTCGCGATACCAAGTTCCTCTCATAAAGGAAACAATA 2880
Qy 2881 AGAAGCGACTGTATGATGGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAA 2940
Db 2881 AGAAGCGACTGTATGATGGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAA 2940
Qy 2941 AGTTTGTAGTCTCTGTCATCTGATTTTCACAGAATGTGTAAACGAAACGGCGTATGAT 3000
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Db 2941 AGTTTGTAGTCTCTGTCATCTGATTTACAGAATGTGTAAACGAAACGGCGTATGAT 3000
Qy 3001 GTCCCTGAATGATGGAATGTGATATCTGCTCTTTTTCAGTAAATCACTTCGAACA 3060
Db 3001 GTCCCTGAATGATGGAATGTGATATCTGCTCTTTTTCAGTAAATCACTTCGAACA 3060
Qy 3061 AAAAAA 3070
Db 3061 AAAAAA 3070

RESULT 2
ADH75529
ID ADH75529 standard; DNA; 3070 BP.
XX
AC ADH75529;
XX
DT 22-APR-2004 (first entry)
XX
DE Eucalyptus grandis superubiquitin related sequence #49.
XX
ds; Monterey pine; superubiquitin; promoter; gene expression;
transgenic plant.
XX
OS Eucalyptus grandis.
XX
PN WC2003093475-A1.
XX
PD 13-NOV-2003.
XX
PP 30-APR-2003; 2003WO-NZ000076.
XX
PR 30-APR-2002; 2002US-00137036.
XX
(GENE-) GENESIS RES & DEV CORP LTD.
(RUBI-) RUBICON FORESTS HOLDINGS LTD.
PA
PI Rice SJ, Wood M, Eagleton CK, Visser ES, Perera R;
XX
WPI; 2003-903678/82.
XX
New polynucleotide of the superubiquitin promoter from Pinus radiata,
useful in modifying gene expression in a target organism.
XX
Disclosure; SEQ ID NO 113; 123bp; English.
XX
The invention relates to a new isolated polynucleotide comprising the
Pinus radiata (Monterey pine) superubiquitin promoter sequence, its
complement, reverse complement, reverse sequence or inverted repeat or a
sequence having at least 40, 60, 75 or 90% identity with the promoter.
The polynucleotide is useful in modifying gene expression in a target
organism, especially in transgenic plants. This sequence corresponds to a
superubiquitin promoter related sequence.
XX
SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 3070; DB 10; Length 3070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCACCATCAGCAAAAAATAGATGGGATAGAGTGGGACACACCTGTTTCAGTTTGATTCC 60
Db 1 AGCACCATCAGCAAAAAATAGATGGGATAGAGTGGGACACACCTGTTTCAGTTTGATTCC 60
Qy 61 CTTGAGATGACCTACAGTGTAGTCTGATGAATAAGATGGGAAATAGATTCCACGAGG 120
Db 61 CTTGAGATGACCTACAGTGTAGTCTGATGAATAAGATGGGAAATAGATTCCACGAGG 120
Qy 121 GATAAAAAAGGTAGGGAGATAGGGGATCTCCCGTCTGATGCCCTCGGGTAGGTTGAAATA 180
Db 121 GATAAAAAAGGTAGGGAGATAGGGGATCTCCCGTCTGATGCCCTCGGGTAGGTTGAAATA 180
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181	AGGCAAAAGTTCGCGCTTGAATTTGACAGCAAAAGACACCGTGTGATGCAATTCATGAT	240	1261	CATCCAGATCGCGCCAGTAAGGGTAATATATTAATTTAACTAATAGCTCTTTGTACCGGAA	1320
181	AGGCAAAAGTTCGCGCTTGAATTTGACAGCAAAAGACACCGTGTGATGCAATTCATGAT	240	Qy		
241	CCATTGTACCCATGTAGGTGAATCCTAGAGTGAAGAGATAGTCTCTTTAGAAAGTCCCA	300	Db		
241	CCATTGTACCCATGTAGGTGAATCCTAGAGTGAAGAGATAGTCTCTTTAGAAAGTCCCA	300	Qy		
301	TTCCACCCCTATCATAGCTTTCTGCAATCCATTTTAAAGAACAGCCCGGAATGACGTCT	360	Db		
301	TTCCACCCCTATCATAGCTTTCTGCAATCCATTTTAAAGAACAGCCCGGAATGACGTCT	360	Qy		
361	ACATTTTCTGACCTTAAATGTAGTGAACCTCTTAGACTATTAATAATATCTCTGGAAT	420	Db		
361	ACATTTTCTGACCTTAAATGTAGTGAACCTCTTAGACTATTAATAATATCTCTGGAAT	420	Qy		
421	TTGACGTCCATGACAAAGCGCTTTGCTCTCGAAATAAAGTACAGGACAGGTAGGCTT	480	Db		
421	TTGACGTCCATGACAAAGCGCTTTGCTCTCGAAATAAAGTACAGGACAGGTAGGCTT	480	Qy		
481	AAGCGGATTTGGCAATCACTTAGAATGATCTTATATGCGTAAATTAACAAGACTGATGG	540	Db		
481	AAGCGGATTTGGCAATCACTTAGAATGATCTTATATGCGTAAATTAACAAGACTGATGG	540	Qy		
541	GGGTTATTTGGTCTAAATTTGTCAGGATGTTGATGCTTGGGTATTTAGGGCTATGATGTT	600	Db		
541	GGGTTATTTGGTCTAAATTTGTCAGGATGTTGATGCTTGGGTATTTAGGGCTATGATGTT	600	Qy		
601	ATTGAGATTCGGTGTGATGATGCCAGAAATTAATAAAGTGTGCTGATGAGATAGTTC	660	Db		
601	ATTGAGATTCGGTGTGATGATGCCAGAAATTAATAAAGTGTGCTGATGAGATAGTTC	660	Qy		
661	ATCTCGGAGTATATCCCAATGATGCTGTGAGAGTCCATTTCAAGCCATCTGACCGGG	720	Db		
661	ATCTCGGAGTATATCCCAATGATGCTGTGAGAGTCCATTTCAAGCCATCTGACCGGG	720	Qy		
721	GGCTTGTGTAAGTCCAGTTGGAAAGTAGCCCTCTCTAACTTCTTCTTGGTAAAGGAGC	780	Db		
721	GGCTTGTGTAAGTCCAGTTGGAAAGTAGCCCTCTCTAACTTCTTCTTGGTAAAGGAGC	780	Qy		
781	TATTAGGGACATATTCATCTCATTTAGTAACTTAAAGACACTGGTTTCAAGATAGGCAA	840	Db		
781	TATTAGGGACATATTCATCTCATTTAGTAACTTAAAGACACTGGTTTCAAGATAGGCAA	840	Qy		
841	GTAGTCTCGATGTCACACTGTCTGAAATAGATGTGAAAGTAACTTATCTGCTCATCTT	900	Db		
841	GTAGTCTCGATGTCACACTGTCTGAAATAGATGTGAAAGTAACTTATCTGCTCATCTT	900	Qy		
901	CAAAATTTCAAGATTCGGCAACCCAGCTTGAATGTCATCTGCAACATCTAATCTTGT	960	Db		
901	CAAAATTTCAAGATTCGGCAACCCAGCTTGAATGTCATCTGCAACATCTAATCTTGT	960	Qy		
961	TCGTTGTGTTGTATGATGTTGTCATGAAATAAATTTAGTATTTTGTCTCCCGCAGCT	1020	Db		
961	TCGTTGTGTTGTATGATGTTGTCATGAAATAAATTTAGTATTTTGTCTCCCGCAGCT	1020	Qy		
1021	GAGCAATTTAATTCGAGACACATTCGCCAAAATTTATCTTCTGTCGCAATCTGCTG	1080	Db		
1021	GAGCAATTTAATTCGAGACACATTCGCCAAAATTTATCTTCTGTCGCAATCTGCTG	1080	Qy		
1081	AATTTTCTCTTTAGTAAAGTAAACCAATGATGCGCCATGTTGACAAATAAGGCTGATAGT	1140	Db		
1081	AATTTTCTCTTTAGTAAAGTAAACCAATGATGCGCCATGTTGACAAATAAGGCTGATAGT	1140	Qy		
1141	ATGATCTTTGGAGTGTGTTGGTCCAAATTTGCAAGTGAAGTGAAGGCTGATAGT	1200	Db		
1141	ATGATCTTTGGAGTGTGTTGGTCCAAATTTGCAAGTGAAGTGAAGGCTGATAGT	1200	Qy		
1201	GGGGCAACCCAGATTTGAAAGACACAAAGACACAGACCCCAACTTCTTCTTAAACAGAT	1260	Db		
1201	GGGGCAACCCAGATTTGAAAGACACAAAGACACAGACCCCAACTTCTTCTTAAACAGAT	1260	Qy		
1261	CATCACAGATCGGCGCAGTAAGGGTAATATTAATTTAACTAATAGCTCTTTGTACCGGAA	1320	Qy		

Db 2341 TCAATGAAGGGATCAACTTCGACGCCCAACGGAATTGAAGACGCCCAACCCCTTCCTG 2400
Qy 2401 GTGTCAGACAGCTCGGAGGCGACATGTCGTCAGCGTTCCAAAGGGAGATGCCATTTTCA 2460
Db 2401 GTGTCAGACAGCTCGGAGGCGACATGTCGTCAGCGTTCCAAAGGGAGATGCCATTTTCA 2460
Qy 2461 TGAAGTGGATATGCCATGACTGAGTGCAGACCAATTCGCGGAAGTTCTCTCAAGAACTGCT 2520
Db 2461 TGAAGTGGATATGCCATGACTGAGTGCAGACCAATTCGCGGAAGTTCTCTCAAGAACTGCT 2520
Qy 2521 ACAGTGGCTTCCCAACAATGGAAGTGATGCTGTCAGAGTGGCTATCTCCTGTGTACC 2580
Db 2521 ACAGTGGCTTCCCAACAATGGAAGTGATGCTGTCAGAGTGGCTATCTCCTGTGTACC 2580
Qy 2581 CAGACAGAGCTAGCGACCAAGATGTGATCCACATCGATGTCATGTTGGCCCA 2640
Db 2581 CAGACAGAGCTAGCGACCAAGATGTGATCCACATCGATGTCATGTTGGCCCA 2640
Qy 2641 ACCAGCGGGGAAAGAGAGGACACAGAAAGGATTCGAGGCAATTCGCCAAAGGGGCCGGAT 2700
Db 2641 ACCAGCGGGGAAAGAGAGGACACAGAAAGGATTCGAGGCAATTCGCCAAAGGGGCCGGAT 2700
Qy 2701 TTCAGGCTTCCAAAGTCAATGCTGCTGCGCTTTCGGCACTCAAGTCAAGAGTTCTGTAAGA 2760
Db 2701 TTCAGGCTTCCAAAGTCAATGCTGCTGCGCTTTCGGCACTCAAGTCAAGAGTTCTGTAAGA 2760
Qy 2761 CCGCTTGATGCTCCTCTGCTGGTGATGTTTCATGGTTCCTGGATTTGAAAGTCTGTAAG 2820
Db 2761 CCGCTTGATGCTCCTCTGCTGGTGATGTTTCATGGTTCCTGGATTTGAAAGTCTGTAAG 2820
Qy 2821 GAGCCCTTTTCTACAGTTGCTTCGGCATACCAAGTTCTTCTCATAAAGGAAACAATA 2880
Db 2821 GAGCCCTTTTCTACAGTTGCTTCGGCATACCAAGTTCTTCTCATAAAGGAAACAATA 2880
Qy 2881 AGAAGCGACTGTATGATGGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAA 2940
Db 2881 AGAAGCGACTGTATGATGGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAA 2940
Qy 2941 AGTTTTCAGTCTTCGATGATGATTTTTCAGATGTTGTAACGAAACGGGTATATGAT 3000
Db 2941 AGTTTTCAGTCTTCGATGATGATTTTTCAGATGTTGTAACGAAACGGGTATATGAT 3000
Qy 3001 GTGCTGAATGATGGAATTTGTATATTTCTGCTCTCTTTTTCAGTAATCACTTCGAACA 3060
Db 3001 GTGCTGAATGATGGAATTTGTATATTTCTGCTCTCTTTTTCAGTAATCACTTCGAACA 3060
Qy 3061 AAAAAAAAAA 3070
Db 3061 AAAAAAAAAA 3070

RESULT 3

ADW80563
ID ADW80563 standard; cDNA; 3070 BP.
XX AC ADW80563;
XX AC
XX 21-APR-2005 (first entry)
XX DE E. grandis caffeic acid O-methyltransferase cDNA SEQ ID NO:113.
XX DE ss; wood; plant; transcription; caffeic acid O-methyltransferase;
XX DE transgenic plant.
XX OS Eucalyptus grandis.
XX FH Key Location/Qualifiers
XX FH 5'UTR 1..1643
XX FT /*tag= a
XX FT 1019..1676
XX FT /*tag= b
XX FT
XX PN US2005026162-A1.

XX 03-FEB-2005.
XX PD
XX PF
XX 06-NOV-2003; 2003US-00702319.
XX 25-MAR-1999; 99US-00276599.
XX 30-JUL-1999; 99US-0146591P.
XX 24-FEB-2000; 2000WO-NZ000018.
XX 20-JUN-2000; 2000US-00598401.
XX 28-NOV-2000; 2000US-00724624.
XX 03-NOV-2001; 2001US-0345397P.
XX 30-APR-2002; 2002US-00137036.
XX 08-NOV-2002; 2002US-00291447.
XX 08-NOV-2002; 2002US-0425087P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (RUBI-) RUBICON FORESTS HOLDINGS LTD.
XX Perera R, Rice SJ, Bagleton CK;
XX WPI; 2005-131806/14.
XX New isolated polynucleotide sequences comprising a functional vascular
tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase
promoter, useful for modifying gene expression.
XX Claim 2; SEQ ID NO 113; 82pp; English.
XX The invention relates to a novel isolated polynucleotide sequence
comprising a functional vascular tissue-specific Eucalyptus grandis
caffeic acid O-methyltransferase (cOMT) promoter (ADW80462 or ADW80563).
XX Also claimed is a genetic construct comprising the above polynucleotide
sequence or a sequence having 2096 base pairs fully defined in the
specification (ADW80510), a host cell comprising the above genetic
construct, a plant comprising the genetic construct, a method for
producing a plant with modified gene expression, and a method for
identifying a gene responsible for a desired function or phenotype. The
composition and methods are useful for modifying gene expression or for
modifying the transcription of endogenous and/or heterologous
polynucleotides involved in wood formation. The present sequence is used
in the exemplification of the invention.
XX Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;
Query Match 100.0%; Score 3070; DB 14; Length 3070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCACCATCAGCAAAAAATAGATGGGATAGATGGGACACACCTGTTCAGTTTGATTC 60
Db 1 AGCACCATCAGCAAAAAATAGATGGGATAGATGGGACACACCTGTTCAGTTTGATTC 60
Qy 61 CTTGAGATGACCTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 120
Db 61 CTTGAGATGACCTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 120
Qy 121 GATAAAAAGGTAGGAGATAGGAGATCTCCCGCTGATGCTCCGGTAGGTGAAATA 180
Db 121 GATAAAAAGGTAGGAGATAGGAGATCTCCCGCTGATGCTCCGGTAGGTGAAATA 180
Qy 181 AGCAAAAAGTTCCCGTTGAAATTTGACAGAAAAGACACCGTGTATGATTCATGATGAT 240
Db 181 AGCAAAAAGTTCCCGTTGAAATTTGACAGAAAAGACACCGTGTATGATTCATGATGAT 240
Qy 241 CCATTGTACCATGTAGGGTGAATCCTAGAGTGGAGATAGTCTCTTTTGAAGTCCCA 300
Db 241 CCATTGTACCATGTAGGGTGAATCCTAGAGTGGAGATAGTCTCTTTTGAAGTCCCA 300
Qy 301 TTCACCCCTATCAGCTTTCTGCATATCCATTTTAAGAACAGCCGGATTCACCTCT 360
Db 301 TTCACCCCTATCAGCTTTCTGCATATCCATTTTAAGAACAGCCGGATTCACCTCT 360
Qy 361 ACATTTTCTGACTTTAAATTTGATGTAGAACCTCTTAGACTATTAAATATTTGCTCTGAAT 420

Db	361	ACATTTTCTGACCTTAAATTTGATGTAGAACCTTTAGACTATTAATAATTTGTCCTGAAT	420
Qy	421	TTGACGTCCACTGACAAAAGCGTTTGCTCCTGGAAAAATTAAGTACAGGAGGTAGGGCTT	480
Db	421	TTGACGTCCACTGACAAAAGCGTTTGCTCCTGGAAAAATTAAGTACAGGAGGTAGGGCTT	480
Qy	481	AAGCGGATTTGGCAATGACCTTAGAATGATCTATATGCGTAAATACAAAGACTGATGGG	540
Db	481	AAGCGGATTTGGCAATGACCTTAGAATGATCTATATGCGTAAATACAAAGACTGATGGG	540
Qy	541	CGCGTATTGGTCTAAATTTGTTTACAGATGTGTACCTTTGGGTATTTAGGGCTTATGATGGTTCG	600
Db	541	CGCGTATTGGTCTAAATTTGTTTACAGATGTGTACCTTTGGGTATTTAGGGCTTATGATGGTTCG	600
Qy	601	ATTGAGATTCGGTGGTATGATGCCAGAAATTAATAAAGTGTGACATGATGAGAAATAGTTTC	660
Db	601	ATTGAGATTCGGTGGTATGATGCCAGAAATTAATAAAGTGTGACATGATGAGAAATAGTTTC	660
Qy	661	ATCCTGGAGTATATCCCAATGATCTCGTGTAGAGAGTCCATTTCAAGCCATCTGGACCGGG	720
Db	661	ATCCTGGAGTATATCCCAATGATCTCGTGTAGAGAGTCCATTTCAAGCCATCTGGACCGGG	720
Qy	721	GGCCTTGGTAAAGTCCAGTTCGGAAGTAGCCCTCTAACTCTTCTTGTGTACAGGAGC	780
Db	721	GGCCTTGGTAAAGTCCAGTTCGGAAGTAGCCCTCTAACTCTTCTTGTGTACAGGAGC	780
Qy	781	TATTAGGGACATATTTCATCTCATTTAGTAACAACTTAAGGACACTGGTTTCAAGAAATAGGCCAA	840
Db	781	TATTAGGGACATATTTCATCTCATTTAGTAACAACTTAAGGACACTGGTTTCAAGAAATAGGCCAA	840
Qy	841	GTAGTCTCGATCTCCCACTGTCTGAATATAGATGTGAAAAGTAAACCTATCGTCATCATCTT	900
Db	841	GTAGTCTCGATCTCCCACTGTCTGAATATAGATGTGAAAAGTAAACCTATCGTCATCATCTT	900
Qy	901	CAAAATTTCAGATCGCGCACCAAGCTTGATGTTCATCTCGCAACATACCTAATCTTGT	960
Db	901	CAAAATTTCAGATCGCGCACCAAGCTTGATGTTCATCTCGCAACATACCTAATCTTGT	960
Qy	961	TCGCTTGTGCTTTGTATAGTTTGTGCATGAAAAAATTTAGTATTTTGTCCCCCAAGCT	1020
Db	961	TCGCTTGTGCTTTGTATAGTTTGTGCATGAAAAAATTTAGTATTTTGTCCCCCAAGCT	1020
Qy	1021	GAGCCATTTAATTCGAGAGACAATGCCCAAAATTTATCTTCTTGTCTGCCATACTGTGCG	1080
Db	1021	GAGCCATTTAATTCGAGAGACAATGCCCAAAATTTATCTTCTTGTCTGCCATACTGTGCG	1080
Qy	1081	AATTTCTCTTTTAGTATAGTAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTAGT	1140
Db	1081	AATTTCTCTTTTAGTATAGTAACCAATGATGCGCCATGTTGACAAAAAGGCTGATTAGT	1140
Qy	1141	ATGATCTVTGGAGTTTGTGGTCAAAATTTGCAAGCTGACATGCGCCCTCAGGGAAATTA	1200
Db	1141	ATGATCTVTGGAGTTTGTGGTCAAAATTTGCAAGCTGACATGCGCCCTCAGGGAAATTA	1200
Qy	1201	GGCGCCAAACCAAGTTCGAAAGGCAACAAGACGACGACCACTTTCTTTAAACAAGAT	1260
Db	1201	GGCGCCAAACCAAGTTCGAAAGGCAACAAGACGACGACCACTTTCTTTAAACAAGAT	1260
Qy	1261	CATCACAGATTCGGCCAGTAAAGGTAAATTAATTTAAACAATPAGCTTTGTACCGGNA	1320
Db	1261	CATCACAGATTCGGCCAGTAAAGGTAAATTAATTTAAACAATPAGCTTTGTACCGGNA	1320
Qy	1321	CTCCGTATTTCTCTCACTTCCATTAACCCCTGATTAAATTTGGGAAAGCCAGACCCAA	1380
Db	1321	CTCCGTATTTCTCTCACTTCCATTAACCCCTGATTAAATTTGGGAAAGCCAGACCCAA	1380
Qy	1381	CCCAAAAGGTCAGATGTCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGATTT	1440
Db	1381	CCCAAAAGGTCAGATGTCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGATTT	1440
Qy	1441	TTCTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGCATGGTACGATCTACATAT	1500
Db	1441	TTCTCTCTATATTTCTGGTTTCCCGGTTGAGTCAATGGCATGGTACGATCTACATAT	1500
Qy	1501	TGGTGTAGGGTCCAATATTTTTCGGGAGGGTGTGTGAACCCAAAGTTTCTTATATATCGA	1560
Db	1501	TGGTGTAGGGTCCAATATTTTTCGGGAGGGTGTGTGAACCCAAAGTTTCTTATATATCGA	1560
Qy	1561	ACCTCCACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCTCTGCTT	1620
Db	1561	ACCTCCACACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTTCTCTGCTT	1620
Qy	1621	TCCTTTGCTCGAGTCTTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATTTGGTTCGACC	1680
Db	1621	TCCTTTGCTCGAGTCTTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATTTGGTTCGACC	1680
Qy	1681	GGCTCCGAGACCCAGATGACCCCGCAAGTCTCGGACGACGAGCGGAACTCTTTCGCC	1740
Db	1681	GGCTCCGAGACCCAGATGACCCCGCAAGTCTCGGACGACGAGCGGAACTCTTTCGCC	1740
Qy	1741	ATGCAGCTGGCGAGCGCTCCGTCCTCCCATGCTCTTAAGCGCCCATCGAGATCGAC	1800
Db	1741	ATGCAGCTGGCGAGCGCTCCGTCCTCCCATGCTCTTAAGCGCCCATCGAGATCGAC	1800
Qy	1801	CTCTCGAGATCATTTGGCCAAAGGACCGGCGCGCTTCTCTCCACGGGGAAATTCGCG	1860
Db	1801	CTCTCGAGATCATTTGGCCAAAGGACCGGCGCGCTTCTCTCCACGGGGAAATTCGCG	1860
Qy	1861	GCAGAGTCCCGACCCAGAACCCCGAGGACCCCGTCACTGTCACCGGATCTTTCGGCTG	1920
Db	1861	GCAGAGTCCCGACCCAGAACCCCGAGGACCCCGTCACTGTCACCGGATCTTTCGGCTG	1920
Qy	1921	CTGGCCAGCTACTCCGTCGTCACTGTCACCCCTCGGACCTCCCGATGCGCAAGGTCGAG	1980
Db	1921	CTGGCCAGCTACTCCGTCGTCACTGTCACCCCTCGGACCTCCCGATGCGCAAGGTCGAG	1980
Qy	1981	CGGCTCTACGGCTTAGCGCCGCTGCAAGTCTTGTGTCAAGAACGAGGACGGGCTCTCC	2040
Db	1981	CGGCTCTACGGCTTAGCGCCGCTGCAAGTCTTGTGTCAAGAACGAGGACGGGCTCTCC	2040
Qy	2041	ATCGCGGCACTCAACTTGTATGAACACGAGACAAAATCTCATGGAAGACTGATATACCTG	2100
Db	2041	ATCGCGGCACTCAACTTGTATGAACACGAGACAAAATCTCATGGAAGACTGATATACCTG	2100
Qy	2101	AAAGATGCGGCTCTTGAAGGCGGAATCCATTTCAACAGGCTACCGGATGACCGGCTTC	2160
Db	2101	AAAGATGCGGCTCTTGAAGGCGGAATCCATTTCAACAGGCTACCGGATGACCGGCTTC	2160
Qy	2161	GAGTATCATGGCACCGACCCGCGATTTCAACAGATCTTTAAACGGGAAATGCTGTGATC	2220
Db	2161	GAGTATCATGGCACCGACCCGCGATTTCAACAGATCTTTAAACGGGAAATGCTGTGATC	2220
Qy	2221	TCACCATTTACTATGAGAGAGATCTGGGCGGCTTCGAGGGCTTCGAGACC	2280
Db	2221	TCACCATTTACTATGAGAGAGATCTGGGCGGCTTCGAGGGCTTCGAGACC	2280
Qy	2281	GTGCTCGATGTTCGAGGCGGCTTCGAGGGCTTCGAGGGCTTCGAGGGCTTCG	

QY	1915	CGGCTGCTGGCAGCTACTCCGTGCTCAGCGTGCACCCCTCCGGACCTCCCGATGGCAAG	1974
Db	941	CGGCTGCTGGCAGCTACTCCGTGCTCAGCGTGCACCCCTCCCGATGGCAAG	1000
QY	1975	GTGAGCGGCTCTACGGCTTAGCGGCTGTCGAAGTCTTCTGGTCAAGAACGAGACGGG	2034
Db	1001	GTGAGCGGCTCTACGGCTTAGCGGCTGTCGAAGTCTTCTGGTCAAGAACGAGACGGG	1060
QY	2035	GTCTCCATCGCCGACTCAACTTGTATGAACAGGACAAATCCTCATGAAAGCTGTAT	2094
Db	1061	GTCTCCATCGCCGACTCAACTTGTATGAACAGGACAAATCCTCATGAAAGCTGTAT	1120
QY	2095	TACTGAAAGATGGGCTCTTGAAGCGGAATCCCAATCAACAAGCGGTACGGGATGACC	2154
Db	1121	TACTGAAAGATGGGCTCTTGAAGCGGAATCCCAATCAACAAGCGGTACGGGATGACC	1180
QY	2155	GCCTTCAGATCATGCGCAGCCGCGCATTCACAAGATCTTTAAACCGGGATGTCT	2214
Db	1181	GCCTTCAGATCATGCGCAGCCGCGCATTCACAAGATCTTTAAACCGGGATGTCT	1240
QY	2215	GATCACTCCACCATTAATATGAAGAGATATCTGAACATACACAGGCTTCGAGGCGCTC	2274
Db	1241	GATCACTCCACCATTAATATGAAGAGATATCTGAACATACACAGGCTTCGAGGCGCTC	1300
QY	2275	GAGACCGTGGTGGATGTCGAGGCGGCACTGGGCGCGTCTCAGCATGATCGTTGCCAAA	2334
Db	1301	GAGACCGTGGTGGATGTCGAGGCGGCACTGGGCGCGTCTCAGCATGATCGTTGCCAAA	1360
QY	2335	TACCCATCAATGAAGAGGATCAACTTCGACCGCCCAACGGATTAAGACGCCACCC	2394
Db	1361	TACCCATCAATGAAGAGGATCAACTTCGACCGCCCAACGGATTAAGACGCCACCC	1420
QY	2395	TTCTCTGGTGTCAAGCAGCTCGGAGCGACATGTTCTGTCAGCGTTCCAAAGGAGATGCCA	2454
Db	1421	TTCTCTGGTGTCAAGCAGCTCGGAGCGACATGTTCTGTCAGCGTTCCAAAGGAGATGCCA	1480
QY	2455	TTTTTCATGAAGTGGATATGCCATGATGAGTGAAGACCATTCGCGGAGTTCCTCAAGA	2514
Db	1481	TTTTTCATGAAGTGGATATGCCATGATGAGTGAAGACCATTCGCGGAGTTCCTCAAGA	1540
QY	2515	ACTGTACAGTGGCTTCCCAATGGAAGGTGATGTTGTCAGAGTGCCTACTCCCTG	2574
Db	1541	ACTGTACAGTGGCTTCCCAATGGAAGGTGATGTTGTCAGAGTGCCTACTCCCTG	1600
QY	2575	TGTACCCAGACAGCGCTAGCGACCAAGAATGTGATCCATCGACTGCATCATGTGG	2634
Db	1601	TGTACCCAGACAGCGCTAGCGACCAAGAATGTGATCCATCGACTGCATCATGTGG	1660
QY	2635	CCCAACACCCAGCGGGAAGAGAGACACAGAGAGTTCGAGGATTCGCGCAAGGGG	2694
Db	1661	CCCAACACCCAGCGGGAAGAGAGACACAGAGAGTTCGAGGATTCGCGCAAGGGG	1720
QY	2695	CCGGAATTCAGGCTTCCAAAGTCAATGCTGCGCTTTCGGCACTCACTGATGAGTTC	2754
Db	1721	CCGGAATTCAGGCTTCCAAAGTCAATGCTGCGCTTTCGGCACTCACTGATGAGTTC	1780
QY	2755	TGAAGACCGCTTGATCTGCTCTCTGCTGCTGATGTTCAATGTTCTGGAATTTGAAGTTC	2814
Db	1781	TGAAGACCGCTTGATCTGCTCTCTGCTGCTGATGTTCAATGTTCTGGAATTTGAAGTTC	1840
QY	2815	GTGAAGGAGCCCTTTCTCAGTTCGCTTCGGCATACCAAGTCTTCTCATATAAGGAA	2874
Db	1841	GTGAAGGAGCCCTTTCTCAGTTCGCTTCGGCATACCAAGTCTTCTCATATAAGGAA	1900
QY	2875	ACAATAAGAAGCGACTGTATGATCGCGCAAGTGAAGTTACAGATTTGTTTATGT	2934
Db	1901	ACAATAAGAAGCGACTGTATGATCGCGCAAGTGAAGTTACAGATTTGTTTATGT	1960
QY	2935	CTATTAAGTTTGTAGTCTTCTGCTACTGATTTCAACAGATGTGTAAACGGAACGGGTAT	2994
Db	1961	CTATTAAGTTTGTAGTCTTCTGCTACTGATTTCAACAGATGTGTAAACGGAACGGGTAT	2020
QY	2995	ATGGATGTGCTGAATGATGGAATTTGTGATTTCTGCTCTTTTTCAGTAAATCACTT	3054

Db	2021	ATGGATGCGCTGGAATGGAATTTGATATTTCTGCTCTTTTTCAGTAAATCACTT	2080
QY	3055	CGAACAAAAA 3070	
Db	2081	CGAACAAAAA 2096	
RESULT 5			
ABK17075			
ID	ABK17075	standard; cdNA; 2096 BP.	
XX	ABK17075;		
AC	ABK17075;		
XX	26-MAR-2002	(first entry)	
DT			
XX	Eucalyptus grandis promoter polynucleotide #31.		
DE			
XX	Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;		
KW	temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;		
KW	PCR primer.		
XX	Eucalyptus grandis.		
OS			
XX	WO200198485-A1.		
PN			
XX	27-DEC-2001.		
PD			
XX	20-JUN-2001; 2001WO-NZ000115.		
PF			
XX	20-JUN-2000; 2000US-00598401.		
PR			
XX	28-NOV-2000; 2000US-00724624.		
PA	(GENE-) GENESTS RES & DEV CORP LTD.		
XX	(FLET-) FLETCHER CHALLENGE FORESTS IND LTD.		
PI	Perera R, Rice S, Bagleton C, Laeham A;		
XX	WPI; 2002-114583/15.		
DR	P-PSDB; AAU80760.		
XX	Novel polynucleotide promoter sequences from pine and Eucalyptus useful		
PT	for modifying expression of endogenous and/or heterologous		
PT	polynucleotides in transgenic plants.		
XX	Claim 1; Page 78; 121pp; English.		
PS	The invention relates to isolated promoter sequences from Pinus radiata		
XX	and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,		
CC	flower-, pollen-, bud-, meristem-specific promoters or temporally		
CC	regulated promoters such as xylogenesis-specific promoters. The promoter		
CC	polypeptides and their related polynucleotides are useful in the		
CC	production of genetic constructs, used for modifying gene expression in a		
CC	target organism, in particular a plant. The method is useful for		
CC	modifying expression of a polynucleotide that comprises an intron		
CC	sequence, through removal of the intron sequence. The method is useful		
CC	for modifying growth and development of plants, and cellular responses to		
CC	external stimulus, such as environmental factors and disease pathogens.		
CC	The sequences are useful in genome and physical mapping, in positional		
CC	cloning of genes, in various assays to determine biological activity, to		
CC	raise antibodies, to isolate corresponding interacting proteins and other		
CC	compounds, and to quantitatively determine levels of interacting proteins		
CC	or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata		
CC	and Eucalyptus grandis polynucleotides and PCR primers used in the method		
CC	of the invention		
XX	Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;		
SQ			
Query Match	65.8%;	Score 2020.4;	DB 6; Length 2096;
Best Local Similarity	99.3%;	Pred. No. 0;	
Matches 2041; Conservative	0;	Mismatches 11;	Indels 4; Gaps 1;
QY	1019	CTGACCATTTAATTCGAGACACATCGCCCAAAATTTATTTCTTCTGTCGCAATCTGT	1078

DT	22-APR-2004	(first entry)	
XX	Eucalyptus grandis	superubiquitin related sequence #31.	
XX	DE		
XX	ds;	Monterey pine; superubiquitin; promoter; gene expression;	
KW	transgenic plant.		
XX			
XX	Eucalyptus grandis.		
XX	OS		
XX	WO2003093475-A1.		
XX			
XX	13-NOV-2003.		
XX			
XX	30-APR-2003;	2003WO-NZ000076.	
XX	PF		
XX	30-APR-2002;	2002US-00137036.	
XX			
XX	(GENE-)	GENESIS RES & DEV CORP LTD.	
PA	(RUBI-)	RUBICON FORESTS HOLDINGS LTD.	
XX			
XX	Rice SJ,	Wood M, Bagleton CK, Visser ES, Perera R;	
XX	WPI;	2003-903678/82.	
XX			
XX	New polynucleotide of the superubiquitin promoter from Pinus radiata,		
PT	useful in modifying gene expression in a target organism.		
XX			
XX	Disclosure;	SEQ ID NO 60; 123pp; English.	
XX			
XX	The invention relates to a new isolated polynucleotide comprising the		
CC	Pinus radiata (Monterey pine) superubiquitin promoter sequence, its		
CC	complement, reverse complement, reverse sequence or inverted repeat or a		
CC	sequence having at least 40, 60, 75 or 90% identity with the promoter.		
CC	The polynucleotide is useful in modifying gene expression in a target		
CC	organism, especially in transgenic plants. This sequence corresponds to a		
CC	superubiquitin promoter related sequence.		
XX			
XX	Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 U; 0 Other;		
XX			
XX	Query Match	65.8%; Score 2020.4; DB 10; Length 2096;	
XX	Best Local Similarity	99.3%; Pred. No. 0;	
XX	Matches 2041; Conservative	0; Mismatches 11; Indels 4; Gaps 1;	
QY	1019	CTGAGCCATTTAAATTCGAGACACATCGCCCAAATTAATTCCTTCTGCTGCCATAACTGT	1078
Db	41	CTGAGCCATTTAAATTCGAGACACATCGCCCAAATTAATTCCTTCTGCTGCCATAACTGT	100
QY	1079	CGAATTTTCTCTTTAGTAGTAACCAATGATGCGCATGTTCGCAAAAAGCGTGATTA	1138
Db	101	CGAATTTTCTCTTTAGTAGTAACCAATGATGCGCATGTTCGCAAAAAGCGTGATTA	160
QY	1139	GTATGATCTTGAGTGTGTTGGTCGCAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT	1198
Db	161	GTATGATCTTGAGTGTGTTGGTCGCAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT	220
QY	1199	AAGGCCCAACCCAGATTGCAAGAGCAAAAGAGCAGACCCCAACTTTCCTTTAAACAAG	1258
Db	221	AAGGCCCAACCCAGATTGCAAGAGCAAAAGAGCAGACCCCAACTTTCCTTTAAACAAG	280
QY	1259	ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGCTTTGTACCGGG	1318
Db	281	ATCATCACCAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGCTTTGTACCGGG	340
QY	1319	AACTCGGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGCTGGGAAGCGACAGCC	1378
Db	341	AACTCGGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGCTGGGAAGCGACAGCC	400
QY	1379	AACCCCAAAAGGTCAGATGTCATCCAC- --GAGAGAGAGAGAGAGAGAGAGAG	1434
Db	401	AACCCCAAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAG	460
QY	1435	AGAGTTTTCTCTCTATATTCTGTGTTCAACCGGTTGAGTCATGGCATCGTGACGAATGT	1494

QY	1675	TCGACCGGCTCCGAGACCCAGATGATCCCGGACCCCAAGTCTCGAGCAGGCGCAACCTC	1734	Db	1781	TGAAGACCGCTGATCTGCTCTCTCTGTTGGTGGTTCATGGTTCTGGAATTTGAAAGGTC	1840
Db	701	TCGACCGGATCCGAGACCCAGATGATCCCGGACCCCAAGTCTCGAGCAGGCGCAACCTC	760	QY	2815	GTGAAGGAGCCCTTTTCTCACAGTTGGCTTCGCGATACCAAGTCTCTCATAAAGGAA	2874
QY	1735	TTCCGCAATGAGTGGCAGCGCTCCGTTGCTCCCATGCTCTAAAGCGCCCATCGAG	1794	Db	1841	GTGAAGGAGCCCTTTTCTCACAGTTGGCTTCGCGATACCAAGTCTCTCATAAAGGAA	1900
Db	761	TTCCGCAATGAGTGGCAGCGCTCCGTTGCTCCCATGCTCTAAAGCGCCCATCGAG	820	QY	2875	ACAATAAGAGGAGCTGATGATGCGCAAGTGGGAAGTTACAAGATTTGTTGTTTATGT	2934
QY	1795	ATCGACTCTCTGAGATCATGTGCAAGGACGGCGCGGCTTCTCTCAACGGGGAA	1854	Db	1901	ACAATAAGAGGAGCTGATGATGCGCAAGTGGGAAGTTACAAGATTTGTTGTTTATGT	1960
Db	821	CTGACTCTCTGAGATCATGTGCAAGGACGGCGCGGCTTCTCTCAACGGGGAA	880	QY	2935	CTATAAGTTTGGTCTTCTGCATCTGATTTTCAAGATGTGTAACGAACCGCGTAT	2994
QY	1855	ATCGCGGACAGTCCCGACCCGAGACCCCGAGGACCCGCTCATCTCGACCGGATCTTC	1914	Db	1961	CTATAAGTTTGGTCTTCTGCATCTGATTTTCAAGATGTGTAACGAACCGCGTAT	2020
Db	881	GTGCGGCCAGCTCCCGACCCAGAACCCCGAGGACCCCGTCTGCTCGACCGGATCTTC	940	QY	2995	ATGGATGTCCCTGAATGATGGAATTTGATATTTCTCTTCTTTCAGTAAATCACTT	3054
QY	1915	CGGCTGTGCGGAGCTACTCCGTGCTCAGTGTGACCTCCGCGACCTCCCGATGGCAAG	1974	Db	2021	ATGGATGTCCCTGAATGATGGAATTTGATATTTCTCTTCTTTCAGTAAATCACTT	2080
Db	941	CGGCTGTGCGGAGCTACTCCGTGCTCAGTGTGACCTCCGCGACCTCCCGATGGCAAG	1000	QY	3055	CGAACAATAAAAAA 3070	
QY	1975	GTGAGCGGCTCTACGGCTTAGCGCGGTGTGAAGTTCTTGGTCAAGAACGAGACGGG	2034	Db	2081	CGAACAATAAAAAA 2096	
Db	1001	GTGAGCGGCTCTACGGCTTAGCGCGGTGTGAAGTTCTTGGTCAAGAACGAGACGGG	1060				
QY	2035	GTCTCCATCGCGCACTCACTTGAAGGCGGATCTTGAAGGCGGATCTTGAAGGCGGATCTT	2094				
Db	1061	GTCTCCATCGCGCACTCACTTGAAGGCGGATCTTGAAGGCGGATCTTGAAGGCGGATCTT	1120				
QY	2095	TACCTGAAAGATGCGGCTCTTGAAGGCGGATCTTGAAGGCGGATCTTGAAGGCGGATCTT	2154				
Db	1121	TACCTGAAAGATGCGGCTCTTGAAGGCGGATCTTGAAGGCGGATCTTGAAGGCGGATCTT	1180				
QY	2155	GGTTCGAGTATCATGGACCGACCCCGGATTTCAAGATCTTAAACCGGCAATGTCT	2214				
Db	1181	GGTTCGAGTATCATGGACCGACCCCGGATTTCAAGATCTTAAACCGGCAATGTCT	1240				
QY	2215	GATCACTCCACCATTTACTATGAAGAGATCTGGAAGATCTGGAAGATCTGGAAGATCTG	2274				
Db	1241	GATCACTCCACCATTTACTATGAAGAGATCTGGAAGATCTGGAAGATCTGGAAGATCTG	1300				
QY	2275	GAGACCGTGGTCTGATGTGGAGCGGCTGCGGCGGCTGCTCAGCATGATCGTTGCCAAA	2334				
Db	1301	GAGACCGTGGTCTGATGTGGAGCGGCTGCGGCGGCTGCTCAGCATGATCGTTGCCAAA	1360				
QY	2335	TACCCATCAATGAAGGATCAACTTCGACCGCCCAACGAGTGAAGACGCCCAACCC	2394				
Db	1361	TACCCATCAATGAAGGATCAACTTCGACCGCCCAACGAGTGAAGACGCCCAACCC	1420				
QY	2395	TTCTCTGATGTCAGGCGGACATGTTGTCAGCGTTTCCAAAGGAGATGCGA	2454				
Db	1421	TTCTCTGATGTCAGGCGGACATGTTGTCAGCGTTTCCAAAGGAGATGCGA	1480				
QY	2455	TTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2514				
Db	1481	TTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1540				
QY	2515	ACTGCTACGATGGCTTCCCAACAATGGAAGGATGATGATGATGATGATGATGATGATGAT	2574				
Db	1541	ACTGCTACGATGGCTTCCCAACAATGGAAGGATGATGATGATGATGATGATGATGATGAT	1600				
QY	2575	TGTACCCAGACACAGCTAGCCAGCCAGGATGATGATGATGATGATGATGATGATGATGAT	2634				
Db	1601	TGTACCCAGACACAGCTAGCCAGCCAGGATGATGATGATGATGATGATGATGATGATGAT	1660				
QY	2635	CCCAACAACCCAGGCGGGAAGAGAGGACACAGAGGATGTCGAGGATTTGGCCCAAGGGG	2694				
Db	1661	CCCAACAACCCAGGCGGGAAGAGAGGACACAGAGGATGTCGAGGATTTGGCCCAAGGGG	1720				
QY	2695	CCGATTTTCAGGCTTCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2754				
Db	1721	CCGATTTTCAGGCTTCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1780				
QY	2755	TGAAGACCGCTTGTATCTGCTCTCTGTTGGTGTATGTTTATGTTTCTTGGATTTGAAGGTC	2814				

RESULT 8

AAA68014 standard; DNA; 1630 BP.

AC AAA68014;

DT 24-OCT-2000 (first entry)

DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:107.

KW Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;

OS Eucalyptus grandis.

PN WO200022099-A1.

PD 20-APR-2000.

PF 06-OCT-1999; 99WO-NZ000168.

PR 09-OCT-1998; 98US-00169789.

PR 14-JUL-1999; 99US-0143811P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Bloksberg LN, Havukkala IJ;

XX WPI; 2000-317962/27.

XX Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and structure.

XX Claim 1; Page 90-91; 213pp; English.

XX The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate-CoA ligase (4CL), coniferol glucosyl transferase (CGR), coniferin beta-glucosidase (CBG), laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, caffeic acid methyl transferase, caffeoyl CoA methyl transferase, coumarate CoA ligase, cytochrome P450 1X1A, diphenol oxidase, flavanol glucosyl transferase, flavanol hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure

PT /product= "STOMT protein"
XX W02003046163-A2.
PN 05-JUN-2003.
XX 26-NOV-2002; 2002WO-EP013320.
XX 26-NOV-2001; 2001US-0332534P.
PA (UYBA-) UNIV BAYERISCHE JULIUS MAXIMILIANS WUERZ.
XX Schwab W, Kaldenhoff R, Wein M;
XX WPI; 2003-532772/50.
XX P-PSDB; AAO30114.
XX Novel isolated strawberry O-methyltransferase polypeptide useful for
PT methylating ortho-dihydroxy substituted ring system such as catechol,
PT caffeic acid, protocatechuic aldehyde or pyrogallol.
XX Claim 1; Page 75-76; 78pp; English.
XX The invention relates to novel strawberry O-methyltransferase (STOMT)
CC polypeptides capable of methylating an ortho-dihydroxy substituted ring
CC system and nucleic acid molecules encoding such polypeptides. The
CC invention is useful for methylating of an ortho-dihydroxy substituted
CC ring system and/or its mimetics (such as 2,5-dimethyl-4-hydroxy-3(2H)-
CC furanone (DMHF) or dithiothreitol (DTT)). The invention is also useful
CC for the synthesis of naturally occurring substances preferably aroma
CC compounds such as 2-methoxyphenol, vanillin, ferulic acid, feruoyl-CoA or
CC DMHF, for enhancing the function of naturally-occurring STOMT in plants
CC or tissue cultured cells, or to enhance the production of flavour-
CC enhancing substances such as vanillin or 2,5-dimethyl-4-methoxy-3(2H)-
CC furanone (DMHF). The present sequence is Fragaria x ananassa (strawberry)
CC O-methyltransferase DNA
SQ Sequence 1876 BP; 432 A; 449 C; 429 G; 566 T; 0 U; 0 Other;
Query Match 22.0%; Score 676; DB 9; Length 1876;
Best Local Similarity 77.0%; Pred. No. 7e-176;
Matches 850; Conservative 0; Mismatches 250; Indels 4; Gaps 2;
QY 1666 AGAATGGGTTTCGACCGGCTCCGAGACCCAGATACCCGACCCAAAGTCTCGAGACGAG 1725
DB 103 AATATGGGTTTCACCGG---CGAGACTCAGATGACTCCGACCCCATGTCTCGAGAGAA 159
QY 1726 GCGAACCTCTTGGCCATGCGAGTGGCGAGCGCTCCGCTGCTCCCGCATGTCCTAAAGGCC 1785
DB 160 GCCAACCTCTTGGCCATGCAACTGCCGAGCGCTCCGCTCCCGCATGTCCTCAAGCC 219
QY 1786 GCGATCGAGATCGACCTCTCGAGATCATGCCAAGACGCGCGCGGCTTCCTCTCC 1845
DB 220 GCCATCGAGTTCGACCTCTTGGAGATCATGCCAAGCGCGACCCCGGCTCTTTCCTCTCC 279
QY 1846 ACGGGGGAATCGCGGCACAGCTCCCGACCCAGAACCCCGAGGACCCCGTCATGCTCGAC 1905
DB 280 CTTAGTATCTAGCTCTCAGCTTCCGACCAAGAACCCCGAAGCTCCGGTCATGCTCGAC 339
QY 1906 CGGATCTTCCGGCTGCTGGCCAGCTACTCCGCTGCTCAGTGCACCTCCCGGACCTCCCC 1965
DB 340 CGTATGCTTCGCCCTCTCGGCCAGCTACTCCATTCTAACCTGCTCATTTGCGTACGCTCCG 399
QY 1966 GATGGCAAGTTCGAGCGGCTCTACGGCTTACGGCGCGGTGTGCAAGTCTTGGTCAAGAAC 2025
DB 400 GACGGCAAGTTGAGAGGCTCTACTGTTGGGACCTGTGTGTAAGTCTTTGACCAAGAT 459
QY 2026 GAGGACGGGTCTTCATCGCGGCACTCACTTGTATGACACGAGCAAAATCTTCATCGAA 2085
DB 460 GAAGATGGGCTCTCTATTGTGCTCTCTGCTCATGAACACGAGCAAGGTCCTGCTCGAG 519
QY 2086 AGCTGGTATTACCTGAAAGATCGGCTCTTGAAGCGGGAATCCCATTTCAACAGGCGGTAC 2145

DB 520 AGCTGGTATCATTTGAAGGATGCAAGTCTTTGATGGTGGGATTCATTTAAACAAGGCTAT 579
QY 2146 GGGATGACCGCGTTTCGAGTATCATGCAACGACCGCGGATTTCAACAGGATCTTTAAACCGG 2205
DB 580 GGCATGACTGCAATTTGATTACCATGGAACCTGACCCCTAGATTCAACAGGCTTTCAACAAG 639
QY 2206 GGAATGCTGATCACTCCACCATTTACTATGAAGAAGATACCTGGAAACATCAAGGGCTTC 2265
DB 640 GGAATGGCTGACCACTCCACCATTTACATGAAGAAATCTTGGAGACTTTACAAAGGCTTC 699
QY 2266 GAGGGCTCGAGACCGTGTGCTGATGTCGAGGGCGGCACTGGGGCCGCTGCTCAGCATGATC 2325
DB 700 GAGGGCTTCAATTCATTCGTTGATGTCGTTGGCGGCACTGGGGCTGTGGTGAACATGATC 759
QY 2326 GTTGGCCAAATACCCATCAATGAAGGATCAACTTCGAC-CGCCCCCAACGAGATTGAAGAC 2384
DB 760 GTTTCGAAGTACCTTCGATCAAGGCACTCACTTCGACTTGCTCATGTTATCGAAGAT 819
QY 2385 GCGCCACCCCTTCTGTTGTCAGACGTCGAGGCGACATGTTGCTCAGCGTTCCAAAG 2444
DB 820 GCTCCTCAATATCTCTGTTTCAACACGTTGGAGGGGACATGTTGTAAGTGTACCAAG 879
QY 2445 GGAATGCCATTTTCATGAAGTGGATATGCCATGACTGAGTGCACGACCATTTGGCGAAG 2504
DB 880 GGAATGCAATTTTCATGAAGTGGATATGTCAGACTGGAGTGCAGGCAATTCATATAA 939
QY 2505 TTCTTCAAGAACCTGCTACGATGCGCTTCCCAACAATGGAAGGTGATCGTTGCAGAGTGC 2564
DB 940 TTCTTGAAGAACCTGCTACGCTGCGCTTCAGACGATGGCNAAGTATCTTGTCTGAGTGC 999
QY 2565 GTACTCCTCTGTGTACCCAGACGAGCTAGCCAGCAAGAAATGTGATCCACATCGACTGC 2624
DB 1000 ATTCTTCTGTTGCCACGACACTAGCTTCCACCAAGGAGTGTGTCATATGGATGTG 1059
QY 2625 ATCATGTTGGCCCAACACCCAGCGGGAAGAGAGACACAGAGGATTCGAGGCAATTG 2684
DB 1060 ATCATGTTGGCGCAACACCCCTGGCGCAAGAGAGGAGCGAGGAGAAATTTGAAGCCCTG 1119
QY 2685 GCCAAGGGCGCGGATTTCAAGGCTTCCAGTCAATGCTGCGCTTTCCGCACTCAGCTC 2744
DB 1120 GCTAAGGGTCTGGATTCAGGCAATTCGCGCTGCTGATGCTTTCAACACCTATGTC 1179
QY 2745 ATGGAGTTCCTGGAAGCCGCTTGA 2768
DB 1180 ATTGAGTTCCTTGAAGAGATCTGA 1203
RESULT 11
AAC62762
ID AAC62762 standard; DNA; 661 BP.
XX AAC62762;
AC AAC62762;
XX 02-FEB-2001 (first entry)
DT 02-FEB-2001 (first entry)
XX O-methyl transferase promoter coding sequence #1.
DE Promoter; eucalyptus; pine; gene transcription; ds.
XX Eucalyptus grandis.
OS OS
XX WO200058474-A1.
PN PN
XX 05-OCT-2000.
PD 24-FEB-2000; 2000WO-NZ000018.
XX 25-MAR-1999; 99US-00276599.
PR 30-JUL-1999; 99US-0146591P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX

PI Perera R, Rice SJ, Eagleton CK;
XX WPI; 2000-647236/62.
XX Novel promoter sequences useful for modulating transcription of plant DNA
XX sequences of interest and production of polypeptides.
XX Claim 1; Page 48; 93pp; English.
XX The present invention relates to promoter sequences from eucalyptus and
XX pine. The present sequence is one such promoter. This sequence is useful
XX for modulating the transcription of DNA sequences of interest. The
XX sequences may also be used to tag or identify an organism or its
XX reproductive material
XX
XX SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;
Query Match 20.8%; Score 638.2; DB 3; Length 661;
Best Local Similarity 98.9%; Pred. No. 1.2e-165;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
Qy 1019 CTGAGCCATTAAATTCGAGAGCAGATCGCCCAAAATTTCTTCTGCTGCCATACTGT 1078
Db 1 CTGAGCCATTAAATTCGAGAGCAGATCGCCCAAAATTTCTTCTGCTGCCATACTGT 60
Qy 1079 CGAATTTTCTTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 1138
Db 61 CGAATTTTCTTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 120
Qy 1139 GTATGATCTTGGAGTTGTTGGTGCAAATTTGCAAGCTGAGATGGCCCTCAGGGAAT 1198
Db 121 GTATGATCTTGGAGTTGTTGGTGCAAATTTGCAAGCTGAGATGGCCCTCAGGGAAT 180
Qy 1199 AAGGGCCCAACCCAGATGCAAGAGCAGACAGCCCAACCTTCTCTTAAACAAG 1258
Db 181 AAGGGCCCAACCCAGATGCAAGAGCAGACAGCCCAACCTTCTCTTAAACAAG 240
Qy 1259 ATCATCACAGATCGGCCAGTAAGGGTAATTAATTAACAATAGCTCTGTACCGGG 1318
Db 241 ATCATCACAGATCGGCCAGTAAGGGTAATTAATTAACAATAGCTCTGTACCGGG 300
Qy 1319 AACTCCGTATTTCTCTCATCTTCCATAACCCCTGATTAATTTGGTGGAAAGCAGAGCC 1378
Db 301 AACTCCGTATTTCTCTCATCTTCCATAACCCCTGATTAATTTGGTGGAAAGCAGAGCC 360
Qy 1379 RACCCACAAAAGTCCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1434
Db 361 RACCCACAAAAGTCCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 1435 AGAGTTTCTCTCTATATTTCTGGTTTCAACCGTTGAGTCAATGGCATGCGTACGAATGT 1494
Db 421 AGAGTTTCTCTCTATATTTCTGGTTTCAACCGTTGAGTCAATGGCATGCGTACGAATGT 480
Qy 1495 ACATATTTGTTAGGTTCCATATTTTTCGGGGGGTTGGTGAACCGCAAAAGTTCCCTATA 1554
Db 481 ACATATTTGTTAGGTTCCATATTTTTCGGGGGGTTGGTGAACCGCAAAAGTTCCCTATA 540
Qy 1555 TATCGAACTCCACACCATACCTCACTTCAATCCCCCACTTTATCCGTTTATTTCCCT 1614
Db 541 TATCGAACTCCACACCATACCTCACTTCAATCCCCCACTTTATCCGTTTATTTCCCT 600
Qy 1615 CTGCTTTCTTGTCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGAGATGGGT 1674
Db 601 CTGCTTTCTTGTCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGATGGGT 660
Qy 1675 T 1675
Db 661 T 661
RESULT 12
ABK17027
. ID ABK17027 standard; cDNA; 661 BP.

XX ABK17027;
XX AC
XX DT
XX 26-MAR-2002 (first entry)
XX Eucalyptus grandis promoter polynucleotide #6.
XX Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;
XX temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
XX PCR primer.
XX Eucalyptus grandis.
XX WO200198485-A1.
XX 27-DEC-2001.
XX 20-JUN-2001; 2001WO-NZ000115.
XX 20-JUN-2000; 2000US-00598401.
XX 28-NOV-2000; 2000US-00724624.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
XX Perera R, Rice S, Eagleton C, Lasham A;
XX WPI; 2002-114583/15.
XX Novel polynucleotide promoter sequences from Pine and Eucalyptus useful
XX for modifying expression of endogenous and/or heterologous
XX polynucleotides in transgenic plants.
XX Claim 1; Page 63-64; 121pp; English.
XX The invention relates to isolated promoter sequences from Pinus radiata
XX and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,
XX flower-, pollen-, bud-, meristem-specific promoters or temporally
XX regulated promoters such as xylogenesis-specific promoters. The promoter
XX polypeptides and their related polynucleotides are useful in the
XX production of genetic constructs, used for modifying gene expression in a
XX target organism, in particular a plant. The method is useful for
XX modifying expression of a polynucleotide that comprises an intron
XX sequence, through removal of the intron sequence. The method is useful
XX for modifying growth and development of plants, and cellular responses to
XX external stimulus, such as environmental factors and disease pathogens.
XX The sequences are useful in genome and physical mapping, in positional
XX cloning of genes, in various assays to determine biological activity, to
XX raise antibodies, to isolate corresponding interacting proteins and other
XX compounds, and to quantitatively determine levels of interacting proteins
XX or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata
XX and Eucalyptus grandis polynucleotides and PCR primers used in the method
XX of the invention
XX SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;
Query Match 20.8%; Score 638.2; DB 6; Length 661;
Best Local Similarity 98.9%; Pred. No. 1.2e-165;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
Qy 1019 CTGAGCCATTAAATTCGAGAGCAGATCGCCCAAAATTTCTTCTGCTGCCATACTGT 1078
Db 1 CTGAGCCATTAAATTCGAGAGCAGATCGCCCAAAATTTCTTCTGCTGCCATACTGT 60
Qy 1079 CGAATTTTCTTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 1138
Db 61 CGAATTTTCTTTTAGTAAAGTAAACCAATGATCGCCCATGTTGACAAAAGGCTGATTA 120
Qy 1139 GTATGATCTTGGAGTTGTTGGTGCAAATTTGCAAGCTGAGATGGCCCTCAGGGAAT 1198
Db 121 GTATGATCTTGGAGTTGTTGGTGCAAATTTGCAAGCTGAGATGGCCCTCAGGGAAT 180
Qy 1199 AAGGGCCCAACCCAGATGCAAGAGCAGACAGCCCAACCTTCTCTTAAACAAG 1258

[illegible]

RESULT 15	
ABK48067	
ID	ABK48067 standard; cDNA; 1501 BP.
XX	
XX	ABK48067;
XX	
DT	15-JUL-2002 (first entry)
XX	
XX	cDNA encoding 5-hydroxyconiferaldehyde O-methyltransferase (AldOMT) .
DE	
XX	plant; aspen; phenylpropanoid pathway; agronomic; lignin; paper;
XX	4-coumarate-CoA ligase; 4CL; coniferyl aldehyde 5-hydroxylase; CAlc5H;
KW	S-adenosyl-L-methionine-dependent; SAM; AldOMT: transgenic; grass;
KW	5-hydroxyconiferaldehyde O-methyltransferase; cellulose; pulp;
KW	coniferyl alcohol dehydrogenase; CAD; sinapyl alcohol dehydrogenase; SAD;
KW	syringyl; guaiacyl; agriculture; gene; ss.
XX	
XX	Populus tremuloides.
OS	
XX	
FH	Key
FD	Location/Qualifiers
FT	65..1162
FT	/*tag= a
FT	/product= "5-hydroxyconiferaldehyde O-methyltransferase
FT	(AldOMT)"
XX	
FN	WO200220717-A2.
XX	
PD	14-MAR-2002.
XX	
PF	05-SEP-2001; 2001WO-US027445.
XX	
PR	05-SEP-2000; 2000US-0230086P.
XX	
PA	(UNMT) UNIV MICHIGAN TECHNOLOGICAL.
XX	
PI	Chiang VLC, Li L;
XX	
XX	WPI; 2002-351773/38.
DR	P-PSDB; AAU80015.
XX	
PT	Genetically transforming plant with multiple genes from phenylpropanoid

XX	Eucalyptus grandis.
XX	OS
XX	Key Location/Qualifiers
FT	TATA_signal 537..543
FT	/tag= a
XX	
XX	US2005026162-A1.
PN	
XX	
PD	03-FEB-2005.
XX	
PF	06-NOV-2003; 2003US-00702319.
XX	
XX	25-MAR-1999; 99US-00276599.
PR	30-JUL-1999; 99US-0146591P.
PR	24-FEB-2000; 2000WO-NZ000018.
PR	20-JUN-2000; 2000US-00598401.
PR	28-NOV-2000; 2000US-00724624.
PR	09-NOV-2001; 2001US-0345397P.
PR	30-APR-2002; 2002US-00137036.
PR	08-NOV-2002; 2002US-00291447.
PR	08-NOV-2002; 2002US-0425087P.
XX	
XX	(GENE-) GENESIS RES & DEV CORP LTD.
PA	(RUBI-) RUBICON FORESTS HOLDINGS LTD.
XX	
PI	Perera R, Rice SJ, Eagleton CK;
XX	
DR	WPI; 2005-131806/14.
XX	
PT	New isolated polynucleotide sequences comprising a functional vascular tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase promoter, useful for modifying gene expression.
PT	
XX	
PS	Claim 2; SEQ ID NO 12; 82pp; English.
XX	
CC	The invention relates to a novel isolated polynucleotide sequence comprising a functional vascular tissue-specific Eucalyptus grandis caffeic acid O-methyltransferase (COMT) promoter (ADW80462 or ADW80563). Also claimed is a genetic construct comprising the above polynucleotide sequence or a sequence having 2096 base pairs fully defined in the specification (ADW80510), a host cell comprising the above genetic construct, a plant comprising the genetic construct, a method for producing a plant with modified gene expression, and a method for identifying a gene responsible for a desired function or phenotype. The composition and methods are useful for modifying gene expression or for modifying the transcription of endogenous and/or heterologous polynucleotides involved in wood formation. The present sequence is used in the exemplification of the invention.
XX	
SQ	Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;
	Query Match 20.8%; Score 638.2; DB 14; Length 661;
	Best Local Similarity 98.9%; Pred. No. 1.2e-165;
	Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY	1019 CTGAGCCATTTAAATTCGAGACCATCGCCCAAAATTATCTTCTTGCTGCCATAACTGT 1078
Db	1 CTGAGCCATTTAAATTCGAGACCATCGCCCAAAATTATCTTCTTGCTGCCATAACTGT 60
QY	1079 CGAATTTTCTCTTTTAGTAAGTAACCAATGATCGGCATGTTGACAAAAGGCTGATTA 1138
Db	61 CGAATTTTCTCTTTTAGTAAGTAACCAATGATGCATCATGTTGACAAAAGGCTGATTA 120
QY	1139 GTATGATCTTGAGTTGTTGGTGC AAATTCGAAGCTGACGATGGCCCCCTCAGGAAATT 1198
Db	121 GTATGATCTTGAGTTGTTGGTGC AAAATTTTGAAGCTGACGATGGCCCCCTCAGGAAATT 180
QY	1199 AAGGGCCCAACCAGATTGCAAAGAGCACAAAGAGCAGACCCCAACCTTCTTTAACAAAG 1258
Db	181 AAGGGCCCAACCAGATTGCAAAGAGCACAAAGAGCAGATCCCAACCTTCTTTAACAAAG 240
QY	1259 ATCATCACCAGATCGGCCCAAGTAGGGTAAATTAATTTAAACAATAGCTCTTGATACCGGG 1318

PT pathways, comprises incorporating number of genes into the genome of the
 XX plant, to produce plants displaying altered agronomic traits.

PS Example 2; Fig 4A; 95pp; English.

XX The invention relates to a method of genetically transforming a plant
 CC simultaneously with multiple genes from the phenylpropanoid pathways,
 CC comprising incorporating into the genome of the plant, a number of genes,
 CC their substantially similar fragments or their combinations, to produce
 CC plants displaying altered agronomic traits. The genes are selected from 4
 CC -coumarate-CoA ligase (4CL), coniferyl aldehyde 5-hydroxylase (C4H5H), S
 CC -adenosyl-L-methionine (SAM), coniferyl alcohol dehydrogenase (CAD) and
 CC methyltransferase (AldomT), coniferyl alcohol dehydrogenase (CAD) and
 CC sinapyl alcohol dehydrogenase (SAD). The method is useful for the
 CC transformation of plant tissue for the alteration of lignin monomer
 CC composition, increased syringyl/guaiacyl (S/G) lignin ratio and increased
 CC cellulose content and transgenic plants resulting from such
 CC transformations. This is an improved method to simultaneously control the
 CC lignin quantity, lignin compositions, and cellulose contents in plants,
 CC and is applicable to all plant species that are susceptible to the
 CC transfer of genetic information by Agrobacterium or other gene delivery
 CC system. The method is of particular value to paper and pulp industries
 CC because lignin containing higher syringyl monomer content is more
 CC susceptible to chemical delignification. Woody plants transformed with
 CC DNA constructs offer a significant advantage in the delignification
 CC process over conventional paper feedstocks. Similarly, modification of
 CC the lignin composition in grasses by insertion and expression of
 CC heterologous SAD gene offers a unique method for increasing the
 CC digestibility of grasses and is of significant potential economic benefit
 CC to the farm and agricultural industries. The present sequence represents
 CC the coding sequence of 5-hydroxyconiferaldehyde O-methyltransferase
 CC (AldomT) used in the method of the invention

XX Sequence 1501 BP; 396 A; 344 C; 331 G; 430 T; 0 U; 0 Other;

Query Match 20.6%; Score 631; DB 631; Length 1501;
 Best Local Similarity 74.5%; Pred. No. 1.8e-163;
 Matches 807; Conservative 0; Mismatches 275; Indels 1; Gaps 1;
 1687 GAGACCAGATGACCCGACCCAAAGTCTCGGACGACGAGGGGAACTCTTCGCCATGCGAG 1746
 80 GAAACTCAGATGACTCCAACTCAGGTATCAGATGAGAGGACACACCTCTTTGGCCATGCAA 139
 1747 CTGCGAGCGCTCCGCTGCTCCCATGCTCTTAAGCGCCGATCGAGATCGACTCTCTC 1806
 140 CTAGCCAGTCTTCTCAGTCTTACCAATGATCTCTCAAAACAGCCATTGAACCTGACTCTT 199
 1807 GAGATCATGGCCAAAGGACGGGCGCGCTTCTCTCCACGGGGGAAATCGCGGCACAG 1866
 200 GAAATCATGGCTAAAGCTGGCCCTGGTCTTCTTGTCCACATCTGAGATAGCTTCTCAC 259
 1867 CTCCCGACCCAGAACCCGAGGACACCGTATGCTCGACCGGATCTTCGGGCTGCTGGCC 1926
 260 CTCCCTACCAAAACCCCTGATGCGCTGTCTATGTTAGACCGTATCTCTCGGCTCTGGCT 319
 1927 AGCTACTCCGTGCTCAGTGTGACCTCTCGGACCTCTCCGATGCGAGGCTCGAGGCTC 1986
 320 AGCTACTCCATTTCTTACCTCTCTCTGAAAGATCTTCTGATGGGAGGTTGAGAGACTG 379
 1987 TACGGCTTAGCGCGGTGTGCAAGTCTTGGTCAAGAACGAGGACGGGCTCTCCATCGCC 2046
 380 TATGGCTCTGCTCTGTTGTAAATTTCTTGACCAAGAACGAGGACGGTGTCTGTGACG 439
 2047 GCACTCAACTTGTATGAACCAAGGACAAATCTCTCATGGAAAGCTGTTATTAACCTGAAAGAT 2106
 440 CCTCTGTCTCTCATGAACCAAGGACAAAGTCTCTCATGGAAAGCTGTTATTTGAAAGAT 499
 2107 GCGGTCTTTGAGCGGGAATCCCAATTCAAAGCGGTACGGGATGACGGGTTCCAGTAT 2166
 500 GCAATTTCTGTATGAGGAAATTCATTTTAAAGAGGCTATGGGATGACTGCAATTTGAATAT 559
 2167 CATGGCACCGACCGCGGATTCACCAAGATCTTTTAAACGGGGAATGTCTGATCACTCCACC 2226

Db 560 CATGGCACCGATCAAGATTTCAAAAGGTCTTCAACAAGGAATGTCTGACCACTCTTACC 619
 Qy 2227 ATTACTATGAAGAAGATACATGGAAGGCTTCGAGGCTTCGAGGCTTCGAGAGCGTGGTC 2286
 Db 620 ATTACCATGAAGAAGATTTCTTGAGACCTCAAAAGGCTTTTGAAGGCTTCACGTCTCTGGTG 679
 Qy 2287 GATGTCGGAGCGGCACTGGGCGCGTCTCAGCATGATCTGTCGCAATACCCATCAATG 2346
 Db 680 GATGTTGGTGGGACTGGAGCGCTGTTAAACACCATCTCTCTAAATACCTTCAATC 739
 Qy 2347 AAGGAGATCAACTTGA - CGGCCCCAACGGAATTGAAGAGCCGCCACCCCTTCTGGTGGTC 2405
 Db 740 AAGGCAATTAACCTTCGATCTGCCCCACGCTATTGAGGATCCCCCATCTTATCCCGGAGTG 799
 Qy 2406 AAGCAGCTCGAGCGACATGTTCTGTCAGCGTTTCCAAAGGGAGATGCCATTTTCATCAAG 2465
 Db 800 GAGCATGTTGGTGGGACATGTTTGTAGTGTGCCCAAGCAGATGCCGTTTTCATGAAG 859
 Qy 2466 TGGATATGCCATGACTGGAGTGACGACCATTTGGCGCAAGTTCTCAAGAACTGCTACGAT 2525
 Db 860 TGGATATGCCATGATTGGAGCGAGCCCACTGCTTAAATTTCTTGAAGATTTGCTATGAC 919
 Qy 2526 GCCTTCCCAACAATGGAAGGTGATGTTGTCAGAGTGTGCTACTCCCTGTGTACCCAGAC 2585
 Db 920 GCGTTGCCGGAACCGCAAGGTGATCTTGTGAGTGCATTTCTTCCGCTGGCTCTTGAC 979
 Qy 2586 ACAGGCTTAGCGACCAAGATGTGATCCACATCGATCGATCTGTTGGCCCAACCCCA 2645
 Db 980 ACAAGCTTGGCCACCAAGGAGTGTGTCACGTTGATGTCTATCATGTTGGCGCACACCCC 1039
 Qy 2646 GCGCGGAAAGAGAGGACACAAAGGAGTTTCGAGGCAATTCGCAAAAGGGGCGGATTTTCAG 2705
 Db 1040 GGTGGGAAAGAGAGGACCCGAGAGGAATTTGAGGGCTTACCTAAGGGAGCTGGCTTCAA 1099
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 Db 1160 TAA 1162

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Listing first 45 summaries

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6: gb_est7.*
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8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535.4	17.4	1315	6	CNS09ZRE
2	533	17.4	901	10	DT546163
3	512	16.7	907	8	CO072302
4	504.2	16.4	930	10	DT566827
5	504	16.4	840	4	CB975481
6	494.8	16.1	958	10	DT566827
7	490.8	16.0	853	8	CO071813
8	489.6	15.9	864	8	CO082948
9	489.2	15.9	895	10	DT558009
10	489	15.9	880	8	CO087218
11	488.6	15.9	961	9	DT566827
12	484.8	15.8	931	9	DT566827
13	480.6	15.7	964	9	DT566827
14	479.8	15.6	917	9	DT566827
15	473	15.4	911	10	DT566827
16	472	15.4	879	9	DT566827
17	471.6	15.4	848	8	CO080744
18	469.4	15.3	891	10	DT566827
19	468.4	15.3	874	9	DT566827

20	466.4	15.2	838	5	CK319716
21	466.4	15.2	936	9	CK665083
22	464.2	15.1	904	9	CK664451
23	462.8	15.1	847	10	DT571100
24	461.6	15.0	833	8	CO080205
25	460.4	15.0	778	8	CO113461
26	459.4	15.0	809	8	CO094187
27	458.6	14.9	903	9	CK664005
28	457	14.9	892	9	CK664055
29	456	14.9	901	8	CK053237
30	454.8	14.8	865	10	DT566827
31	454.6	14.8	812	8	CNS24481
32	454	14.8	939	9	CK670522
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34	449.6	14.6	881	10	DT572664
35	440.8	14.4	834	10	DT534066
36	438	14.3	759	5	CF235608
37	436.4	14.2	853	10	DM016705
38	436	14.2	782	5	CK319284
39	435.2	14.2	821	8	CO127529
40	433.2	14.1	817	10	DT558669
41	431.6	14.1	794	8	CO079925
42	431	14.0	585	10	DR919300
43	430.2	14.0	925	9	CK665084
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ALIGNMENTS

RESULT 1	CNS09ZRE	1315 bp	mrna	linear	HTC 06-FEB-2004
LOCUS	Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSTRPGH15ZH04 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).				
DEFINITION	Arabidopsis thaliana (thale cress)				
ACCESSION	BX831565				
VERSION	1				
KEYWORDS	HTC; GSTR cDNA.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1 (bases 1 to 1315)				
AUTHORS	Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.				
TITLE	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1315)				
AUTHORS	Genoscope.				
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)				
COMMENT	- Web : www.genoscope.cns.fr The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.				
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/tissue_type="Hormone Treated Callus"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
1. .1315
/gene="At5g54160"

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Query Match 17.4%; Score 535.4; DB 6; Length 1315;
Best Local Similarity 70.0%; Pred. No. 9.4e-143;
Matches 780; Conservative 0; Mismatches 326; Indels 9; Gaps 4;

QY 1685 CCGAGACCCAGATGACCCGACCAAGTCTCGGACGACGAGCGAACCCTTCGCGCATGC 1744
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QY 1745 AGCTGGGAGCGGCTCCGTCCTCCCATGTCTCTAAAGCGCGCATCGAGATCGACCTCC 1804
DB 133 AACTAGCAGTGTCTCCGTCCTTCCGATGGCTTTAAGATCCGCTTAGAGCTTGACCTTC 192
QY 1805 TCGAGATCATGCGCAAGCGGCGCGGCGGTCTCTCCAGCGGGGAAATCGCGGCAC 1864
DB 193 TTGAGATTATGGCAAGAAATGTTCTCCATGTCTCTACC-----GAGATCGCTTCG 246
QY 1865 AGCTCCGACCCAGAACCCGAGGACCCGTCATGTCGACGCGATCTCCGCTCGCTGG 1924
DB 247 AACTTCCGACCAAAATCCTGAAGTCGCGTCATGTCGACCGTATCTCCGCTCTCTTA 306
QY 1925 CCAGTACTCCGTCGTCAGTGCACCTCCGCGACCTCCCGATGCGCAAGTCTCCATCG 1984
DB 307 CGCTTACTCCGCTTAACTCCGCTCCCAACCTTAACCTTCCGCTGATGGCTTGAACGA 366
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DB 487 ATGCAATTTTGTGTTGGATTCCTTCAAGGCTTATGCAATGAGCTCGTTCGAGT 546
QY 2165 ATCATGCGACCGACCGCG-ATTCACAGATCTTTTACCGGGGAAATGTCTGATCACTCC 2223
DB 547 ACCACGGGACTGAACCTAGCATTTCAACCAAGGCTTTTAAACATGGAAATGTCTAACCATTC 606
QY 2224 ACCATTACTATGAAGAGTACTGGAACATACCAAGGCTTCGAGGCGCTCGAGACCGTG 2283
DB 607 ACAATACCATGATGAAGAGATCTTGAAGCTTATGAGCTTAAAGGTTTGAAGGATTAACTTCTTTG 666
QY 2284 GTCCATGTTCGAGGCGGACATGGGCGGTCTCAGCATGATCGTTCGCCAAATACCATCA 2343
DB 667 GTTGATGTGTGGTGGAAATGGTGTCTTAAACTCAAAATGATGTCTCCAAGTACCCCTAAT 726
QY 2344 ATGAAGGATCAACTTTCGACCGCGC-CAACGGATTTGAAGACCGCCGCCCTTCCTGCT 2402
DB 727 CTTAAAGGCATCAACTTTTGAATCTCCCATGTCTCATCGAGATGCTCTCTCATCCTGCT 786
QY 2403 GTCAGACAGCTCGGAGGCGCATGTTTGTGAGCGTTCCTCAAGGAGATGCCATTTTCATG 2462
DB 787 ATTGAGCATGTGGAGGAGATATGTTTGAAGTGTCTTAAAGTGTGATGATGATTCATG 846
QY 2463 AAGTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2522
DB 847 AAGTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
QY 2523 GATGCGCTTCCCAACAAGGAGTGTGTTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2582

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Db 907 GAGTCACCTTCAGAGGATGGAAAGTGTATATTAGCAGTGTATATTCCAGAGACCA 966
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DB 967 GACTCAAGCTCTCAACCAAGTAGTCCATGTCGATTCGATTCGATTCGATTCGAT 1026
QY 2643 CCAGCGGGAAGAGAGGACACAGAGGATTCAGGAGCATTCGCAAGGCGCGGATTT 2702
DB 1027 CCGGAGGCAAGAGAACGAAACCGAGAAAGTTTGGGCAATTAGCCAAAGCATCAGGCTTC 1086
QY 2703 CAGGCTTCCAAAGTCATGTGCTGCGCTTTTCGCGACTCACGTGTCAGGATTCCTCAAGACC 2762
DB 1087 AAGGGGATCAAGT-TTCTGCGAGCTTTTGGTGTAACTTATTGATTTACTCAAGAAG 1145
QY 2763 GCTTGATCTGCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2797
DB 1146 CTCATAAAACAAACATATGTTCTCTATGAAGATGATT 1180

RESULT 2
DT546163 951 bp mRNA linear EST 31-OCT-2005
LOCUS EST1056803 TMO Gossypium hirsutum cDNA, mRNA sequence.
DEFINITION DT546163
ACCESSION DT546163
VERSION DT546163.1 GI:78325889
KEYWORDS EST.
SOURCE Gossypium hirsutum (upland cotton)
ORGANISM Gossypium hirsutum
REFERENCE 1 (bases 1 to 951)
AUTHORS Yang, S.S., Cheung, F., Wei, N.B., Lee, J.J., Ha, M., Stelly, D.M.,
Thaxton, P., Sze, S.H., Triplett, B.A., Town, C.D. and Chen, Z.J.
TITLE ESTs from immature ovule (-3 to 3 DPA) of G. hirsutum TM-1
JOURNAL Unpublished (2005)
COMMENT Contact: Z. Jeffrey Chen
The Chen lab: A Home of Polyploidy (http://polyploidy.tamu.edu)
Texas A&M University
Department of Soil & Crop Sciences, MS2474, College Station, TX
77842-2474, USA
Tel: 979 862 2359
Fax: 979 845 0456
Email: zjchen@neo.tamu.edu
TIGR sequence name: GOAB447TR
Seq primer: CAG GAA ACA GCT ATG ACC.
Location/Qualifiers
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/organism="Gossypium hirsutum"
/mol_type="mRNA"
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/db_xref="taxon:3635"
/tissue_type="Immature ovules"
/dev_stage="Immature ovules (-3 to 3 days post anthesis,
DPA) with or without fibers"
/clone_lib="TMO"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRI; Site 2: NotI;
G. hirsutum L. Texas Marker-1 (TM-1) plants were grown in
a greenhouse at the Texas A&M University and in the field
at the USDA-ARS, New Orleans. The bolls were tagged and
harvested at 3 days before anthesis (-3DPA), the day of
anthesis (0 DPA), and 3 days post anthesis (3DPA) from a
pool of ~20 plants. Total RNA was extracted from immature
ovules or fiber-bearing ovules. An equal amount of total
RNA from three samples was mixed and sent to Invitrogen
Corp. (Carlsbad, California) for full-length cDNA library
construction. Messenger RNA was isolated from the total
RNA using a filter syringe containing oligo (dT). The
first-strand cDNA was synthesized from 15 ug mRNA using
SuperScriptTMIII reverse transcriptase, and the
second-strand cDNA was synthesized using E. coli RNase H,
DNA polymerase I, and DNA ligase. The double-stranded cDNA

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was blunt-ended using T4 DNA polymerase, digested with NotI, size-selected using agarose gel electrophoresis, and directionally cloned into the NotI-EcoRV sites of the pCMV-SPORT6.1. The ligated products were transformed using ELECTROMAX DH10BT cells. The library contained 4.2x10⁶ cfu with ~100% of colony growth rate. It is estimated that over 60% clones contained full-length cDNA inserts with an average insert size of 1.53-kb. A total of 51,072 colonies were arrayed in duplicate sets each with 133 384-well plates for sequencing and storage, respectively."

ORIGIN	
Query Match	17.4%; Score 533; DB 10; Length 951;
Best Local Similarity	75.5%; Pred. No. 4.2e-142;
Matches	687; Conservative 0; Mismatches 221; Indels 2; Gaps 2;
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Qy	760 GAGCATGTTGGTGGAGACATGTTTGAAGTGTTCGAAGGGAGAGCGCACTTCATGAAG 819
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ACCESSION	CO072302
VERSION	CO072302.1 GI:48741783
KEYWORDS	EST.
SOURCE	Gossypium raimondii
ORGANISM	Gossypium raimondii
REFERENCE	1 (bases 1 to 907)
AUTHORS	Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.
TITLE	Global assembly of Cotton ESTs
JOURNAL	Unpublished (2004)
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu Plate: 31 row: G column: 13.
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Query Match	16.7%; Score 512; DB 8; Length 907;
Best Local Similarity	75.6%; Pred. No. 5e-136;
Matches	662; Conservative 0; Mismatches 210; Indels 4; Gaps 2;
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Qy      1964  CCGATGGCAAGGTCGAGCGGCTTAGCGCTTAGCGCGGTGCAAGTCTTGGTCAAGA 2023
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Qy      2024  ACAGGACCGGGTCTCCATCGCGCACTCAACTGATGAACACGAGCAAAATCTCATGG 2083
Db      389  ATGAAGATGGCGTCACTCTTTCGGCCCTCAGTCTCATGAATCAAGACAGGTCCTTATGG 448
Qy      2084  AAGCTGTGTATACCTGAAGATGCGGTCTTGAAGCGGATCCCATTCACACAGGCT 2143
Db      449  AGAGCTGTGTACTTGAAGATGCGGTCTGGAAGGTGAATTCCTTCAACAAGCT 508
Qy      2144  ACGGATGACCGGTTCGAGTATCATGCAACCGACCGCGGATTCACACAGATCTTTAAC 2203
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Db      809  AAGGAGACGCGCATCTTATGAAGTGGATGATGCGACGATGCGATGCGATGCGCA 868
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Db      869  AGTTCTCTCAAGAACTGCTAGGATGCGCTTCCCAACA 2538

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LOCUS   DT566827
DEFINITION EST1077467 TWO Gossypium hirsutum cDNA, mRNA sequence.
ACCESSION DT566827
VERSION   DT566827.1 GI:78346553
KEYWORDS EST.
SOURCE   Gossypium hirsutum (upland cotton)
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 930)
Yang,S.S., Cheung,F., Wei,N.E., Lee,J.J., Ha,M., Stelly,D.M.,
Thaxton,P., Sze,S.H., Triplett,B.A., Town,C.D. and Chen,Z.J.
ESTs from immature ovule (-3 to 3 DPA) of G. hirsutum TM-1
Unpublished (2005)
Contact: Z. Jeffrey Chen
The Chen lab: A Home of Polyploidy (http://polyploidy.tamu.edu)
Texas A&M University
Department of Soil & Crop Sciences, MS2474, College Station, TX
77842-2474, USA
Tel.: 979 862 2359
Fax: 979 845 0456
Email: zjchen@neo.tamu.edu
TIGR sequence name: GOARE57R
Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES
Location/Qualifiers
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/note="Vector: pCMV-SPORT6.1; Site 1: EcoRI; Site 2: NotI;
G. hirsutum L. Texas Marker-1 (TM-1) plants were grown in
a greenhouse at the Texas A&M University and in the field
at the USDA-ARS, New Orleans. The bolls were tagged and
harvested at 3 days before anthesis (-3DPA), the day of
anthesis (0 DPA), and 3 days post anthesis (3DPA) from a
pool of ~20 plants. Total RNA was extracted from immature
ovules or fiber-bearing ovules. An equal amount of total
RNA from three samples was mixed and sent to Invitrogen
Corp. (Carlsbad, California) for full-length cDNA library
construction. Messenger RNA was isolated from the total
RNA using a filter syringe containing oligo (dT). The
first-strand cDNA was synthesized from 15 ug mRNA using
SuperScriptTMIII reverse transcriptase, and the
second-strand cDNA was synthesized using E. coli RNase H.
DNA polymerase I, and DNA ligase. The double-stranded cDNA
was blunt-ended using T4 DNA polymerase, digested with
NotI, size-selected using agarose gel electrophoresis, and
directionally cloned into the NotI-EcoRV sites of the
pCMV-SPORT6.1. The ligated products were transformed using
ELECTROMAXTMHI0B1 cells. The library contained 4.2x106
cfu with ~100% of colony growth rate. It is estimated that
over 60% clones contained full-length cDNA inserts with an
average insert size of 1.53-kb. A total of 51,072 colonies
were arrayed in duplicate sets each with 133 384-well
plates for sequencing and storage, respectively."

ORIGIN
Query Match      16.4%; Score 504.2; DB 10; Length 930;
Best Local Similarity 74.5%; Pred. NO. 9.2e-134;
Matches 662; Conservative 0; Mismatches 223; Indels 4; Gaps 2;

Qy      1687  GAGACCCAGATGACCCCGACCAAGTCTCGGACGAGGCGAACTCTTCGCCATGCGAG 1746
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Db      102     CTGGCAGTGCATCAGTCTCTCCCATGTCCTCAATCAGCCATTGAACTTGCTCTC 161
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Qy      2047  GCATCTCAACTTGATGAACCAAGGACCAAAATCCTCATGAAAGCTGGTATTACCTGAAGAT 2106
Db      402     GCCCTTAGTCTCATGAATCAAGCAAGGTCCTTATGAGAGCTGGTACTTACTTGAAGAT 461
Qy      2107  GCGGTCTTTGAAGCGGAAATCCCATTCACAGGGGTACGGGATGACCCCGTTCGATAT 2166
Db      462     GCTGTGCTGGATGGTGAATTCATTCACAAAGGCTTATGGTATGACTGCACTTGTAGTAC 521
Qy      2167  CATGGCACCGGACCGGATTCACAGATCTTTAACCGGGGATGCTGATCACTCACTCCACC 2226

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Db 522 CATGGCACTGATCTAGATTCAACAAGGTTTTCACAGGGGAATGTCTGATCACTTACC 581
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Db 882 GAAGCTTTGCCAGACAAACGGGAAGTGTATGTTGCCGAATGCATTTCTTC 930

RESULT 5
CB975481
LOCUS
DEFINITION
CB975481
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

CB975481 848 bp mRNA linear EST 01-MAY-2003
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CB975481
CB975481.1 GI:30298687
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Vitis vinifera
Vitis vinifera
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 848)
Goes da Silva,F., Randolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave. Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
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berry set from field-grown vines during stage I of berry
growth, 17 days after full bloom. The average berry size
was 6 millimeters. Sampled vines were located at the
University of California, Davis, Experimental Vineyard.
cDNAs were made by oligo-dT priming and directionally

cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AAGCTAGGTTATCAAGCGAGTGGCAATTCACCGGG-3' and
5'-ATTCTAGAGCCGAGCGGCGACATG-dt(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 16.4%; Score 504; DB 4; Length 848;
Best Local Similarity 75.6%; Pred. No. 1e-133;
Matches 639; Conservative 0; Mismatches 205; Indels 1; Gaps 1;

Qy 1826 GGCGGGCGGTTCTCTCCACGGGGGAAATCGCGGCACAGTCCCGACCCAGAACCCCG 1885
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Qy 2006 GCAAGTCTTGTGTCAGAAACGAGGACGGGTTCTCCATCGCCGACCTCAATTTGATGAACC 2065
Db 181 GCAAGTACTTGTAGTACGAAACGAGATGGGGTGTCTGTAGCCCTCTTCTCTCATGAATC 240
Qy 2066 AGGACAAATCTCATGGAAGCTGTATTACCTGGAAGTGGCTCTTGAAGGCGGAA 2125
Db 241 AGGACAAAGTCTTCATGGAGAGCTGTGTTATTTGAAGATGAGTCTTGTGATGGTGA 300
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Db 361 TCACAAAGGTTTCAACAATGGAATGTCTGGTCACTTCCACATTAATCCATGAAGAAATTC 420
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DV465073 958 bp mRNA linear EST 20-OCT-2005
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 ACCESSION DV465073
 VERSION DV465073.1 GI:77989246
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 ORGANISM Populus fremontii x Populus angustifolia
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 REFERENCE 1 (bases 1 to 958)
 AUTHORS Harding S.A., Elliott S.G., Montag J.D. and Tsai C.-J.
 TITLE Expressed sequence tags from Populus fremontii x Populus angustifolia
 JOURNAL Unpublished (2005)
 COMMENT Contact: Chung-Jui Tsai
 Biotech Research Center
 Michigan Technological University, School of Forest Resources & Environmental Science
 1400 Townsend Drive, Houghton, MI 49931-1295, USA
 Tel: 906 487 2914
 Fax: 906 487 2915
 Email: chtsai@mtu.edu.

FEATURES
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ORIGIN
 Query Match 16.1%; Score 494.8; DB 10; Length 958;
 Best Local Similarity 73.7%; Pred. No. 4.9e-131;
 Matches 656; Conservative 0; Mismatches 232; Indels 2; Gaps 2;
 QY 1687 GAGACCGAGTACCCCGACCAAGTCTCGGACGACGAGGCGAACCTTTCGCCATCGAG 1746
 DB 69 GAAACTCAGATGACTCCAACTCAGATATCAGATGAAGGACACCTCTTGGCAGTCAA 128
 QY 1747 CTGGCGAGCGCTCGTCTGCCATGGTCTTAAGGCGCGCATCGAGATGACCTCTC 1806
 DB 129 CTAGCCAGTGTTCAGTTCTACCAATGATCTCAAAACAGGCAATGAATCGACCTTCT 188
 QY 1807 GAGATCATGGCCAGGACGGCGGGCG - CTTTCTCTCCAGCGGGGAAATCGGGGACA 1865
 DB 189 GAAATCATGGCTAAAGCTGGCCCTGGTGCCTTTCTGTCCACATCTGAGATAGTCTTCA 248
 QY 1866 GCTCCCGACCGAGACCCCGAGGACCGTCTATGCTCGACCGGATCTTCCGGCTGCTGGC 1925
 DB 249 CTTCCCTACCAAAACCTTGATGCGCTGTCTATGTAGACCGTATCTTGGCCCTCTGGC 308
 QY 1926 CAGTACTCTCGTGTCTCAGTGCACCTCCCGGACCTCCCGATGGCAGGCTGAGCGCT 1985
 DB 309 TAGTACTCTCAATCTTACTTGTCTCTGAAAGATCTTCTGATGGAAAGTTGAGAGCT 368
 QY 1986 CTAGCGCTTAGCGCGGTGTCAAGTCTTGTGTAAGAACGAGGACGGGTCTCCATCGC 2045
 DB 369 GTATGGCCTTGTCTCTGTGTAAGTCTTGTGTAAGAACGAGGACGGGTGTCTGTGTCAG 428
 QY 2046 CGCACTCAACTTGTGTAAGAACGAGGACAAATCTCTATGGAAGCTGGTATTACCTGAAAGA 2105

Db 429 CCCTCTCTGCTCATGTAACGAGCAAGGTCCTCATGTAAGCTGGTATTATTGAAAGA 488
 QY 2106 TGGCGTCTTTGAAGCGGAATCCCATTAACAAGGCTAGCGGATGACCCGCTTCAGTA 2165
 Db 489 TGCATTTCTTTGGTGAGGAATTCATTTAAACAAGGCTATGGGATGACTGCATTTGAATA 548
 QY 2166 TCATGGCACCGACCGCGGATTCACAGATCTTTAAACCGGGGAATGCTCATCACTCCAC 2225
 Db 549 TCATGGCAGCGATCCAAAGATTCACAAAGGCTTTCATTAAGGAATGCTGACCACTTAC 608
 QY 2226 CATTACTATGAAGAAGTACTTCGAAACATACAAGGGCTTCGAGGGCTTCGAGACCGTGGT 2285
 Db 609 CATTACCATGAAGAAGCTTCTTGAGACCTACAAGGCTTTGAAGGCTCCACATCCTTGGT 668
 QY 2286 CGATGTGGAGGCGGACCTGGGGCCGTGCTCAGCATGATCGTTGCCAAATACCCATCAAT 2345
 Db 669 GGATGTTGGTGGGACTGGAGCTGTCGTAAACACCATGCTCTCTAAATACCCCTTCAAT 728
 QY 2346 GAAAGGATCAACTTCGA - CGGCCCAACGGAATGAAGAGCGCCCAACCCCTTCTCGTGT 2404
 Db 729 TAAGGCAATTAACCTTTGATCTGCCCCACGTCATTGAGGATGCCCATCTTATCCGGTGT 788
 QY 2405 CAAGCACGTCGGAGCGGACATGTTGTCAGCGTTCGAGGGATGATGCGATTTTCATGAA 2464
 Db 789 GGAGCATGTTGGTGGGACATGTTGTTAGTGTGCCAAGCAGATGCGGTTTCATGAA 848
 QY 2465 GTGGATATGCAATGATGAGTGAGGACCATTCGCGGAAGTTCCTCAAGAATGCTCAGA 2524
 Db 849 GTGGATATGCCATGATTGGAGCGGACGACATGCTCTTAAATTCCTGAAGAATGCTATGA 908
 QY 2525 TGCCTTCCCAACATGAAAGGTGATCGTTGCGAGAGTGCCTACTCCCTG 2574
 Db 909 GCGCTTGGCGGAAAGAACGCGAGTGATCTTTGTGAGTGATCTTCTCCG 958

RESULT 7
 LOCUS CO071813
 DEFINITION GR_Ea30H18.r GR_Ea Gossypium raimondii cDNA clone linear EST 15-JUN-2004
 mRNA sequence.
 ACCESSION CO071813
 VERSION CO071813.1 GI:48741294
 KEYWORDS EST.
 SOURCE Gossypium raimondii
 ORGANISM Gossypium raimondii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 REFERENCE 1 (bases 1 to 853)
 AUTHORS Kim H., Yu Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and Wing, R.A.
 TITLE Global assembly of Cotton ESTs
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 Plate: 30 row: H column: 18.
 Location/Qualifiers
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 /organism="Gossypium raimondii"
 /mol_type="mRNA"
 /db_xref="taxon:29730"
 /clone="GR_Ea30H18"
 /tissue_type="whole seedlings"
 /dev_stage="first true leaves"
 /lab_host="DH10B"
 /clone_lib="GR_Ea"
 /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:

ECORV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

ORIGIN		Query Match		Best Local Similarity		Matches		Conservative		0; Mismatches		217; Indels		1; Gaps		1;	
Qy	1702	CCGACCAAGTCTCGGACGAGGCGAAGCTCTTCCCATGCGAGTGGGAGGCGCTCC	1761														
Db	4	CCACCAAGTCTCAGATGAGGAGCCACTTATTCGCTATGCAACTTGGCAGTGCATCA	63														
Qy	1762	GTGCTCCCATGCTCTTAAAGGCGCCATCGAGATCGACCTCTCCGAGATCATGGCCAAAG	1821														
Db	64	GTCTCCCATGCTCTTAAAGGCGCCATCGAGATCGACCTCTCCGAGATCATGGCCAAAG	1821														
Qy	1822	GACGGCGCGGCGGCTTCTCTTCCACGGGGAAATCGCGACACAGTCTCCGACCCAGAAC	1881														
Db	124	GCTGTCCAGTGTCTTCTTGTGCCCAAGAGAGTGGCTTCCAAGCTCCCAACCAAC	183														
Qy	1882	CCGAGGACCGCTATGCTCGACCGGATCTTCGGGTGCTGGCAGTACTCGGTGCTC	1941														
Db	184	CCTGATGACCGGCTATGCTGGACCGTATCTTGGCTCTCCTGGCTAGCTACAAGTCTC	243														
Qy	1942	ACGTGACACCTTCGCGACCTCCCGATGGCAAGTTCGAGCGGCTTACGGCTTAGCGCG	2001														
Db	244	ACTTGTCTTGTGCTACCTCTCTGATGGCAAGTGGTGAAGACTATATGGCTTGGCCCT	303														
Qy	2002	GTGTGCAAGTCTTGTGTCAAGAACGAGGAGGGGTCTCCATCGCGCACTCAACTTGATG	2061														
Db	304	GTGTGCAAGTCTTGTGTCAAGAACGAGGAGGGGTCTCCATCGCGCACTCAACTTGATG	2061														
Qy	2062	AACGAGCAAAATCTCTATGGAAGTGTGTATTAACCTGAAAGATGGGCTTCTTGAAGGC	2121														
Db	364	AATCAAGACAAAGTCTTATGAGAGCTGTGTACTTACTTGAAGATGTGTGCTGGATGT	423														
Qy	2122	GGATCCCATTCACAAAGGCTGAGGATGACCGGCTTCAGTATCATGCGACCGACCCG	2181														
Db	424	GGATCCCATTCACAAAGGCTGAGGATGACCGGCTTCAGTATCATGCGACCGACCCG	2181														
Qy	2182	CGATTTCAACAAAGTCTTTTAAACCGGGGAATGCTGATCACTCCACATTACTATGAAGAG	2241														
Db	484	AGATTTCAACAAAGTCTTTTAAACCGGGGAATGCTGATCACTCCACATTACTATGAAGAG	2241														
Qy	2242	ATACTGAAACATACAAAGGCTTGAAGGCTCGAGACCGTGTGATGTGCGAGGCGGC	2301														
Db	544	ATTCGATACATATGATGTTTCCAAAGGACTAAACACATTGGTTCGATGTTGGCGGTGT	603														
Qy	2302	ACTGGGCGGTGCTCAGCATGATGTTGCCAATATACCATCATGAAAGGATCACTTC	2361														
Db	604	ACGGTGCCACGCTTAGCATGATGCTCTTAAGTACCCCAACCAATGAAAGGATTAACCTT	663														
Qy	2362	GA-CCGCCCCAACCGAATTGAAGACGCCGCCCTTCTCGTGTCAAGACAGCTCGGAGGC	2420														
Db	664	GAATTGCTCATGTCATGAGTGTCTTCTAGTGTCTCCGGTGTGAGCATGTTGTGGA	723														
Qy	2421	GACATGTTGTGACGCTTCCAAAGGAGATGCCATTTTCATGAAGTGGATATGCGATGAC	2480														
Db	724	GACATGTTGTGACGCTTCCAAAGGAGATGCCATTTTCATGAAGTGGATATGCGATGAC	783														
Qy	2481	TGGAGTGACCAACATTGCGCGAAGTCTCTCAGACACTGCTACGATGCGCTTCCCAACAT	2540														
Db	784	TGGAGTGACCAACACTGCGCAAGTCTTGAAGAACTGCTATGAAGCTTTTGCCAGACAAC	843														
Qy	2541	GGAAAGGTGA	2550														
Db	844	GGGAAAGTGA	853														
RESULT 8		CO082948		LOCUS		864 bp		mRNA		linear		EST 15-JUN-2004					

DEFINITION		GR_Ea47M18.r GR_Ea Gossypium raimondii cDNA clone GR_Ea47M18 3', mRNA sequence.	
ACCESSION		CO082948	
VERSION		CO082948.1	
KEYWORDS		GI:48752429	
SOURCE		EST.	
ORGANISM		Gossypium raimondii	
REFERENCE		Gossypium raimondii	
AUTHORS		Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.	
TITLE		Global assembly of Cotton ESTs	
JOURNAL		Unpublished (2004)	
COMMENT		Contact: Rod A. Wing Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu Plate: 47 row: M column: 18.	
FEATURES		Location/Qualifiers	
source		1..864	
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		/tissue_type="whole seedlings"	
		/dev_stage="first true leaves"	
		/lab_host="DH10B"	
		/clone_lib="GR_Ea"	
		/notes="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."	
ORIGIN		Query Match 15.9%; Score 489.6; DB 8; Length 864; Best Local Similarity 75.9%; Pred. No. 1.5e-129; Matches 617; Conservative 0; Mismatches 195; Indels 1; Gaps 1;	

Qy	1687	GAGACCCAGATGACCCGACCCCAAGTCTCGGACGAGGCGGACCTTTCGCCATGCAG	1746
Db	52	GAAACCCAAATGACTCCACCCCAAGTCTCGGATGAGGAGCCAACTATTTCGCCATGCAA	111
Qy	1747	CTGGCGAGCGCTTCGCTGCTCCCATGGTCTCTAAAGCGCCCATCGAGATCGACCTCTC	1806
Db	112	CTCACCAGTGCCTCAGTCTTCCATGGTCTCTCAAGTCGCGCATAGACTTGACCTGCTG	171
Qy	1807	GAGATCATGSCCAAGACGCGGCGGCGGTCTCTTCCACGCGGGGAAATTCGGGCAACAG	1866
Db	172	GAGATCATGSCCAAGACGCGGCGGCGGTCTCTTCCACGCGGGGAAATTCGGGCAACAG	231
Qy	1867	CTCCGACCCAGACCCCGAGGCAACCGTCTGATGCTCGACCGATCTTCGGCTGCTGGCC	1926
Db	232	CTCCGACCCAGACCCCGAGGCAACCGTCTGATGCTCGACCGATCTTCGGCTGCTGGCC	291
Qy	1927	AGCTACTCTCGTGTCTACGTCACCTCCCGACCTCCCGATGGCAAGGTCGAGCGGCTC	1986
Db	292	ACCTACTCTCATCTCTACTTGTCTCTTGGCGACTCTTCTGATGCGCAAGTGGAGACTC	351
Qy	1987	TACGGCTTAGCGCGGTGTGCAAGTCTTGGTCAAGAACGAGACCGGGGTCTCCATCGCC	2046
Db	352	TATGGTCTTGGCCCTGTCTGCAAAATTCGTGACCAAGATGAAGATGSCGTCACTCTTTC	411
Qy	2047	GCACTCAACTTGATGAACCGAGCAAAATCTCATGGAAGCTGGTATTACCTGGAAGAT	2106
Db	412	GCCCTCAGTCTCATGAATCAAGCAAGGCTCTTATGAGAGCTGGTACTACTTTGAAAGAT	471
Qy	2107	GCGGTCTTGAAGCGGGAATCCCATTCACAAAGCGGTACGGGATGACCGGTTTCGAGTAT	2166

RNA from three samples was mixed and sent to Invitrogen Corp. (Carlsbad, California) for full-length cDNA library construction. Messenger RNA was isolated from the total RNA using a filter syringe containing oligo (dT). The first-strand cDNA was synthesized from 15 ug RNA using SuperScriptTMIII reverse transcriptase, and the second-strand cDNA was synthesized using E. coli RNase H, DNA polymerase I, and DNA ligase. The double-stranded cDNA was blunt-ended using T4 DNA polymerase, digested with NotI, size-selected using agarose gel electrophoresis, and directionally cloned into the NotI-EcoRV sites of the pCMV-SPORT6.1. The ligated products were transformed using ELECTROMAXTM DH10BT1 cells. The library contained 4.2x10⁶ cfu with ~100% of colony growth rate. It is estimated that over 60% clones contained full-length cDNA inserts with an average insert size of 1.53-kb. A total of 51,072 colonies were arrayed in duplicate sets each with 133 384-well plates for sequencing and storage, respectively."

ORIGIN

Query Match	15.9%	Score 489.2	DB 10	Length 895
Best Local Similarity	74.8%	Pred. No. 2e-129		
Matches 639	Conservative 0	Mismatches 213	Indels 2	Gaps 2
QY	1687	GAGACCCAGATGACCCCGACCCCAAGTCTCGAGACGAGCGAAGACCTCTTCGCCCATCGAG	1746	
Db	42	GAACCTCAATGACACCCACCCCAAGTCTCAGATGAGGAAGCCAACTTATTTCGCTTATGCAA	101	
QY	1747	CTGGCGAGCGCTCGGTCTCCCATATGGTCTCTAAAGCCGCCATCGAGATCGACTCTCTC	1806	
Db	102	CTTGCCAGTGCATCAGTTCTCCCATATGGTCTCTAAATCAGCCATTTGAATTTGACTTGTCTG	161	
QY	1807	GAGATCATGGCCAGGACGCGCGCGCTCTCTCCACGCGGGGAAATCCGCGGACAG	1866	
Db	162	GAGATCATGGCCAAAGCTGGTCTCAGTCTTCTTGTCCCCCAAGAGTGGCTTCCAAAG	221	
QY	1867	CTCCGACCCAGAACCCCGAGGACCCGCTCATGTCTGACCGGATCTCCGGCTGCTGSCC	1926	
Db	222	CTCCCCACCCACCAACCTGATGACCCGCTCATGTCTGGACCGTATCTTTCGCTCTCTGCTG	281	
QY	1927	AGCTACTCGGTCTCAGCTGGACCCCTCCGACCTCCCGATGCGAAGCTGCGAGCGGCTC	1986	
Db	282	AGCTCAACAGCTCCTCATTGCTCTTGGTACCCCTCTCTGATGGCAAGTGGAAAGACTC	341	
QY	1987	TACGGCTTAGCGCCGCTGTGCAAGTTCTTGGTCAAGACGAGGACGGGTCTCCATCGCC	2046	
Db	342	TATGGCTTGGCCCTGCTGCAAAATCTTGAACAAAGACGAAGATGGTGTCTCATCTTTCC	401	
QY	2047	GCACTCAATTTGATGAACGAGGACAAATCTCTCATGGAAGCTGTTTACCTGAAAGAT	2106	
Db	402	GCCCTTAGTCTCATGAATCAAGACAAAGTCTTATGGAGAGCTGTTATGATGCAATTTGAGTAC	461	
QY	2107	GGGCTCTTGAAGGCGGAATCCCATTTCAACAAAGGCTTACGGATGACCGCTGCGAGTAT	2166	
Db	462	GCTGTGCTGGATGGTGAATTCATTTCAACAGGCTTATGTTATGATGCAATTTGAGTAC	521	
QY	2167	CATGGCACCGACCCCGCATTTCAACAAAGATCTTTTAAACGGGGAATGCTTCATCATCTCCACC	2226	
Db	522	CATGGCACGTACTAGATTCAACAAAGTCTTCAACAGGGGAATGCTCATCACTCTACC	591	
QY	2227	ATTACTATGAAGAAGATACATCGAAGGCTTCGAGGGCTTCGAGGCGCTCGAGACCGTGGTC	2286	
Db	582	ATCACCATGAAGAAGATTTCTCGATACATATGATGGTTCGAGGCTTCAAGGACTAATAAATTTGGTC	641	
QY	2287	GATGTCGAGGCGGCACCTGGGCGCGTCTCAGCATGATGTTGCCAAATACCCATCAATG	2346	
Db	642	GATGTTGGCGGTGGTACCGGTGCACCGCTTAGCATGATGCTCTTAAGTACCCACCATTA	701	
QY	2347	AAAGGATCAACTTCGA-CCGCCCCAACGATTTGAAGACGCCGCCACCTTCTCTGTGTGTC	2405	
Db	702	AAAGGCAATTAATTCGATTTGCTCATGTCATTTGAGGATGCTCTTAGCTGCTCTGTGTGTG	761	
QY	2406	AAGCACGTCGAGGCGGACATGTTTCGTGTCAGCGCTTCCAAAGGAGATGTCATTTTCATGAAG	2465	

Db	472	GCGTCTGGAAGGTGAATTCCTTCAACAAGCTATGTTATGACCGCATTCGAGTAC	531	
QY	2167	CATGGCACCGACCCCGCATTTCAACAAGATCTTTTAAACGGGGAATGTTGATCATTCCACC	2226	
Db	532	CATGGCACCGATCCTAGATTCAACAAGTCTTCAACAGGGAATGTTGATCATTCTTACC	591	
QY	2227	ATTACTATGAAGAAGTACATCGAAGGCTTCGAGGCGCTCGAGACCGTGGTC	2286	
Db	592	ATTACCATGAAGAAGATCTTTGAGACCTATGATGGCTTTGAGGACTCAAAACATGGTCT	651	
QY	2287	GATGTCGAGGCGGCACCTGGGCGCGTCTCAGCATGATGTTGCCAAATACCCATCAATG	2346	
Db	652	GATGTTGGCGCGTACTGAGTACGCTTAAATGTTGTCACCAAGCACCTTCTATA	711	
QY	2347	AAAGGATCAACTTCGA-CCGCCCCAACGATTTGAAGACGCCGCCACCTTCTCTGTGTGTC	2405	
Db	712	AAGGCAATCACTTGAATTTGCTCATGTCATTTGAGGATGCTCTTATCTCTGTGTG	771	
QY	2406	AAGCACGTCGAGGCGGACATGTTTCGTGTCAGCGCTTCCAAAGGAGATGCCATTTTCATGAAG	2465	
Db	772	GAGCATGTTGGTGAGACATGTTTGAAGTGTTCANAGGAGACGCCATCTTCATGAAG	831	
QY	2466	TGATATGCCACGATCGAGTGCAGCATTCGC	2498	
Db	832	TGGATATGCCACGATTTGGAGTGATGAGCACTGC	864	
RESULT 9				
DT558009		895 bp	mRNA	linear
LOCUS	EST1068649	TWO	Gossypium	hirsutum
DEFINITION	EST1068649			hirsutum cDNA, mRNA sequence.
ACCESSION	DT558009			
VERSION	DT558009.1	GI:78337735		
KEYWORDS	EST.			
SOURCE	Gossypium	hirsutum	(upland cotton)	
ORGANISM	Eukaryota			
REFERENCE	Yang, S.S., Cheung, F.H., Wei, N.E., Lee, J.J., Ha, M., Stelly, D.M.,			
AUTHORS	Thaxton, P., Sze, S.H., Triplett, B.A., Town, C.D. and Chen, Z.J.			
TITLE	ESTs from immature ovule (-3 to 3 DPA) of G. hirsutum TM-1			
JOURNAL	Unpublished (2005)			
COMMENT	Contact: Z. Jeffrey Chen			
	The Chen lab: A Home of Polyploidy (http://polyploidy.tamu.edu)			
	Texas A&M University			
	Department of Soil & Crop Sciences, MS2474, College Station, TX			
	77842-2474, USA			
	Tel: 979 862 2359			
	Fax: 979 845 0456			
	Email: zjchen@neo.tamu.edu			
	TIGR sequence name: GOAP684TRC			
	Seq primer: CAG GAA ACA GCT ATG ACC.			
FEATURES				
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	/clone_lib="TMO"			
	/notes="Vector: pCMV-SPORT6.1; Site 1: EcoRI; Site 2: NotI; G. hirsutum L. Texas Marker-1 (TM-1) plants were grown in a greenhouse at the Texas A&M University and in the field at the USDA-ARS, New Orleans. The bolls were tagged and harvested at 3 days before anthesis (-3DPA), the day of anthesis (0 DPA), and 3 days post anthesis (3DPA) from a pool of ~20 plants. Total RNA was extracted from immature ovules or fiber-bearing ovules. An equal amount of total			

	Query Match	15.9%	Score 488.6;	DB 9;	Length 961;
	Best Local Similarity	71.3%;	Pred. No. 3.1e-129;		
	Matches 672; Conservative	0;	Mismatches 269;	Indels 2;	Gaps 2;
QY	1640	GGAGAGGAGAGAGAGAGGAGGAGAGATCGGTTCGACCGGCTCCGAGACCAGATGA	1699		
Db	20	GAAGAAGGGAGAAAAAANAANAACAATAATGGTTCAACCAATTGCAGAAATCAAATAA	79		
QY	1700	CCCCGACCACCAAGTCTCGGACGAGCGGCCAACCTCTTTGGCCATGCAAGCTGGCGAGCGCCT	1759		
Db	80	GTCACGACCAAGGCTCGGATGAAGGCAAAACCTCTTTGGCCATGCAATAACCAAGTCCT	139		
QY	1760	CGGTGCTCCCCCATGGTCTTAAGGCCGCCATTCAGATTCGACTCTTCAGATCATGGCCA	1819		
Db	140	CAGTCTTGCTTATGGTTCTCAAAATCAGCCATTGAGCTTGATCTTTTAGAGATCATCGCTA	199		
QY	1820	AGGACGGGCGGGCGGCTTCTCTCCACGGGGGAAAATCGCGCACAGCTCCCGACCCAGA	1879		
Db	200	AAGCTGGGCGCGGATGTTTTCATGTCTCCAAAGACATATAGCTTCTCAGCTGCCACAAAGA	259		
QY	1880	ACCCCGAGGCAACCGTGCATGCTTCGACCGGATCTTTCGGGCTGTGGCGCACTACTCCGTGC	1939		
Db	260	ACCCAGATGCCATATCGTGTCTGATGTATATTTGGCCTTCTGGCGAGCTATTCAGTCC	319		
QY	1940	TCAGGTGCAACCTCCGCGACCTCCCGATGGCAAGFTCGAGCGGCTCTACGGCTTAGCGC	1999		
Db	320	TTAATTGC-TCTTTGGCAATCTCCCGACGGCAAGTTGAGAGGCTTTATGGCCTTGCCC	378		
QY	2000	CGGTGTGCAAGTCTTGTGTCAAGAACGAGGACGGGCTCTCCATCGCGGCATCAACTTGA	2059		

379	CGGTTTGTAATTCCTCACTAAAAATGAAGATGGTGTACACTTTCCGATCTTGTCICA	438
2060	TGAACGAGGACHAAATCTCATGTGAAAGCTGTGATTACCTGAAAGATGCGGTCTTGAAG	2119
439	TGAACCAAGACAAGGTTCTCATGAGAGCTGGTACTACTTAAAGATGCAGTGTCTGAAG	498
2120	GCGGAATCCCATTCACAAAGGCGTACGGGATGACCGCGTTCGAGTATCATGGCACCGACC	2179
499	GTGGCATTCATTTAAACAAGGCTATGGATGAATGCATTGCATTACCATGGCAAGATC	558
2180	CGCGATTCACAAAGATCTTTAAACCGGGGAATGTCGTACTCTCCACCACTACTATGAAGA	2239
559	TAAGATTCAACAGAATTTTCAACAATGAAGATGTCTCTCATCTTCACTTACCATGAAGA	618
2240	AGATACTGGAACCATACAAGGCGTTTCGAGGCGCTCGAGACCGTGGTGCATGTCGGAGCG	2299
619	AAATTCCTGAAATTTACAAAGGGTTTGAAGGCGCTCAACTCAGTTGTGCGACGTTGGTGGTG	678
2300	GCACCTGGGCGGTGCTCAGCATGATCGTTCGAATATCCCATCAATGAAGGGAATCAACT	2359
679	GAATTGGAGCCACACTTAACATGATATCTCCAAGTATCCATCGATTAAAGGCATCAACT	738
2360	TCGA - CGCGCCCCAAGGATTTGAAGACGCCGCCACCCCTTCTGGTGTCAAGCACGTCGGAG	2418
739	TTGATTTGCCACATGTTATTCAGGATGCTCCAGCTTTTCTGGTGTGAGCATGTGTGGGG	798
2419	GCGCATGTTTCGTACGGTTTCMAAGGGAGATGCCATTTTCATGAAGTGGATATGCCATG	2478
799	GAGACATGTTTGTGTAGTGTTCMAAGGGAGATGCCATTTTATCAAGTGGATATGTCTATG	858
2479	ACTCGAGTGCAGCATTTGCGCGAAGTTCCTCAAGAATCTGTACGATGCGTTCCTCAACA	2538
859	ATTGGAGTGTATGACCATCGCTGGAATTTCTTGAAGACTGCTATGAAGCACTCCCAAGTAA	918
2539	ATGMAAGGTGATCGTTGCAAGTGTGGTACTCTCCTGTGTACCC	2581
919	ATGGGAAGTCAATGTTGCTGAATCTATCTCTCCAGTAACCCC	961

RESULT 12	
LOCUS	CKX668414
DEFINITION	UCCRP01_037_E09 T7 Swingle citrurnelo nematode-challenged root cDNA library - UCCRP01 Citrus x paradisi x Poncirus trifoliata cDNA clone UCCRP01_037_T7_E09, mRNA sequence.
ACCESSION	CKX668414
VERSION	1
KEYWORDS	GI:57927201
SOURCE	EST.
ORGANISM	Citrus x paradisi x Poncirus trifoliata
REFERENCE	Citrus x paradisi x Poncirus trifoliata
AUTHORS	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus x Poncirus.
TITLE	1 (bases 1 to 931)
JOURNAL	Close,T.J., Roose,M.L., Becker,O., Darsow,J., Federici,C.F., Fenton,R.D., Wanamaker,S., Choi,Y.G and Kingan,T.
COMMENT	Development of EST Resources and New Genetic Markers for California Citrus - Swingle citrurnelo nematode-challenged roots - UCCRP01 Unpublished (2005)
	Contact: Timothy J. Close
	Department of Botany & Plant Sciences
	University of California
	Riverside, CA 92521-0124, USA
	Tel: 909-787-3318
	Fax: 909-787-4437
	Email: timothy.close@ucr.edu
	Seq primer: T7
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Twelve seedlings were
transplanted from cones to 4 inch pots of sand mix, then
grown in greenhouses (Barsow, Becker lab). Citrus
nematodes (Tylenchulus semipenetrans) were extracted from
contaminated soil from the UC Riverside Citrus Research
Center then suspended in water and added to pots (Barsow).
Growing roots were collected by clipping them away from
the old root ball 24 hr and 4 days after inoculation
(Federici). Total RNA was extracted using Concert Plant
RNA Reagent (Invitrogen) followed by RNeasy (Qiagen), an
equal amount of RNA was pooled from each of the two
collection times, poly(A) RNA was purified using Oligotex
(Qiagen), a cDNA library was made using a cDNA synthesis
kit (Stratagene), then 0.45 million primary lambda cDNA
clones were in vivo excised to give a population of
pBluescript SK(-) phagemids (Fenton, Close lab). Phagemids
were plated, plasmid DNA purified, cDNA clones archived,
and DNA sequences determined bi-directionally using an
ABI3730 at the University of California Riverside
Institute of Integrative Genome Biology Genomics Core
Instrumentation Facility, (Choi, Kingan). Chromatogram
files were downloaded by FTP by Close, then processed by
Wanmaker (Close lab) using the HarVest pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a phred 17
region of at least 100 bases were assembled, then chimeras
were removed following manual inspection of assemblies
(Close, Roose, Wanmaker). Sequences that survived all
removal steps were submitted to GenBank."

ORIGIN

Query Match 15.8%; Score 484.8; DB 9; Length 931;
Best Local Similarity 71.6%; Pred. No. 3.9e-128;
Matches 650; Conservative 0; Mismatches 257; Indels 1; Gaps 1;

QY 1651 AAGAGGAGGAGGAGAAATGGTTCGACCGGCTCCGAGACCCAGATGACCCGACCCAA 1710
DB 24 AAAAAAATAAACAATAATGGGTTCACACGATTCAGAAATCAATTAATGTCAGGCCAA 83
QY 1711 GTCTCGGACGAGGCGGAACTCTTCGCCATGCGAGCTGCGGCGCTCCGCTGCTCC 1770
DB 84 GGCTCGGATGAGAGGCAACCTCTTGCGCATGCAATTAACAGTGCCTCAGCTTGCT 143
QY 1771 ATGCTCTAAAGGCGCATCGAGATCGACTCTCTCGAGATCATGCGCAAGGACGGGCG 1830
DB 144 ATGCTCTCAATCAGCCATGAGCTTGATCTTTAGAGATCATCGCTAAAGCTGGGCCC 203
QY 1831 GCGCGTCTCTCCACGGGGGAATCGGCGCAGCTCCGACCCAGACCCCGAGGCA 1890
DB 204 GATGCTTTATGCTCTCAAAAGACATAGCTTCTCAGCTGCGCCCAAGAACCCAGATGCC 263
QY 1891 CCGCTCATGCTCGACCGGATCTTCGGGCTGTCGCCAGTACTCCGCTCAGTGCAGTGCA 1950
DB 264 CATATCGTCTTATGATATATGCGCTCTTGCGGAGCTTATCAGTCTTAATGCTCT 323
QY 1951 CTCGCGACTCTCCCGATGCAAGGTCGAGCGGCTCTACGGCTTACGGCTTACGGCTG 2010
DB 324 TTGCGCAATCTCCCGACGCAAGTTGAGAGGCTTATGGCTTGGCCCGTGGTGTAA 383
QY 2011 TTCTTGTCAGAACGAGGAGGGGTCTCCATCGCCGCTCACTTGTATGATGACCGAGC 2070
DB 384 TTCTCTCACTAAATGAAGATGGTGTACACTTTCCGATCTTTTCTCATGAACCAAGC 443
QY 2071 AATACTCTGAAAGCTGTATACCTGAAGATCGGCTCTTGAAGCGGAATCCCA 2130

Db 444 AAGGTTCTCATGAGAGCTGGTACTACTTAAAGATGCAGTGTCTGAAGGTGGCAATCCA 503
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QY 2191 AAGATCTTTAAACCGGGGAATGTCTGATCACTCCACCATTAATGAAGAGATCACTGGAA 2250
Db 564 AAGATTTTCAACAATGGAATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 623
QY 2251 ACATACAAGGCTTCAGAGGCTTCGAGACCGTGTGATGTCGAGGCGGCACTGGGCCC 2310
Db 624 AATTACAAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 683
QY 2311 GTCTCAGCATGATGCTGTCGAATACCCATCAATCAATGAAGGATCACTTCGA-CGCCCC 2369
Db 684 ACATTTAACAATGATTAATCTCAAGTATCAATCAATTAAGGCAATCACTTTGATTTGCCA 743
QY 2370 CAAAGGATTAAGACGCGCCACCCCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2429
Db 744 CATGTTATTCAGGATGCTCCAGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
QY 2430 GTCAAGGCTTCAAGAGGAGATGCAATTTTCATGAAGTGAATGCTGATGCTGATGCTG 2489
Db 804 GTTAGTGTTCGAGGAGATGCAATTTTATCAAGTGAATGCTGATGCTGATGCTGATGCTG 863
QY 2490 GACCATTCGCGAAGTTCCTCAAGACTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2549
Db 864 GAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923
QY 2550 ATCGTTGC 2557
Db 924 ATGTTGC 931

RESULT 13
CX664056/c

LOCUS
DEFINITION
UCRCP01_007_F10_T7 Swingle citrusmelo nematode-challenged root cDNA
library - UCRCP01 Citrus x paradisi x Poncirus trifoliata cDNA
clone UCRCP01_007_T7_F10, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CX664056.1 GI:57922014
EST.
Citrus x paradisi x Poncirus trifoliata
Citrus x paradisi x Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Sapindales; Rutaceae; Citrus x Poncirus.
1 (bases 1 to 964)
Close, T.J., Roose, M.L., Becker, O., Darsow, J., Federici, C.F.,
Fenton, R.D., Wanmaker, S., Choi, Y.G. and Kingan, T.
Development of EST Resources and New Genetic Markers for California
Citrus - Swingle citrusmelo nematode-challenged roots - UCRCP01
Unpublished (2005)
Contact: Timothy J. Close
Department of Botany & Plant Sciences
University of California
Riverside, CA 92521-0124, USA
Tel: 909-787-3318
Fax: 909-787-4437
Email: timothy.close@ucr.edu
Seq primer: T7.
Location/Qualifiers
1. .964
/organism="Citrus x paradisi x Poncirus trifoliata"
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/cultivar="Swingle"
/db_xref="taxon:309804"
/clone="UCRCP01_007_T7_F10"
/tissue_type="root"
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/lab_host="E. coli TJCl21"

FEATURES
source
1. .964

/clone_lib="Swingle citrumelo nematode-challenged root
cDNA library - UCRCP01"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Twelve seedlings were
transplanted from cones to 4 inch pots of sand mix, then
grown in greenhouses (Darsow, Becker lab). Citrus
nematodes (Tylenchulus semipenetrans) were extracted from
contaminated soil from the UC Riverside Citrus Research
Center then suspended in water and added to pots (Darsow).
Growing roots were collected by clipping them away from
the old root ball 24 hr and 4 days after inoculation
(Federici). Total RNA was extracted using Concert Plant
RNA Reagent (Invitrogen) followed by RNeasy (Qiagen), an
equal amount of RNA was pooled from each of the two
collection times, poly(A) RNA was purified using Oligotex
(Qiagen), a cDNA library was made using a cDNA synthesis
kit (Stratagene), then 0.45 million primary lambda cDNA
clones were in vivo excised to give a population of
pBluescript SK(-) phagemids (Fenton, Close lab). Phagemids
were plated, plasmid DNA purified, cDNA clones archived,
and DNA sequences determined bi-directionally using an
ABI3730 at the University of California Riverside
Instrumentation Facility, (Choi, Kingan). Chromatogram
files were downloaded by FTP by Close, then processed by
Wanamaker (Close lab) using the Harvest pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a phred 17
region of at least 100 bases were assembled, then chimeras
were removed following manual inspection of assemblies
(Close, Roose, Wanamaker). Sequences that survived all
removal steps were submitted to GenBank."

ORIGIN

Query Match 15.7%; Score 480.6; DB 9; Length 964;
Best Local Similarity 72.6%; Pred. No. 6.4e-127;
Matches 635; Conservative 0; Mismatches 239; Indels 1; Gaps 1;
QY 1895 TCATGCTCGACCGGATCTTCGGGTGTCGGACACTACTCGTGCTCAGTCGACCTCC 1954
DB 963 TCGTGCTTGATCGTATATTGGGCTTTCTGGCGAGCTATTGAGTCTTTAATTCCTTGC 904
QY 1955 GCGACCTCCCGATGCGGAGTCGAGCGGCTCTACGGCTTAGCGCGGTGCAAGTTCT 2014
DB 903 GCAATCTCCCGACGGCAAGTTGAGAGCTTTATGGCTTGCCCGCTTGTGTAATTC 844
QY 2015 TGGTCAAGAACGAGACGGGGTCTCCATCGCCGCACTCAACTTGATGAACAGACAAA 2074
DB 843 TCACATAAATGAAGATGGTGTACACTTTCCGATCTTTGTCTCATGAACAGACAAAG 784
QY 2075 TCCTCATGGAAGCTGGTATTACTGGAAGATCGGTCTTGAAGCGGATCCATTCA 2134
DB 783 TTCTCATGAGAGCTGGTACTACTTAAAGATGCGAGTCTTGAAGGTGGCATTCAATTA 724
QY 2135 ACAAGCGTACGGATGACCGGTTCGAGTATCATGGCACCGACCGCGATTCACACAGA 2194
DB 723 ACAAGCGCTATGGATGAATTCGATTTACCGGCAAGATCTAGATTCACACAGA 664
QY 2195 TCTTTAACCGGGGAATGTCGTGATCACTCCACCATTACTATGAAGAAGATATCGGAACAT 2254
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DB 603 ACAAGGGTTGAAGGCTTCACATCAGTTGTGCGAGTGGTGGTGAATTTGAGCCACAC 544
QY 2315 TCAGCATGATCGTTGGCAATACCCATCAATGAAGAGGATCACTTCGA-CGCCCCAAC 2373
DB 543 TTAACATGATTAATCTCCAGATATCCATCGATTAAAGGCATTAACTTTGATTGGCCACATG 484
QY 2374 GGATTGAAGACGCCCCACCCCTTCCTGGTGTCAAGCAGTCGAGGGCGACATGTCGCA 2433

Db 483 TTATTAGGATGCTCCAGCTTTTCTCGGTTCGAGCATGTTGGGGGAGACATGTTTGTTA 424
QY 2434 CGCTTCCAAAGGAGATGCCATTTTCATGAAGTGGATATGCCATGACTCGAGTGACGACC 2493
Db 423 GTGTTCAAAGGAGATGCCATTTTATCAGTGGATATGTCATGATTGGAGTGATGAGC 364
QY 2494 ATTGCGGAAAGTTCTCTCAAGAACTGCTAGCATCGGTTTCCAAACAATGGAAGGTCATCG 2553
Db 363 ACTGCGTGAATCTTTGAAGAACTGCTATGAAGCACTCCCAAGTAAATGGGAAAGTCATTG 304
QY 2554 TTGAGAGTGGTACTCTCTGTGTACCCACACAGAGCTAGCGACCAAGAAATGTGATCC 2613
Db 303 TTGCTGAATCTATCTCTCCCAATAACCCCGGACACAAAGCTTTGATCCAAAGTAGTCATCC 244
QY 2614 ACATCGACTGATCATGCTTGGCCCAACACCCAGCGGAAAGAGAGACACAGAGAGT 2673
Db 243 ATGTCGACTGCAATCATGTTGGCTCATTAACCCGGGTGGCAAGAGAGGACTGAACAAGT 184
QY 2674 TCGAGGCAATTTGGCCAAAGGGCGGATTTCAAGGCTTCCAAAGTCATGCTGCGCTTTCG 2733
Db 183 TCAGAGCATTTGGCTTAAGGCTGCTGGAATTCGAAGTTTCCAAGTTGTGAGCTCTGCTTTTA 124
QY 2734 GCATCAGCTCATGAGTTCTCTGAAGACCGCTTGA 2768
Db 123 ATACTTACATTATGGAATTTCTCAAGAGTGTCTTGA 89

RESULT 14

CX663706 917 bp mRNA linear EST 19-JAN-2005
UCRCP01_005_E01_T3 Swingle citrumelo nematode-challenged root cDNA
library - UCRCP01 Citrus x paradisi x Poncirus trifoliata cDNA
clone UCRCP01_005_T3_E01, mRNA sequence.

ACCESSION

VERSION CX663706.1 GI:57921620

KEYWORDS

SOURCE Citrus x paradisi x Poncirus trifoliata

ORGANISM

Citrus x paradisi x Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Sapindales; Rutaceae; Citrus x Poncirus.
1 (bases 1 to 917)

REFERENCE

Authors Close, T.J., Roose, M.L., Becker, O., Darsow, J., Federici, C.F.,
Fenton, R.D., Wanamaker, S., Choi, Y.G and Kingan, T.
Development of EST Resources and New Genetic Markers for California
Citrus - Swingle citrumelo nematode-challenged roots - UCRCP01
Unpublished (2005)

JOURNAL

CONTACT: Timothy J. Close

COMMENT

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Fax: 909-787-4437

Email: timothy.close@ucr.edu

Seq primer: T3

FEATURES

source

1..917
/organism="Citrus x paradisi x Poncirus trifoliata"
/mol_type="mRNA"
/cultivar="Swingle"
/db_xref="taxon:309804"
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/lab_host="E. coli TUC121"
/clone_lib="Swingle citrumelo nematode-challenged root
cDNA library - UCRCP01"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Twelve seedlings were
transplanted from cones to 4 inch pots of sand mix, then
grown in greenhouses (Darsow, Becker lab). Citrus
nematodes (Tylenchulus semipenetrans) were extracted from
contaminated soil from the UC Riverside Citrus Research

propagation."

ORIGIN

Query Match 15.4%; Score 473; DB 10; Length 911;
Best Local Similarity 74.7%; Pred. No. 1e-124;
Matches 607; Conservative 0; Mismatches 205; Indels 1; Gaps 1;

Qy 1687 GAGACCCAGATGACCCCGACCCCAAGTCTCGGACGAGCGGAAACCTTTGCCCATGCGAG 1746
Db 99 GAAACTCAGATGACTCCAACCTCAGGTATCAGATGAGAGGCACACCTTTGCCATGCAA 158
Qy 1747 CTGGCGAGCCCTCCGCTGCTCCCATGCTCTAAAGGCCGCCATCGAGATCGACCTCCTC 1806
Db 159 CTAGCCAGTCTTTCAGTTCTACCAATGATCCTCAAAACACGCCATTGAACTCGACCTTCTT 218
Qy 1807 GAGATCATGCGCCAGGACGCGCGCGGCTCTCTCCACGGGGAAATCGCGGCACAG 1866
Db 219 GAAATCATGGCTAAAGCTGGCCCTGGTCTTTCTTGTCCACATCTGAGATAGCTTCTCAC 278
Qy 1867 CTCCCGACCCAGAACCCCGAGGACCCGCTCATGCTCGACCGGATCTTCGGGCTGTGGCC 1926
Db 279 CTCCCTACCAAAAACCCCTGATGCGCTGTCTATGTAGACCGTATCTTGGCCCTCCTGGCT 338
Qy 1927 AGCTACTCGGTGCTCAGTGCACCCCTCCGCGACTCTCCCGATGGCAAGTTCGAGCGGCTC 1986
Db 339 AGCTACTCCATTTCTTACTTCTCTGAAAAGATCTTCTGATGGGAAAGTTGAGAGACTG 398
Qy 1987 TACGGCTTAGCGCGGTGTGCAAGTCTTGTCTCAAGAAACGAGACGCGGCTCTCCATCGCC 2046
Db 399 TATGGCCCTTGTCTGTTTGGCAATTTCTTACCAAGAACCGAGGATGGTGTCTCTGTGACG 458
Qy 2047 GCACCTCAACTTTGATGAACACGAGCAAAATCCTCATGGAAGCTGGTATTTACCTGAAAGAT 2106
Db 459 CCTCTGTCTCATGAACACGAGCAAGTCTCTATGGAAGCTGGTATTTTGAAGAT 518
Qy 2107 GCGGTCTTTGAAGCGGAATCCGATTCACCAAGCGTACGGGATGACCGGCTTCGAGTAT 2166
Db 519 GCAATTTCTGTGAGGAAATTCATTTAACAAAGGCTTATGGGATGACTGCAATTTGAATAT 578
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Db 819 GAGCATGTTGTGGGGACATGTTGTAGTGTGCCAAAGCAGATGCCGTTTTTCATGAAG 878
Qy 2466 TGGATATGCCATGACTGGAGTGACGACCATTCG 2498
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QY	241	CAATTGTAACCCATGAGGTGAAATCCTAGAGTGGAGAGATAGTCCCTTTAGAAAGTCCCA	300	1321	CTCCGTAATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCCAA	1380
Db	241	CCATTGTACCCATGATAGGTGAAATCCTAGAGTGGAGAGATAGTCCCTTTAGAAAGTCCCA	300	1321	CTCCGTAATTTCTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCCAA	1380
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QY	361	ACATTTCTGACCTTTAAATTTGATGTAGAACCTCTTAGACTATTAATAATTTGCTCGTAAT	420	1441	TTCTCTCTATATTTCTGGTTTCCACCGTTGGAGTCAATGGCATCGTGCAGAAATGTACATAT	1500
Db	361	ACATTTCTGACCTTTAAATTTGATGTAGAACCTCTTAGACTATTAATAATTTGCTCGTAAT	420	1441	TTCTCTCTATATTTCTGGTTTCCACCGTTGGAGTCAATGGCATCGTGCAGAAATGTACATAT	1500
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QY	481	AAGCGGATTTGGCAATCACTTGAAGATGATCTTATATGCGTAATTAACAAGACTGATGG	540	1561	ACCTCCACCAACCATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGCTT	1620
Db	481	AAGCGGATTTGGCAATCACTTGAAGATGATCTTATATGCGTAATTAACAAGACTGATGG	540	1561	ACCTCCACCAACCATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGCTT	1620
QY	541	GGGTAATGCTTAATTTGTTCCAGGATGCTGATCTTTGGGTATTTAGGCTTATGATGGTTGG	600	1621	TCCTTTTCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGGGTTCCGACC	1680
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Db	721	GGCTTGTAGTCCCAAGTACCTCTCTAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	780	1801	CTCTCTCGAGATCATGGCCAAAGACGGCCCGGCGCGTTCCTCTCCACGGGGGAAATCGCG	1860
QY	781	TATTAGGACATATTCATCTCATTAGTAAACCTTAAGGACACTGGTTTCAAGATAGGCAA	840	1861	GCACAGTCTCCGACCCAGAACCCCGAGGACCCCGTCACTGCTCCAGCCGATTCCTCGGCTG	1920
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Db 2761 CCGCTTGATCTGCTCTCTGCTGCTGATGTTTCATGGTTCCTTGGATTTGAAAGGTCGTGAAG 2820
Qy 2821 GAGCCCTTTTCTCAGTGGCTTCGGGATACCAAGTTCCTTCTCATAAAGGAAACAATA 2880
Db 2821 GAGCCCTTTTCTCAGTGGCTTCGGGATACCAAGTTCCTTCTCATAAAGGAAACAATA 2880
Qy 2881 AGAAGCACTGTATGATGGCGCAAGTGGAGTTACAAGATTTGTTGTTTATGTCATATA 2940
Db 2881 AGAAGCACTGTATGATGGCGCAAGTGGAGTTACAAGATTTGTTGTTTATGTCATATA 2940
Qy 2941 AGTTTTCAGTCTTCTGCACTACTGATTTTACAGAAATGTGTAAACGAAACGGCGTATATGGAT 3000
Db 2941 AGTTTTCAGTCTTCTGCACTACTGATTTTACAGAAATGTGTAAACGAAACGGCGTATATGGAT 3000
Qy 3001 GTGCTGAATGATGGAATTTGTGATATCTGCTCTCTTTTTCAGTAAATCACTTCGAACA 3060
Db 3001 GTGCTGAATGATGGAATTTGTGATATCTGCTCTCTTTTTCAGTAAATCACTTCGAACA 3060
Qy 3061 AAAAAAAAAA 3070
Db 3061 AAAAAAAAAA 3070

RESULT 2
US-09-598-401C-60
; Sequence 60, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c2
; CURRENT APPLICATION NUMBER: US/09/598,401C
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2096
; TYPE: DNA
; ORGANISM: Eucalyptus grandis

US-09-598-401C-60
Query Match 65.8%; Score 2020.4; DB 3; Length 2096;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;
Qy 1019 CTGAGCCATTTAATTCGAGAGCACATCGCCCAAAATTTATTTCTTCTGTCGCAATACTGT 1078
Db 41 CTGAGCCATTTAATTCGAGAGCACATCGCCCAAAATTTATTTCTTCTGTCGCAATACTGT 100
Qy 1079 CGAATTTTCTTTTATAGTAAATCAATGATGCCCATGTTGACAAAAGGCTGATTA 1138
Db 101 CGAATTTTCTTTTATAGTAAATCAATGATGCCCATGTTGACAAAAGGCTGATTA 160
Qy 1139 GTATGATCTTGGAGTTGTTGGTGCATAATTTGCAAGCTGAGATGGCCCTCAGGGAATTT 1198
Db 161 GTATGATCTTGGAGTTGTTGGTGCATAATTTGCAAGCTGAGATGGCCCTCAGGGAATTT 220
Qy 1199 AAGCGCCCAACCCAGATTTGCAAAAGAGACACAAAGAGACACGACCCCAACTTTCTTAAACAAG 1258
Db 221 AAGCGCCCAACCCAGATTTGCAAAAGAGACACAAAGAGACACGACCCCAACTTTCTTAAACAAG 280
Qy 1259 ATCATCAACAGATCGGCCAGTAAGGTAATATTTAATTTTAAACAATAGCTCTTGTACCGGG 1318
Db 281 ATCATCAACAGATCGGCCAGTAAGGTAATATTTAATTTTAAACAATAGCTCTTGTACCGGG 340
Qy 1319 AACTCGGTATTTCTCTCACTTCCATTAACCCCTGATTTAATTTGTTGGGAAAGGACAGCC 1378
Db 341 AACTCGGTATTTCTCTCACTTCCATTAACCCCTGATTTAATTTGTTGGGAAAGGACAGCC 400
Qy 1379 AACCCCAAAAAGGTCAAGATGTCTATCCAC --- GAGAGAGAGAGAGAGAGAGAGAGAG 1434
Db 401 AACCCCAAAAAGGTCAAGATGTCTATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
Qy 1435 AGAGTTTCTCTCTATATTTCTGTTTCAACCGGTTGAGTCAATGGCATGCGTGACGAATGT 1494
Db 461 AGAGTTTCTCTCTATATTTCTGTTTCAACCGGTTGAGTCAATGGCATGCGTGACGAATGT 520
Qy 1495 ACATATTGTTAGGTTCCAAATTTTTCGGGAGGGTTGGTGAACCGCAAGTTCTCTATA 1554
Db 521 ACATATTGTTAGGTTCCAAATTTTTCGGGAGGGTTGGTGAACCGCAAGTTCTCTATA 580
Qy 1555 TATCGAACCTTCCACCAACCATACCTCACTTCAATCCCACTTATTCCTTATTTTCT 1614
Db 581 TATCGAACCTTCCACCAACCATACCTCACTTCAATCCCACTTATTCCTTATTTTCT 640
Qy 1615 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1674
Db 641 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
Qy 1675 TCAGACCGGCTCCGAGACCCAGATGACCCGACCCCAAGTCTTCGACCGAGCGGACCTC 1734
Db 701 TCAGACCGGATCCGAGACCCAGATGACCCGACCCCAAGTCTTCGACCGAGCGGACCTC 760
Qy 1735 TTGCGCATGAGCTGGCGAGCGCTCCGTGCTCTCCCATGGTCTTAAAGGCGGCATCGAG 1794
Db 761 TTGCGCATGAGCTGGCGAGCGCTCCGTGCTCTCCCATGGTCTTAAAGGCGGCATCGAG 820
Qy 1795 ATCGACCTCTCTGAGATCATGCGCAAGAGACGGGCGGGCTTCTCTTCAACGGGGAA 1854
Db 821 CTGACCTCTCTGAGATCATGCGCAAGAGCGGGCGGGCGGCTTCTCTCTCCCGGGGAA 880
Qy 1855 ATCGCGGCACAGCTCCGACCCAGAACCCCGAGGACCCGTCATGCTCCGACCGATCTTC 1914
Db 881 GTGCGGCGCCAGCTCCGACCCAGAACCCCGAGGACCCGTCATGCTCGACCGGATCTTC 940
Qy 1915 CGGCTGCTGGCCAGCTACTCCGTGCTCAAGTGCACCTCCGCGACCTCCCGGATGGCAAG 1974
Db 941 CGGCTGCTGGCCAGCTACTCCGTGCTCAAGTGCACCTCCGCGACCTCCCGGATGGCAAG 1000
Qy 1975 GTGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGTGCAAGACGAGGACGG 2034
Db 1001 GTGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGTGCAAGACGAGGACGG 1060

601 ACCGGGAATGCTGATCACTCCACCATTACTATGAAGAAGATACCTGAAACATACAAGG 660
2261 GCTTCGAGGGCTCGAGACCGTGTGATGTCGAGGGCGGACCTGGGGCGGTCTCAGCA 2320
661 GCTTCGAGGGCTCGAGACCGTGTGATGTCGAGGGCGGACCTGGGGCGGTCTCAGCA 720
2321 TGATCGTTGGCAATACCCATCAATGAAGGGATCAACTTCGACC-GCCCCAACCGGATTG 2379
721 TGATCGTTGGCAATACCCATCAATGAAGGGATCAACTTCGACCCTGACCTCAGCTGATTG 780
2380 AAGACGGCCCAACCCCTTCCTGGTGTCAAGCACTGTCGAGGGCGGACATGTTGTCAGCTTC 2439
781 AAGACGGTCCACCCCTTCCTGGTGTCAAGCACTGTCGAGGGCGGACATGTTGTCAGCTTC 840
2440 CAAAGGAGATGTCATTTTCATGAAGTGGATATGCCATGACTGAGTGAGCAGCATTCGCG 2499
841 CAAAGGAGATGTCATTTTCATGAAGTGGATATGCCATGACTGAGTGAGCAGCATTCGCG 900
2500 CGAAGTTTCCTCAAGAACTGCTACGATCGCTTCCCAACAATGGAAAGGTGATCGTTGCAG 2559
901 CGAAGTTTCCTCAAGAACTGCTACGATCGCTTCCCAACAATGGAAAGGTGATCGTTGCAG 960
2560 AGTCGCTACTCCCTGTGTACCAAGACAGAGCTTAGCGACCAAGATGTGATCCACATCG 2619
961 AGTCGCTACTCCCTGTGTACCAAGACAGAGCTTAGCGACCAAGATGTGATCCACATCG 1020
2620 ACTGCATCATGTTGGCCCCAACACCCAGCGGGGAAGAGAGACACAGAAGGTTTCGAGG 2679
1021 ACTGCATCATGTTGGCCCCAACACCCAGCGGGGAAGAGAGACACAGAAGGTTTCGAGG 1080
2680 CATTTGGCCAAAGGGCGCGGATTTTCAGGGCTTCCAAAGTCATGTGCTGGCGCTTTCGGCACTC 2739
1081 CATTTGGCCAAAGGGCGCGGATTTTCAGGGCTTCCAAAGTCATGTGCTGGCGCTTTCGGCACTC 1140
2740 ACCTCATGAGTTCCTGAAGACCGCTTGAATGCTGCTCTCTGTGTGATGTTTCATGTTCT 2799
1141 ACCTCATGAGTTCCTGAAGACCGCTTGAATGCTGCTCTCTGTGTGATGTTTCATGTTCT 1200
2800 TGGATTTGAAGGTCGTCGAGGAGCCCTTTCTCAGATTTGGCTTTCGGCATACCAAGTTC 2859
1201 TGGATTTGAAGGTCGTCGAGGAGCCCTTTCTCAGATTTGGCTTTCGGCATACCAAGTTC 1260
2860 TTCTCATAAAGGAAACAATAAGAACGCACTGTATGATGGCGCAAGTGGAGTTTACAAGA 2919
1261 TTCTCATAAAGGAAACAATAAGAACGCACTGTATGATGGCGCAAGTGGAGTTTACAAGA 1320
2920 TTTGTTGTTTATGCTATATAAGTTTGAATGCTTCTGCATACCTGATTTTCAAGATGTTG 2979
1321 TTTGTTGTTTATGCTATATAAGTTTGAATGCTTCTGCATACCTGATTTTCAAGATGTTG 1380
2980 AACGAAACGGGTATATGATGCTGCTGAATGATGGAATTTGATATTTCTGTTCTTTT 3039
1381 AACGAAACGGGTATATGATGCTGCTGAATGATGGAATTTGATATTTCTGTTCTTTT 1440
3040 TTCAGTAAATCAGTTTCGAAACAAA 3063
1441 TTCAGTAAATCAGTTTCGAAACAAA 1464

RESULT 4

US-09-169-789-107
; Sequence 107, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316
; EARLIER FILING DATE: 1997-11-21

; EARLIER APPLICATION NUMBER: US 08/713,000
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-107

Query Match 46.8%; Score 1429.6; DB 3; Length 1630;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

Qy 1601 CCGTTTTATTTCCTCTGCTTTTCGTTTCGAGTCTCGGGAAGAGAGAGAGAGAGAG 1660
Db 1 CCGTTTTATTTCCTCTGCTTTTCGTTTCGAGTCTCGGGAAGAGAGAGAGAGAGAG 60
Qy 1661 AGGAGAGAATGGGTTTCGACCGGCTCCGAGACCCAGATGACCCGACCCCAAGTCTCGAG 1720
Db 61 AGGAGAGAATGGGTTTCGACCGGATCCGAGACCCAGATGACCCGACCCCAAGTCTCGAG 120
Qy 1721 ACAGGCGCAACCTTCCTTCGCAATGCACTGCGGAGCGCTCCGTCGCTCCCATGCTCTAA 1780
Db 121 AGGAGCGCAACCTTCCTTCGCAATGCACTGCGGAGCGCTCCGTCGCTCCCATGCTCTAA 180
Qy 1781 AGSCCCCAATCGAGATCGACCTCCTCGAGATCATGCGCAAGGACGGCGGCGCTTC 1840
Db 181 AGSCCCCAATCGAGATCGACCTCCTCGAGATCATGCGCAAGGACGGCGGCGCTTC 240
Qy 1841 TCTCCACGGGGGAAATCGGGGACACAGCTCCCGACCCAGAACCCCGAGGCAACCCGTCATGC 1900
Db 241 TCTCCCGGGGGAAGTCCGGGCCAGCTCCCGACCCAGAACCCCGAGGCAACCCGTCATGC 300
Qy 1901 TCAGCCGATTCCTTCGCTGCTGCGCAGCTATCTCGTGTCTACGTTGACCCCTCGGAC 1960
Db 301 TCAGCCGATTCCTTCGCTGCTGCGCAGCTATCTCGTGTCTACGTTGACCCCTCGGAC 360
Qy 1961 TCCCGCATGCGAAGTCGAGCGCTCTAGCGCTTAGCGGCTGTCAGAGTTCTTCGTCTCA 2020
Db 361 TCCCGCATGCGAAGTCGAGCGCTCTAGCGCTTAGCGGCTGTCAGAGTTCTTCGTCTCA 420
Qy 2021 AGAACGAGACGGGGTCTCCATCCCGCACTCAACTTTGATGAACACAGGACAAATCTCTCA 2080
Db 421 AGAACGAGACGGGGTCTCCATCCCGCACTCAACTTTGATGAACACAGGACAAATCTCTCA 480
Qy 2081 TGAAGAGCTGGTATTAACCTGAAAGATGCGGTCTCTGAAGCGGGAATCCCATTCACAAAG 2140
Db 481 TGAAGAGCTGGTATTAACCTGAAAGATGCGGTCTCTGAAGCGGGAATCCCATTCACAAAG 540
Qy 2141 CGTACGGGATGACCGGTTTCGAGTATCATGGCACCCGACCCGCGATTCACAAAGATCTTTA 2200
Db 541 CGTACGGGATGACCGGTTTCGAGTATCATGGCACCCGACCCGCGATTCACAAAGATCTTTA 600
Qy 2201 ACCGGGGAATGCTGATCACTCCACCATTAATGAAGAAGATACCTGGAACACATACAAGG 2260
Db 601 ACCGGGGAATGCTGATCACTCCACCATTAATGAAGAAGATACCTGGAACACATACAAGG 660
Qy 2261 GCTTCAGGGCTTCGAGACCGTGTGATGTCGAGCGGCGACTGGGGCGGTCTCAGCA 2320
Db 661 GCTTCAGGGCTTCGAGACCGTGTGATGTCGAGCGGCGACTGGGGCGGTCTCAGCA 720
Qy 2321 TGAATCGTTGCCAAATACCCATCAATGAAGGGATCAACTTCGACCTGACGTGATTG 2379
Db 721 TGAATCGTTGCCAAATACCCATCAATGAAGGGATCAACTTCGACCTGACGTGATTG 780
Qy 2380 AAGACCCCGACCCCTTCCTGGTGTCAAGCAGCTCGAGGCGGACATGTTGCTCAGCGTTC 2439
Db 781 AAGACCTCCACCCCTTCCTGGTGTCAAGCAGCTCGAGGCGGACATGTTGCTCAGCGTTC 840
Qy 2440 CAAAGGAGATGCAATTTTCATGAAGTGGATATGCCATGATGCTGAGTGGAGCAGCATTCG 2499
Db 841 CAAAGGAGATGCAATTTTCATGAAGTGGATATGCCATGATGCTGAGTGGAGCAGCATTCG 900

QY	2500	CGAAGTTCTCAAGACTGCTAGGTCGCTTCCCAAAAGGAGTGATGCTGTCAG	2559
Db	901	CGAAGTTCTCAAGAACTGCTAGGTCGCTTCCCAAAAGGAGTGATGCTGTCAG	960
QY	2560	AGTGCCTACTCCCTGTGTATCCACAGACAAGAGCTAGCGCAAGAAATGTATCCACATCG	2619
Db	961	AGTGCCTACTCCCTGTGTATCCACAGACACAGAGCTAGCGCAAGAAATGTATCCACATCG	1020
QY	2620	ACTGCATCATGTTGGCCCAACACCCAGGCGGGAAGAGAGGAGGAGGAGGTTTCGAGG	2679
Db	1021	ACTGCATCATGTTGGCCCAACACCCAGGCGGGAAGAGAGGAGGAGGAGGTTTCGAGG	1080
QY	2680	CATTGGCCAAAGGCGCGGATTTTCAGGCTTCCCAAGTCAATGTGCTGCGCTTTTCGCACTC	2739
Db	1081	CATTGGCCAAAGGCGCGGATTTTCAGGCTTTCAGGCTTCCCAAGTCAATGTGCTGCGCTTTTCGCACTC	1140
QY	2740	ACGTTCATGAGTTCTCTGAAGACCGCTTGATCTGCTCTCTCTGCTGCTGCTGCTGCTGCT	2799
Db	1141	ACGTTCATGAGTTCTCTGAAGACCGCTTGATCTGCTCTCTCTGCTGCTGCTGCTGCTGCT	1200
QY	2800	TGGATTTGAAGTCGTCGAGAGGCGCTTTTCACAGTTGGCTTCGGCATACCAAGTTTC	2859
Db	1201	TGGATTTGAAGTCGTCGAGAGGCGCTTTTCACAGTTGGCTTCGGCATACCAAGTTTC	1260
QY	2860	TTCTCATAAAGGAAACAATAAGAGCGACTGTATGATGCGCAAGTGAAGTTACAAGA	2919
Db	1261	TTCTCATAAAGGAAACAATAAGAGCGACTGTATGATGCGCAAGTGAAGTTACAAGA	1320
QY	2920	TTTGTGTTTATGTCATAAAGTTTGTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2979
Db	1321	TTTGTGTTTATGTCATAAAGTTTGTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1380
QY	2980	AACGAAACGGGTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3039
Db	1381	AACGAAACGGGTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440
QY	3040	TTTCAGTAAATCACTTCGAACAAA 3063	
Db	1441	TTTCAGTAAATCACTTCGAACAAA 1464	
RESULT 5			
US-09-276-599-12			
; Sequence 12, Application US/09276599			
; Patent No. 6380459			
; GENERAL INFORMATION:			
; APPLICANT: Perera, J. Ranjan			
; APPLICANT: Rice, Stephen J.			
; TITLE OF INVENTION: Composition and methods for the			
; FILE REFERENCE: 11000.1036			
; CURRENT APPLICATION NUMBER: US/09/276,599			
; NUMBER OF SEQ ID NOS: 21			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 12			
; LENGTH: 661			
; TYPE: DNA			
; ORGANISM: Eucalyptus grandis			
; FEATURE:			
; NAME/KEY: (1)...(654)			
; LOCATION: TATA_signal			
; NAME/KEY: (537)...(543)			
; LOCATION: (537)...(543)			
; NAME/KEY: CAAT_signal			
; LOCATION: (499)...(502)			
US-09-276-599-12			
Query Match			
Best Local Similarity 20.8%; Score 638.2; DB 3; Length 661;			
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;			

QY	1019	CTGAGCCATTTAATTCGAGGACATCGCCCAAAATTTATTTCTTGTGCTGCTGCTGCTGCTGCT	1078
Db	1	CTGAGCCATTTAATTCGAGGACATCGCCCAAAATTTATTTCTTGTGCTGCTGCTGCTGCTGCT	60
QY	1079	CGAATTTTCTCTTTTAGGTAAATGAATGATGCGCCATGTTGACAAAAGGCTGATTATTA	1138
Db	61	CGAATTTTCTCTTTTAGGTAAATGAATGATGCGCCATGTTGACAAAAGGCTGATTATTA	120
QY	1139	GTATGATCTTGGAGTTGTTGTCGCAATTTGCAAGCTGACGATGCGCCCTCAGGGAAATTT	1198
Db	121	GTATGATCTTGGAGTTGTTGTCGCAATTTGCAAGCTGACGATGCGCCCTCAGGGAAATTT	180
QY	1199	AAGCGCCCAACCCAGATTTGCAAGAGACACAAAGAGACACGACCAACCTTTTCTTAAACAAG	1258
Db	181	AAGCGCCCAACCCAGATTTGCAAGAGACACAAAGAGACACGACCAACCTTTTCTTAAACAAG	240
QY	1259	ATCATCACAGATCGGCGCAGTAAAGGTAAATTAATTTAAACAATAGCTCTTGTACCGGG	1318
Db	241	ATCATCACAGATCGGCGCAGTAAAGGTAAATTAATTTAAACAATAGCTCTTGTACCGGG	300
QY	1319	AACCTCCGTTATTTCTCTCACATTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGCC	1378
Db	301	AACCTCCGTTATTTCTCTCACATTTCCATAAACCCCTGATTAATTTGGTGGGAAAGCGACAGCC	360
QY	1379	AACCCACAAAGGTGATGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1434
Db	361	AACCCACAAAGGTGATGATGTCATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420
QY	1435	AGAGTTTCTCTTATATTTCTGCTTACCGGTTGAGTCAATGCGATGCTGCGATGCTGCTTATA	1494
Db	421	AGAGTTTCTCTTATATTTCTGCTTACCGGTTGAGTCAATGCGATGCTGCGATGCTGCTTATA	480
QY	1495	ACATATTTGCTGAGGTTCCCAATATTTTGGGAGGTTGTTGAAACCCGAAAGTTTCTTATA	1554
Db	481	ACATATTTGCTGAGGTTCCCAATATTTTGGGAGGTTGTTGAAACCCGAAAGTTTCTTATA	540
QY	1555	TATCGAACTCCACACACATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTTATA	1614
Db	541	TATCGAACTCCACACACATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTTATA	600
QY	1615	CTGCTTTCTTCTGCTGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT	1674
Db	601	CTGCTTTCTTCTGCTGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT	660
QY	1675	T 1675	
Db	661	T 661	
RESULT 6			
US-09-598-401C-12			
; Sequence 12, Application US/09598401C			
; Patent No. 6596925			
; GENERAL INFORMATION:			
; APPLICANT: Perera, J. Ranjan			
; APPLICANT: Eagleton, Clare			
; APPLICANT: Rice, Stephen J.			
; TITLE OF INVENTION: Compositions and Methods for the			
; FILE REFERENCE: 11000.1036C2			
; CURRENT APPLICATION NUMBER: US/09/598,401C			
; CURRENT FILING DATE: 2000-06-20			
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591			
; PRIOR FILING DATE: 1999-07-30			
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018			
; PRIOR FILING DATE: 2000-02-24			
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599			
; PRIOR FILING DATE: 1999-03-25			
; NUMBER OF SEQ ID NOS: 120			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 12			
; LENGTH: 661			
; TYPE: DNA			

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; ORGANISM: Eucalyptus grandis
US-09-598-401C-12

Query Match      20.8%; Score 638.2; DB 3; Length 661;
Best Local Similarity 98.9%; Pred. No. 4.5e-162;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 1019 CTGAGCCATTAAATTCGAGAGCAGCATCGCCAAATAATTTCTTCTGCTGCCATAACTGT 1078
Db 1 CTGAGCCATTAAATTCGAGAGCAGCATCGCCAAATAATTTCTTCTGCTGCCATAACTGT 60

QY 1079 CGAATTTTCTTTTAGTAAAGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1138
Db 61 CGAATTTTCTTTTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 120

QY 1139 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGAGAGTGGCCCTCAGGAAAT 1198
Db 121 GTATGATCTTGGAGTTGTTGGTCAAAATTTGCAAGCTGAGAGTGGCCCTCAGGAAAT 180

QY 1199 AAGCGCCAAACCCAGATTGCAAGAGCACAAGAGCAGCACCACCTTTCTTAAACAG 1258
Db 181 AAGCGCCAAACCCAGATTGCAAGAGCACAAGAGCAGCACCACCTTTCTTAAACAG 240

QY 1259 ATCATCACAGATCGGCCAGTAAGGTAATTAATTAATTAACAAATAGCTCTTGTACGGG 1318
Db 241 ATCATCACAGATCGGCCAGTAAGGTAATTAATTAATTAACAAATAGCTCTTGTACGGG 300

QY 1319 AACTCGGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGGAAAGCAGACC 1378
Db 301 AACTCGGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGGTGGGAAAGCAGACC 360

QY 1379 AACCCACAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1434
Db 361 AACCCACAAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

QY 1435 AGAGTTTTCTCTCTATATTTCTGTTTACCGGTTGAGTCAATGGCATGCGTGACGAATGT 1494
Db 421 AGAGTTTTCTCTCTATATTTCTGTTTACCGGTTGAGTCAATGGCATGCGTGACGAATGT 480

QY 1495 ACATATGGTGTAGGTCGAATATTTTGGGGAGGTTGGTGAACCGCAAGTTCCTATA 1554
Db 481 ACATATGGTGTAGGTCGAATATTTTGGGGAGGTTGGTGAACCGCAAGTTCCTATA 540

QY 1555 TATCGAACCTCCACCACTACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCT 1614
Db 541 TATCGAACCTCCACCACTACCTCACTTCAATCCCAACCATTTATCCGTTTATTTCT 600

QY 1615 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1674
Db 601 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

QY 1675 T 1675
Db 661 T 661

RESULT 7
US-09-947-027-5
; Sequence 5, Application US/09947027
; Patent No. 685864
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigneh
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIO
; FILE REFERENCE: 066040-9718
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 2001-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
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; LENGTH: 1503
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: ALGOMT; GenBank accession number: X62096
US-09-947-027-5

Query Match      20.6%; Score 631; DB 3; Length 1503;
Best Local Similarity 74.5%; Pred. No. 5.9e-160;
Matches 807; Conservative 0; Mismatches 275; Indels 1; Gaps 1;

QY 1687 GAGACCCAGATGACCCCGACCCCAAGTCTCGAGCAGCAGAGCGCAACCTTTGCGCATCGAG 1746
Db 80 GAAACTCAGATGACTCCAATCTCAGGTATCAGATGAAGAGGACACCTCTTTGCGCATCGCAA 139

QY 1747 CTGGCAGAGCGCTCGTGTCTCCCATGTTCTTAAAGGCGCCCATCGAGATCGACCTCTC 1806
Db 140 CTAGCCAGTGTCTCAGTTCTTACCAATGATCTCAAACAGACCATTTGAACCTCGACCTTCT 139

QY 1807 GAGATCATGCGCAAGGACGCGCGCGTCTCTCCACGGGGGAAATCGGGGCACAG 1866
Db 200 GAAATCATGGCTAAAGCTGGCCCTGCTGTCTTCTGTCCACATCTGAGATAGCTTCTCAC 259

QY 1867 CTCCCGACCCAGAACCCCGAGGCAACCCGTCATGCTCGACCGGATCTTCCGGCTGTGGCC 1926
Db 260 CTCCCTTACCAAAACCCCTGATGGCCCTGTCATGTTAGACCGTATCTCGCCCTCTGGCT 319

QY 1927 AGCTACTCGTGTCTAGTGTGACCCCTCCCGGACCTCCCGATGGCAAGGTGAGCGGCTC 1986
Db 320 AGCTACTCCATCTTACCTGCTCTCTGAAAGATCTTCTCTGATGGGAAGGTGAGAGACTG 379

QY 1987 TAGCGCTTAGCCCGGTGTCAGTCTTGTGTCACAGACGAGACGGGTCTCCATCGCC 2046
Db 380 TAGCGCTCGCTCTCTGTTGTTAAATCTTGAACAGACGAGACCGTGTCTCTGTGACG 439

QY 2047 GCACCTCAACTTGATGAACAGGACAAATCTCTCATGAAAGCTGTGTTATCTGAAAGAT 2106
Db 440 CCTCTCTGTCTCATGAACAGGACAAAGTCTCTCATGAAAGCTGTGTTATTTGAAAGAT 499

QY 2107 GCGGTCTTTGAAGCGGAAATCCATTTCAACAGCGGTACGGATGACCGGTTCGAGTAT 2166
Db 500 GCAATTTCTTGATGGAGGAAATCCATTTTAAACAAAGGCTATGGGATGACTGCAATTTGAAT 559

QY 2167 CATGGCACCGACCGGATTTCAACAGATCTTTTAAACGGGGATGCTGATCACTCCACC 2226
Db 560 CATGGCACCGGATTTCAACAGGTTTCAACAGGTTTCAACAGGAAATGCTGACCACTCTACC 619

QY 2227 ATTACTATCAAGAAAGATCTGGAACATACAAAGGGCTTCGAGGGCTTCGAGACCGTGGT 2286
Db 620 ATTACTATCAAGAAAGATTTCTTGAGACCTACAAAGGCTTTGAGGCTCTCACGTCCTTGGTG 679

QY 2287 GATGTCGAGCGGCACTGGGCGGTGCTCAGCATGATCGTTGCCAAAATACCCATCAATG 2346
Db 680 GATGTTGGTGGGACTGGAGCCGTCGTTAAACACCATGCTCTCTAAATACCCCTTCAATC 739

QY 2347 AAGGGATCACTTGA- CCGCCCAACCGATTTGAGAGCCGCCCTTCTCTGCTGTC 2405
Db 740 AAGGGATTTAACTTCGATCTGCCCCACGTCATTTGAGGATGCCCTCTTATCCCGAGTG 799

QY 2406 AAGCAGCTCGAGGCGACATGTTGTCAGCGTTTCAAGGGAGATGCCATTTTTCATGAAG 2465
Db 800 GAGCATGTTGGTGGCAGCATGTTGTTAGTGTGCCCCAAGAGAGATGCCGTTTTCATGAAG 859

QY 2466 TGGATATGCCATGACTGGAGTGAACCAATTTGCGGAGGTTCTCCTAAGAACTGCTCAGAT 2525
Db 860 TGGATATGCCATGATTGGAGCGACGCCACTGCTTAAATTTCTTGAAGAAATTCCTATGAC 919

QY 2526 GCGCTTCCCAACATGGAAGGTGATCGTTGAGAGTGGTACTCTCTGTTGTTACCCAGAC 2585
Db 920 GCGTTCCGGAACCGGCAAGGTGATCTGTTGTTGATGATCTTCTCCCGGCTCTCTGAC 979

QY 2586 ACGAGCCTAGCGACCAAGAAATGTGATCCACATCGACTGCATCATGTTGGGCCCAACACCA 2645
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Query Match 20.5%; Score 629.4; DB 2; Length 1503;
Best Local Similarity 74.4%; Pred No. 1.6e-159;
Matches 806; Conservative 0; Mismatches 276; Indels 1; Gaps 1;

1687 GAGACCCAGATGACCCCGACCCAAAGTCTCGGACGACGAGGCGCACTCTTCGCCATGAG 1746
80 GAAACTCAGATGACTCAACTCAGGTATCAGATGAAGAGGCACACCTCTTTGCCATGCAA 139
1747 CTGGGAGGCGCTCCGCTGCTCCCATGGTCTTAAGGCGCGCATCGAGATCGACCTCTTC 1806
140 CTAGCCAGTGTCTCACTCTTACCAATGATCCTCAAAAGACCATTTGAACCTCGACCTTC 199
1807 GAGATCATGGCCAAAGACGCGCGCGGCTTCTCTTCCACGGGGGAAATCGGGGACAG 1866
200 GAAATCATGGCTAAAGCTGGCCCTGGTGTCTTCTGTCCACATCTGAGATAGTCTTCAC 259
1867 CTCGCGACCCAGAACCCCGAGGACCCGCTCATGCTCGACGGGATCTTCGGGTGCTGGCC 1926
260 CTCCTTACCAAAAAACCTGATGGCGCTCATGTTAGACCGTATCTCTGGCCTCTTGGCT 319
1927 AGTACTCCGTGCTCAGTGCACCCCTCCGCGACCTCTCCCGATGGCAAGTTCGAGCGGCTC 1986
320 AGTACTCCCATTTTACTGCTCTCTGAAAGATCTTCTGATGGGAAGTTCGAGAGACTG 379
1987 TACGGCTTAGCGCGGTGTGCAAGTTCTTGTCAAGAACGAGACGGGTCTTCATCGCC 2046
380 TATGGCTCGCTCTGTTTGTAAATTTCTTGACCAAGAACGAGACGGGTCTCTGTGACG 439
2047 GCATCAACTTGATGAACCGAGCAAAATCTCATGGAAGCTGGTATTAACCTGAAAGAT 2106
440 CCTCTGCTCATGAACCGAGCAAGTCTCATGGAAGCTGGTATTAATTTGAAAGAT 499
2107 GCGGTCTTTGAAGCGGAATCCCATTTCAAGGCGTACGGGATGACCGGTTCGAGTAT 2166
500 GCAATCTTGATGGGAATTTCCATTTAAACAAGGCTATGGGATGACTGCACTTTGAATAT 559
2167 CATGCACCGACCCCGGATTTCAAGATCTTTAAACGGGGAATGTCTGATCACTCCACC 2226
560 CATGGCAGCGATCCAAAGATTCAAGAGTCTTCAACAAAGGGAATGTCTGACCATCTTACC 619
2227 ATTACTATGAAGAGATACATCGAAACATCAAGGCGCTTCGAGGCGCTCGAGACCGTGTG 2286
620 ATTACATGAAGAGATTTCTTGAGACCTTCAAGGCTTTGAAGGCTTCACGCTCTTGTG 679
2287 GATGTGGAGGCGGCACTGGGGCGTGTGACGATGATCTGCAAAATCCCAATCCCAATGAT 2346
680 GATGTGGTGTGGGACTGGACCGCTGTTAACAACCATCTCTTAAATACCTTCAATC 739
2347 AAAGGATCAACTTCGA-CCGCCCCAAAGGATGAAGACGCCCCACCTTCTGCTGTGTC 2405
740 AAGGCAATTAATCTTGATCTGCCACGCTCATTTGAGGATGCCCATCTTATCCCGAGTG 799
2406 AAGCAGCTCGGAGGCGACATGTTGCTGAGCTTCAAGGGAGATGCCATTTTCATGAAG 2465
800 GAGCATGTTGTTGGCGACATGTTGTTAGTGTGCCCAAGACAGATGCGCGTTTCATGAAG 859
2466 TGGATATGCCATGACTGGGATGACGACCATTCGCGAAGTTCCTCAAGAACTGCTACGAT 2525
860 TGGATATGCCATGATTGGAGCGGACGCCCACTGCTTAAATTTCTTGAAGATTTGCTATGAC 919
2526 GCGCTTCCCAACAATGGAAGGATGATGTTGCGAGAGTGGTATCTCCTGTGTACCCAGAC 2585
920 GCGTTGCCGGAACCGCAAGGTGATCTTGTGAGTGCATCTTCTCCGCTGCTCTGAC 979
2586 ACAGGCTTAGCGACCAAGATGATGATCCACATGCTGATGCTGTCGCCACACACCA 2645
980 ACAAGCCTTGCACCAAGGAGTTCGTGACGCTGATGATCATCATGTCTGGGACACACCC 1039
2646 GCGGGAAAGAGGACACAGAGGAGTTCGAGGCAATTCGCCAAAGGGCGGATTTTCAG 2705
1040 GGTGGAAAGAGGACCGGAGAGGATTTGAGGGCTTAGCTAAGGAGCTGCTTCCAA 1099
2706 GGCTTCCAAAGTCACTGCTGCGCTTTCCGGCACTCAGCTCATGGAGTTCCTTGAAGACGCT 2765

980 ACAAGCCTTGCACCAAGGAGTGTGACGTTGATGTCATCATGCTGCGCACAAACCC 1039
2646 GCGGGAAAGAGAGGACACAGAGGATTCGAGGCAATTCGCCAAAGGGCGGATTTTCAG 2705
1040 GGTGGAAAGAGAGGACCGGAGGAAATTTGAGGGCTTAGCTAAGGGAGCTGGCTTCCAA 1099
2706 GGCTTCCAAAGTCACTGCTGCGCTTTCCGCACTCAGCTCATGGAGTTCCTGAAGACCGCT 2765
1100 GGTTTGAAGTAATGCTGTGCATTTCAACACACATGTCATTTGAATTCGCGAAGAGCC 1159
2766 TGA 2768
1160 TAA 1162

RESULT 8
US-08-715-325-1
; Sequence 1, Application US/08715325
; Patent No. 5886243
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Tsai, Chung-Jui
; APPLICANT: Podila, Gopi
; TITLE OF INVENTION: Genetic Engineering of Wood Color
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael, Best & Friedrich
; STREET: 100 E. Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: United States of America
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS 6.22
; SOFTWARE: WordPerfect for Windows 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,325
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US60/007727
; FILING DATE: 30 NOV 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Genignani, Joseph A
; REGISTRATION NUMBER: 19,482
; REFERENCE/DOCKET NUMBER: 66040/9627
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-6560
; TELEFAX: (414) 277-0656
; TELEX: 262057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1503 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Populus Tremuloides
; DEVELOPMENTAL STAGE: four year old sapling
; DEVELOPMENTAL STAGE: undergoing lignification in summer
; TISSUE TYPE: secondary xylem
; IMMEDIATE SOURCE: to total mRNA
; LIBRARY: cdna
; CLONE: pLOWTI
US-08-715-325-1

Db 1100 GGTATTAAGTAATGTGTGTCATTCAACACACATGTCAATTGGAATCCCGCAAGAGGCC 1159
 QY 2766 TGA 2768
 Db 1160 TAA 1162

RESULT 9

US-08-204-288-1
 ; Sequence 1, Application US/08204288
 ; Patent No. 5959178
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN DOORSSELAERE, Jan
 ; APPLICANT: FRITIG, Bernard J.M.
 ; APPLICANT: INZE, Dirk G.
 ; APPLICANT: JOUANIN, Lise
 ; APPLICANT: KNIGHT, Mary E.
 ; APPLICANT: VAN MONTAGU, Marc
 ; APPLICANT: LEGRAND, Michel
 ; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D. C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3518
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/204,288
 ; FILING DATE: 10-MAR-1994
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9119279.9
 ; FILING DATE: 10-SEP-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB92/01460
 ; FILING DATE: 09-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, Paul N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1368 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-204-288-1

Query Match 20.1%; Score 618.2; DB 2; Length 1368;
 Best Local Similarity 73.5%; Pred. No. 1.6e-156;
 Matches 802; Conservative 0; Mismatches 288; Indels 1; Gaps 1;
 QY 1687 GAGACCCAGATGATCCCGAGCCCAAGTCTCGAGCGACGAGCGAACCTCTTCGCCATGCGAG 1746
 Db 64 GAAACTCAGATGACTCCAACTCAGGTATCAGATGAGAGGCGACACCTCTTTTGCATGCAA 123
 QY 1747 CTGCGAGCGCCTCCGTCCTCCCATGCTCTAAAGCGCCCATCGAGATCGACCTCTC 1806
 Db 124 CTAGCCAGTGCTTCAGTGTCTACCAATGATCCTCAAAACAGCCATTGAACTCGACCTTCTT 183

QY 1807 GAGATCATGSCCAAGCAGCGGCGGGCGGCTTCTCTCCACGGGGGAAATTCGGGCGACAG 1866
 Db 184 GAAATCATGGCTAAAGCTGGCCCTGGTCTTCTTGTCCACATCTGAGATAGCTTCTCAC 243
 QY 1867 CTCGCCAGCCAGAACCCCGAGGCAACCGCTCATGCTCGACCGGATCTTCGGCTGCTGGCC 1926
 Db 244 CTCCTTACCAAAAACCTGATGCGCTGTCTATGAGCCGTATCTTGGCCCTCTGGCT 303
 QY 1927 AGCTACTCCGTGCTCAGCTGCACCCCTCCGCGACCTCCCGATGCGAAGCTCGAGCGGCTC 1986
 Db 304 AGCTACTCCATACTGACTTGTCTCTGAAAGATCATCTCTGGAAGAGTTGAGAGACTG 363
 QY 1987 TAGCGGCTTAGCGCGCGGTGTGCAAGTCTTGGGTCAAGAAACGAGGACGGGTCTCCATCGCC 2046
 Db 364 TATGGCTTGTCTCTGTTGCAAACTTCTTGACCAGAACGAGGAGGTGTCTCTGTGTCAGC 423
 QY 2047 GCATCAACTGTATGAACACGAGCAAAATCTCTCATGGAAGCTGTGTATTAACCTGAAAGAT 2106
 Db 424 CCTCTCTGTCTCATGAACACGAGCAAGGTCTCTCATGAAAGCTGTGTATTAATTTGAAAGAT 483
 QY 2107 GCGGTCTTTGAAGCGGGAATCCCAATTCACAAAGCGGTACGGGATGACCGGTTTCGAGTAT 2166
 Db 484 GCAATTTCTTGATGGAGGAATTCCAATTTAAACAAGGCTTATGGGATGACTGCAATTTGAATAT 543
 QY 2167 CATGGCACCGACCCCGGATTTCAACAAGATCTTTAAACGGGGAATGTCTGATCACTCCACC 2226
 Db 544 CATGGCACCGATCCAAGATTTCTTGAGACTTCAACAAGGTCTTCAATAAGGGAATGTCTGACCACTTACC 603
 QY 2227 ATTACTATGAAGAGATACATGGAACATACAAGGGTTCAGAGGCTTCGAGACCGTGGTC 2286
 Db 604 ATTACCATGAAGAAAGATTTCTTGAGACTTCAACAAGGTCTTCAATAAGGGAATGTCTGACCACTTACC 663
 QY 2287 GATGTCGAGGCGGCACTGGGCGGTGCTCAGCATGATGTTGCCAAATACCATCAATG 2346
 Db 664 GATGTTGGTGGTGAGCTGGAGCTGCTGTTAAACACCATGCTCTCTAAATAACCTTCAAT 723
 QY 2347 AAAGGATCAACTTTGCA - CCGCCCCCAACGAGTTGAAGAGCGCCCAACCTCTCTCGGTGTC 2405
 Db 724 AAGGCAATTAACTTTGATTTGCCACGCTCATGAGATGCCCATCTTATCCCGGTGTG 783
 QY 2406 AAGCAGCTCGAGGCGACATGTTTCGTGAGGTTCCAAAGGAGATGCCATTTTCATGAAG 2465
 Db 784 GAGCATGTTGGTGGGACATGTTTGTAGTGTGCCCAAGACAGATGCCGTTTTTCATGAAG 843
 QY 2466 TGGATATGCATGACTGGAGTGAACGACCATTTGGCGAAGTTCCTCAAGAACTGCTAGCAT 2525
 Db 844 TGGATATGCCATGATTTGGAGCGACGACACTGCTTAAATTTCTTGAAGAAATTCCTATGAC 903
 QY 2526 GCGCTTCCCAACAATGGAAGAGTGTGTTGACAGAGTGGTACTCCTGTGTATCCCGACAGAC 2585
 Db 904 GCGTTGCCGGAANAACGCGAAGGTGATCTTGTGAGTGCATTTTCCCGTGGCTCTGAC 963
 QY 2586 ACAGGCTTAGCGACCAAGAAATGTGATCCACATCGATGATCATGTTGGCCCAACACCCA 2645
 Db 964 ACAAGCTTTGCCACCAAGGAGTTCGTTACATTTGATGTTTATCATGCTGGGCGCAACCC 1023
 QY 2646 GCGCGGAAGAGAGGACACAGAAGAGTTCGAGGCAATTCGCCAAAGGGGCGGATTTTCAG 2705
 Db 1024 GGTGGGAAGAGAGAGGACCCGAAAGAAATTTGAGGGCTTAGCTAAGGAGAGTGTGCTTCAA 1083
 QY 2706 GCGTTCCAAAGTCAATGCTGCGCTTTCGGCAGCTCAGTGTGAGTTCCTTGAAGACCGCT 2765
 Db 1084 GGTGTTGAAGTGTGCTGTGCTGATTCACACACATGTCATTTGAACTCCGCAAGAACTAA 1143
 QY 2766 TGATCTGCTCC 2776
 Db 1144 GGCTCAAGTCC 1154

RESULT 10
 US-09-500-569-3
 ; Sequence 3, Application US/09500569

[illegible]

Db 394 TATGCTCTGCCCGCCGTTGCCAAGTACTTGGTTAAGAACGAAGATGGTGTCTCCATTGCT 453
Qy 2047 GCATCTCAACTTGTATGAACAGACAAATCCTCATGGAACTGCTATTAATCTCAAGAT 2106
Db 454 GCGCTCAACCTCTATGAACAGACAAATCCTCATGGAACTGCTATTAATCTCAAGAT 513
Qy 2107 GCGTCTCTTGAAGCGGGAATCCCATTTCAACGAAGCGTACGGGATGACCGGCTTCGAGTAT 2166
Db 514 GCAGTCTCTTGAAGCGGGAATCCCATTTCAACGAAGCGTATGAATGACAGCGCTTTGAGTAC 573
Qy 2167 CATGGACCGGACCGCGGATTTCAACAGATCTTTAAACCGGGAATGTCTGATCACTCCACC 2226
Db 574 CATGGAACAGATCCAAAGGTTTTAAACAGGTTTTCAACGAAGGAATGGCTGATCACTCTACC 633
Qy 2227 ATTAATATGAAGAGATATCTGAACATACAAAGGCTTCGAAGGCTTCGAGCGCTTCGAGCGTGTG 2286
Db 634 ATCAATATGAAGAAATTTCTTGAGACCTTACAGGTTTGGAGTCTTAAATCTCTGGTT 693
Qy 2287 GATGTCGAGCGGCACTGGGGCGGTGCTCAGCATGATCGTTGCCAAATACCCATCAATG 2346
Db 694 GATGTTGGTGGGACTGGAGCTGTAATCAACATGATTTGCTCAAGCATCCCACTATT 753
Qy 2347 AAGGGATCAACTTCCA-CGCGCCCAACGGATGAAGACGCCGCCACCGCTTCCTGGTGTG 2405
Db 754 AAGGGCATTAATTTTGAATTTGCTCTCATGCTATTGAAGATGCCCATCTTATCTCTGGAGTG 813
Qy 2406 AAGCAGCTCGAGCGGACATGTTGCTCAGCGTTCGAAGGAGATGCAATTTTCATGAAG 2465
Db 814 GAGCATGTAGTGGAGATATGTTTGGAGTGTTCGAAGCTGATGCTATTTTATGAAG 873
Qy 2466 TGGATATGCCATGACTGGAGTGACGCCATTTGCCGGAATTTCTCAAGAACTGTACGAT 2525
Db 874 TGGATTTGCCACGATTTGGAGTGATGAGCATGCTGTTGAATTTTGAAGACTGTCTAG 933
Qy 2526 GCGCTTCCCAACAAATGAAGGTGATCGTTCAGAGTGCCTGCTCCTGTGTACCCAGAC 2585
Db 934 GCATACAGACAAATGGAGGTGATTTGGCAGATGCAATTTCTCCAGTGGCTCCAGAC 993
Qy 2586 ACGAGCTAGCGACCAAGATGATCCACATGCACTGCATCATGTTGGCCCAACCCCA 2645
Db 994 TCTAGCTTGGCCCAAAAGGTGTGGTTCACATGATGTGATCATGTTGGCACAATATCCA 1053
Qy 2646 GCGGGGAAAGAGAGACACAGAGAGTTTCAGAGCATTTGGCAAGGCGCGGATTTTCAG 2705
Db 1054 CGTGGGAAAGAGAGAACAGAGAGATTTGAGGCTCTGGCAAGGCTGTGATTTCAA 1113
Qy 2706 GGCTTCCAAGTCACTGTCTGCGCTTTCCGCACTCACGTCTATGGAGTTCTTGAAGACCGCT 2765
Db 1114 GGTTCGAGTTGTTGCTGTGCTTTCAATACCAACATCATGGAATTTCTCAAAAGATT 1173
Qy 2766 TGATCTGCTCTGTGTGATGTTTCATGTTCTT 2800
Db 1174 TAAGTTCTTTGGCATGATTCATGTCAGCTGCAT 1208

RESULT 12

US-08-991-677-5
; Sequence 5, Application US/08991677A
; Patent No. 6252135
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Caraway, Daniel T
; APPLICANT: Smeltzer, Richard H
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
; FILE REFERENCE: 50617
; CURRENT APPLICATION NUMBER: US/08/991.677A
; CURRENT FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: US 60/033.381
; EARLIER FILING DATE: 1996-12-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1380

; TYPE: DNA
; ORGANISM: Liquidambar styraciflua
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1170)
US-08-991-677-5

Query Match 19.2%; Score 589; DB 3; Length 1380;
Best Local Similarity 72.8%; Pred. No. 1.3e-148;
Matches 787; Conservative 0; Mismatches 290; Indels 4; Gaps 2;

Qy 1710 AGTCTCGACGACGAGCGAACTCTTTCGCCATGACAGTGGCGAGCGCTCCGTCGTCCTCC 1769
Db 1.11 AGCAGCAGAAAGAAAGCAATTCGTATTTCGCTATGCAATTAACCAAGTCTTCAGTCTCTCC 170
Qy 1770 CATGGTCTTAAAGCGGCCCATCGAGATCGAGCTCTCGAGATCATGCGCAAGGACGGCC 1829
Db 171 CATGGTCTTAAATTCAGCCCATGAGCTCGACGCTTTAGAAATCATGGCTAAAGCTGTGCC 230
Qy 1830 GGGCGGCTTCTCTCCACGGGGAAATCGCGGCACAGCTCCCGACCCAGAAACCCCGAGGC 1889
Db 231 AGTGGCACAATATCCACATCTGACATAGCTCTAAGCTGCCACAAAGAAATCAGATGC 290
Qy 1890 ACCGCTCATGCTCGACCGGATCTTTCGGCTGTGTCGCGAGTACTCTCGTGTCTCAGTGCAC 1949
Db 291 AGCGTCTATGCTTGAACCGTATGCTCGGCTCTTGGCTAGTACTCTCTCTTAACGCTGCTC 350
Qy 1950 CTTCCGGGACCTCCCGATGGCAAGTTCGAGCGGCTCTAGGCTTAGCGCGGTGTGCA 2009
Db 351 TCTCCGCACTCTCTTCGACCGCAAGATTCGAGAGGCTTTACGGGCTTTCACCCGCTTTGTAA 410
Qy 2010 GTTCTTGGTCAAGAACGAGGACGGGTCTCCATCGCGCACTCAACTTGTATGAACCAAGGA 2069
Db 411 ATTCTTGACCAAGAAACGATGATGAGTCTCCATAGCGCTCTGTCTCTATGAATCAAGA 470
Qy 2070 CAAATCTCTCATGAAAGCTGGTATTACCTGAAAGATGCGGTCTTGAAGCGGAAATCCC 2129
Db 471 CAAGGTCTCATGAGAGCTGGTACCACTTGAACCGAGGCAAGTCTTGAAGCGGAAATCCC 530
Qy 2130 ATTCAACAGGCTACGGGATGACCGGTTTCGAGTATATGCGACCCAGCCCGGATTTCAA 2189
Db 531 ATTAAACAGGCTATGGAATGACAGCAATTTGAGTACCATTTGGCAACCATCCGATTTCAA 590
Qy 2190 CAAGATCTTTAAACGGGGAATGCTGATCACTCCACCATTTATGAAGAGATFACCTGGA 2249
Db 591 CACAGTTTTCAACAATGGAATGCCATCAATTCACCATTTACCAATGAAGAAATTCCTTGA 650
Qy 2250 AACATACAAGGCTTTCGAGGCTTCGAGACCGTGGTTCGATGTTCGAGGCGGCACTGGGCG 2309
Db 651 GACTTACAAGGCTTCGAGGCTTCGAGTCTGTGGTTCGATGTTGGTGTGTCACCTGGTGC 710
Qy 2310 CGTGTCTCAGATGATGTTGCCAAATACCCATCAATGAAGAGGATCACTTCGAC-CGCC 2368
Db 711 CCACCTTAAACATGATTTATCGCTAAATACCCCATGATCAAGGCGCATTAACCTTCGACTTGC 770
Qy 2369 CCAACGATTTGAAGACGCCCGCCCTCTCTCTGTGTCAACAGCTCGAGCGGACATGTT 2428
Db 771 TCATGTTATTGAGAGGCTCCCTCTCTCTGTGTGGAGCATGTTGGTGGAGATATGTT 830
Qy 2429 CGTCAGGCTTCCAAAGGGAGATGCCATTTTCATGAAGTGGATATGCCATGCTGGAGTGA 2488
Db 831 TGTAGTGTTCCAAAGAGGAGATGCCATTTTCATGAAGTGGATATGTCATGATTGGAGCGA 890
Qy 2489 CGACCATTTGCGGAGGTTCTCCTCAAGAACTGCTCAGTGCCTTCCCAACCAATGAAGAGGT 2548
Db 891 TGAACACTGCTTGAAGTTTTTGAAGAAATGTTTATGAAGCACTTCCCAACCAATGGGAAGGT 950
Qy 2549 GATCGTTGACAGTGGCTACTCTCTGTGTACCCAGACACAGGCTACGACCAAGATGT 2608
Db 951 GATCCTTGTGTAATGCACTCTCCCGTGGCGCAGACGCAAGCTTCCCACTAAGGAGT 1010
Qy 2609 GATCCACATGCACTGCAATCATGTTGGCCCAACCCAGGCGGGAAGAGAGGACACAGAA 2668

Db	1011	GGTCCATATTGATGTCATCATGTTGGCTCATTAACCCAGGTGGGAAGAGAGAACTGAGAA	1070
QY	2669	GGAGTTTCGAGGCAATTGGCCAAAGGGCCGGATTTTCAGGGCTTCCAAGTCAT---GTGCTG	2725
Db	1071	GGAGTTTCGAGGCTTGGCCAAAGGGGCTGGATTTGAAGGTTTCCGAGTAGTAGCCTCGTG	1130
QY	2726	CGCTTTCCGCACTCACGTGATGAGTTCTCTGAAGACCGCTTGATCTGCTCTCTCTGTGGTG	2785
Db	1131	CGCTTACATATACGATCATCGAATTTTGAAGAGATTTCAGTCCCTTACTCGGCTTTG	1190
QY	2786	A 2786	
Db	1191	A 1191	
RESULT 13			
US-09-500-569-17			
; Sequence 17, Application US/09500569			
; Patent No. 6329204			
; GENERAL INFORMATION:			
; APPLICANT: Cahoon, Rebecca E.			
; APPLICANT: Rafalski, Antoni			
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs			
; FILE REFERENCE: BB1327 US NA			
; CURRENT APPLICATION NUMBER: US/09/500,569			
; CURRENT FILING DATE: 2000-02-09			
; EARLIER APPLICATION NUMBER: 60/119,587			
; EARLIER FILING DATE: 1999-February-10			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: Microsoft Office 97			
; SEQ ID NO 17			
; LENGTH: 1314			
; TYPE: DNA			
; ORGANISM: Glycine max			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: (472)			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: (1156)			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: (1180)			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: (1262)			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: (1302)			
; US-09-500-569-17			
Query Match 18.1%; Score 556.6; DB 3; Length 1314;			
Best Local Similarity 72.2%; Pred. No. 7.2e-140;			
Matches 765; Conservative 0; Mismatches 290; Indels 5; Gaps 3;			
QY	1687	GAGACCCAGATGACCCCGACCCCAAGCTCGGACGAGCGGGAACCTCTTCGCCATCGAG	1746
Db	87	GAGACTCAGATTACTCCAAACCCATGATCTGATGAAGAGGCAAACTTTTCGCCATGCAA	146
QY	1747	CTGGGAGCGCTTCCTGCTCCCATGGTCTTAAAGGCGCGCATCGAGATCGACTCCTC	1806
Db	147	CTAGCCAGTGCTCAGTACTCCCTATGGTTCTCAAATCAGCTCTTGAGCTTGATCTGTG	206
QY	1807	GAGATCATGCCAAGACGCGGCGGCTTCCTCTCAACGGGGGAATCCGGCACAG	1866
Db	207	GAATCATAGCCAAAGGCTGGCCCTGTGTTCACCTTTCCCTCCGACATTCCTTCGG	266
QY	1867	CTCCGACCCAGAACCCCGAGGACCCGTCATGCTCGACCGGATCTTCGGGTGTGGCC	1926
Db	267	CTCCCAACACACACCTGATGACCCGTTATGTTGACCGGTATATTGGCGCTCTTGGCT	326
QY	1927	AGCTACTCCGTGCTCAGTGCAACCTCCCGGACCTCCCGATGGCAAGGTCGAGCGGCTC	1986

Db	327	TGCTACATATCTCTCTTTTCTCTTCGACTCTCCCTCATGGCAAGGTTGAGAGGCTC	386
QY	1987	TACGGCTTACGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGACGGGCTCTCCATCGCC	2046
Db	387	TATGGTCTGCGCCCTGTGTCTAGTACTTGGTTCAGGAACGAAGATGGTGTCTCCATGCT	446
QY	2047	GCACTCACTTGATGAACAGGACAAATCCTCATGGAAGCTGGTATTACCTCGAAAGAT	2106
Db	447	GCTCTCAACTCATGAACACGAGACAAATCCTCATGGAAGCTGGTACTATTATGAAAGAT	506
QY	2107	GCGTCTCTGAAGCGGAATCCCATTTCAACAAGCGCTACGCGGATGACCGGTTTCGAGTAT	2166
Db	507	GCAGTCTTGAAGGGGTATTCCATTAAACAAAGCATATGGAATGACAGCTTTGAATAC	566
QY	2167	CATGGCACCGACCGCGATTTCAACAAGATCTTTAAACGGGGAATGCTGATCACTCCACC	2226
Db	567	CATGGAACGGATCCAAAGGTTTAAACAGGTTTCAACAAAGGGATGGCTGATCACTTACC	626
QY	2227	ATTACTATGAAGAGATACTTGGAAACATACAAAGGCTTTCGAGGGCTTCGAGACCGTGGTC	2286
Db	627	ATTACATGAAGAAATTTCTTGAGACCTACACAGGCTTTGAGGGACTTAAATCCCTGGT	686
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Db	747	AAGGCATTAATTTTGTATTTGCCCATGTCATTGAAGATGCCCATCTTATCCAGGATG	806
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QY	2466	TGGATATGCCATGACTCGAGTGAAGACCATTTGCGGAAGTTTCCTCAAGAACTGTGTACAT	2525
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QY	2586	ACGAGCTTAGCCACCAAGAAATGTGATCCACATCGACTGCATCATGCTGCCCCACAACCCA	2645
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QY	2646	GCGGG---AAAGAGAGGACACAGAGGAGTTTCGAGGCAATTTGGCCAAAGGGCCGGATTT	2702
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; Sequence 17, Application US/09971823B			
; Patent No. 6610521			
; GENERAL INFORMATION:			
; APPLICANT: Cahoon, Rebecca E.			
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs			
; FILE REFERENCE: BB1327 US NA			
; CURRENT APPLICATION NUMBER: US/09/971,823B			
; CURRENT FILING DATE: 2002-05-17			
; PRIOR APPLICATION NUMBER: 60/119,587			
; PRIOR FILING DATE: 1999-02-10			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: Microsoft Office 97			
; SEQ ID NO 17			
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; TYPE: DNA			

ORGANISM: Glycine max
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 LOCATION: (472)
 OTHER INFORMATION: n = A, C, G or T
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 Best Local Similarity 72.2%; Pred. No. 7.2e-140;
 Matches 765; Conservative 0; Mismatches 290; Indels 5; Gaps 3;
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Thu Nov 2 13:35:51 2006

us-10-702-319a-113.rni

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 Job time : 572.583 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:25:56 ; Search time 3927.54 Seconds
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9604.757 Million cell updates/sec

Title: US-10-702-319A-113

Perfect score: 3070

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /EMC_Celerra_SID33/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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- 15: /EMC_Celerra_SID33/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SID33/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3070	100.0	3070	9	US-10-702-319A-113
3	3070	100.0	3070	10	US-10-927-641-113
4	2020.4	65.8	2096	6	US-10-137-036-60
5	2020.4	65.8	2096	9	US-10-702-319A-60
6	2020.4	65.8	2096	10	US-10-927-641-60
7	1429.6	46.6	1630	7	US-10-174-693-107
8	638.2	20.8	661	6	US-10-137-036-12
9	638.2	20.8	661	9	US-10-702-319A-12
10	638.2	20.8	661	10	US-10-927-641-12
11	631	20.6	1503	3	US-09-947-027-5
12	631	20.6	1503	6	US-10-091-009-5
13	631	20.6	1503	13	US-11-057-518-5
14	613.4	20.0	2037	8	US-10-424-599-20299
15	613	20.0	1486	8	US-10-469-993-11
16	603.8	19.7	1370	8	US-10-464-610-3
17	589	19.2	1380	3	US-09-796-256A-5

18	589	19.2	1380	10	US-10-681-878A-5	Sequence 5, Appli
19	556.6	18.1	1314	8	US-10-464-610-17	Sequence 17, Appli
20	554.2	18.1	1098	8	US-10-239-463-3	Sequence 3, Appli
21	534.4	17.4	1460	3	US-09-129-298-3	Sequence 3, Appli
22	534	17.4	534	8	US-10-703-091-1	Sequence 1, Appli
23	529.2	17.2	1124	8	US-10-425-114-15205	Sequence 15205, A
24	523	17.0	1418	3	US-09-129-298-4	Sequence 4, Appli
25	485	15.8	485	8	US-10-703-091-2	Sequence 2, Appli
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27	475.4	15.5	1452	10	US-10-955-745-42	Sequence 42, Appli
28	472.8	15.4	1428	7	US-10-289-757-149	Sequence 149, App
29	472.8	15.4	1428	10	US-10-955-745-149	Sequence 149, App
30	472.8	15.4	1455	7	US-10-289-757-150	Sequence 150, App
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44	419.6	13.7	1440	8	US-10-425-114-23028	Sequence 23028, A
45	419.6	13.7	1478	8	US-10-425-114-17765	Sequence 17765, A

ALIGNMENTS

RESULT 1

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; Sequence 113, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-113

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2281 GTGTGCGATGTCGAGGCGGACCTGGGGCCGTGTCTCAGCATGATCGTTGCCAATACCCA 2340
Qy 2341 TCAATGAAGGATCAACTTCGACCGGCCCAACGGATTTGAAGCGCCCAACCTTCCTG 2400
Db 2341 TCAATGAAGGATCAACTTCGACCGGCCCAACGGATTTGAAGCGCCCAACCTTCCTG 2400
Qy 2401 GTGTCAAGACGTCGAGGCGGACATGTTGTCGACGCTTCAAAAGGGAGATGCCATTTC 2460
Db 2401 GTGTCAAGACGTCGAGGCGGACATGTTGTCGACGCTTCAAAAGGGAGATGCCATTTC 2460
Qy 2461 TGAAGTGGATATGCCATGACTGGAGTGACGACCAATTCGCGGAAGTTCCTCAAGAACTGCT 2520
Db 2461 TGAAGTGGATATGCCATGACTGGAGTGACGACCAATTCGCGGAAGTTCCTCAAGAACTGCT 2520
Qy 2521 ACAGTGGCTTCCCAACAAATGGAAGGTGATCGTTGCGAGATGCGTACTCCCTGTGTACC 2580
Db 2521 ACAGTGGCTTCCCAACAAATGGAAGGTGATCGTTGCGAGATGCGTACTCCCTGTGTACC 2580
Qy 2581 CAGACAGCGCTAGCGACCAAGATGTGATCCACATCGACTGCATCATGTGCGCCACA 2640
Db 2581 CAGACAGCGCTAGCGACCAAGATGTGATCCACATCGACTGCATCATGTGCGCCACA 2640
Qy 2641 ACCAGCGGGGAAAGAGAGACACAGAAAGGATTCGAGGCAATTCGCCAAAGGGGCCGAT 2700
Db 2641 ACCAGCGGGGAAAGAGAGACACAGAAAGGATTCGAGGCAATTCGCCAAAGGGGCCGAT 2700
Qy 2701 TTCAGGCTTCCAAAGTCATGTGTCGCTTTCGGGCACTCAGTCATGGAGTTCCTGAAGA 2760
Db 2701 TTCAGGCTTCCAAAGTCATGTGTCGCTTTCGGGCACTCAGTCATGGAGTTCCTGAAGA 2760
Qy 2761 CCGCTTATCTGCTCTGCTGCTGATGTTTCATGGTTCCTGGATTCGAAAGGTCGTGAAG 2820
Db 2761 CCGCTTATCTGCTCTGCTGCTGATGTTTCATGGTTCCTGGATTCGAAAGGTCGTGAAG 2820
Qy 2821 GAGCCCTTTCTCACAGTGGCTTCGGCATAACCAAGTTCCTCATAAAGGAAACAATA 2880
Db 2821 GAGCCCTTTCTCACAGTGGCTTCGGCATAACCAAGTTCCTCATAAAGGAAACAATA 2880
Qy 2881 AGAAGCGACTGTATGATGGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAA 2940
Db 2881 AGAAGCGACTGTATGATGGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAA 2940
Qy 2941 AGTTTTCAGTCTTCGATGCTGATGTTTCAAGATGTTTCAAGATGTTTCAAGATGTTT 3000
Db 2941 AGTTTTCAGTCTTCGATGCTGATGTTTCAAGATGTTTCAAGATGTTTCAAGATGTTT 3000
Qy 3001 GTGCTGAAATGATGAAATGATGATGTTTCTGCTTCTTTTTCAGTAAATCACTTCGAACA 3060
Db 3001 GTGCTGAAATGATGAAATGATGATGTTTCTGCTTCTTTTTCAGTAAATCACTTCGAACA 3060
Qy 3061 AAAAAAAAAA 3070
Db 3061 AAAAAAAAAA 3070

RESULT 2

US-10-702-319A-113
; Sequence 113, Application US/10702319A
; Publication No. US20050026162A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression

FILE REFERENCE: 11000.1036C5
CURRENT APPLICATION NUMBER: US/10/702.319A
PRIOR FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: U.S. No. 10/291,447
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: U.S. No. 60/425,087
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: U.S. No. 10/137,036
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 113
LENGTH: 3070
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-10-702-319A-113

Query Match 100.0%; Score 3070; DB 9; Length 3070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCACCATCAGCAAAAAATAGATGGATAGATGGGACACCACTGTTCAGTTTGTATTC 60
Db 1 AGCACCATCAGCAAAAAATAGATGGATAGATGGGACACCACTGTTCAGTTTGTATTC 60
Qy 61 CTTGAGATGACCTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 120
Db 61 CTTGAGATGACCTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 120
Qy 121 GATAAAGAGTAGGAGATAGGAGATCTCCCGTCTGATGCTCCGGTAGGTGAAATA 180
Db 121 GATAAAGAGTAGGAGATAGGAGATCTCCCGTCTGATGCTCCGGTAGGTGAAATA 180
Qy 181 AGCAAAAGTTCCCGTTCGAATTTGACAGCAAAAGACACCGTCTGATGCTATGATGATGAT 240
Db 181 AGCAAAAGTTCCCGTTCGAATTTGACAGCAAAAGACACCGTCTGATGCTATGATGATGAT 240
Qy 241 CCATTGTACCCATGTAGGGTGAATCCTAGAGTGAGGAGATAGTCTCTTTAGAAAGTCCCA 300
Db 241 CCATTGTACCCATGTAGGGTGAATCCTAGAGTGAGGAGATAGTCTCTTTAGAAAGTCCCA 300
Qy 301 TTCACCCCTATCATAGGCTTTCGCAATATCCATTTTAAAGACAGCCCGGAAATGACGTCT 360
Db 301 TTCACCCCTATCATAGGCTTTCGCAATATCCATTTTAAAGACAGCCCGGAAATGACGTCT 360
Qy 361 ACATTTTCGACTTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 ACATTTTCGACTTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 TTGACGCTCCACTGACAAAGAGCGCTTTCGCTCTGCGAAATAAGTACAGGAGGTAGGGCTT 480
Db 421 TTGACGCTCCACTGACAAAGAGCGCTTTCGCTCTGCGAAATAAGTACAGGAGGTAGGGCTT 480
Qy 481 AAGCGGATGGCAATCACCTTAGAATATGATCTTATATGCGTAATTAACAAAGACGTAGGG 540
Db 481 AAGCGGATGGCAATCACCTTAGAATATGATCTTATATGCGTAATTAACAAAGACGTAGGG 540
Qy 541 GCGGATTCGTCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 GCGGATTCGTCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 601 ATTGAGATTCGGTGGTATGATGCCAGAAATTAAGTCTGCTGATGATGATGATGATGATGAT 660
Db 601 ATTGAGATTCGGTGGTATGATGCCAGAAATTAAGTCTGCTGATGATGATGATGATGATGAT 660

Db 601 ATTGAGATTCGGTGTATGATGCCAGAAATTAABAAAGTGTGCACTGATGAGAAATGTT 660
 Qy 661 ATCTCTGGAGTATATCCCAATGATGTGTGAGAGATGCATTAAGCCATCTGACCGGG 720
 Db 661 ATCTCTGGAGTATATCCCAATGATGTGTGAGAGATGCATTAAGCCATCTGACCGGG 720
 Qy 721 GGCCCTTGGTAAAGTCCAGTGGAAAGTAGCCTCTCTAACTTCCTTCTTGGTAAACAGAGAC 780
 Db 721 GGCCCTTGGTAAAGTCCAGTGGAAAGTAGCCTCTCTAACTTCCTTCTTGGTAAACAGAGAC 780
 Qy 781 TATTAGGACATATTCATCTCAATAGTAAACAACTTAAGGACACTGCTGTCAGAAATAGGCAA 840
 Db 781 TATTAGGACATATTCATCTCAATAGTAAACAACTTAAGGACACTGCTGTCAGAAATAGGCAA 840
 Qy 841 GTAGTCTCGATGTCCTGCTGAAATAGATGTAAGAGTAACTTATCGTCAATCATCTT 900
 Db 841 GTAGTCTCGATGTCCTGCTGAAATAGATGTAAGAGTAACTTATCGTCAATCATCTT 900
 Qy 901 CAAATTTTCAGGATCGGCGACCCAAAGCTTGATTTGTCATCTGCAACATATACTTGT 960
 Db 901 CAAATTTTCAGGATCGGCGACCCAAAGCTTGATTTGTCATCTGCAACATATACTTGT 960
 Qy 961 TCGTGTGTGCTTTGTATAGTGTGATGCAAAAAATTTAGTATTTTGTCCCCAGCT 1020
 Db 961 TCGTGTGTGCTTTGTATAGTGTGATGCAAAAAATTTAGTATTTTGTCCCCAGCT 1020
 Qy 1021 GAGCCATTTAATTCGAGGACATCGGCCCAAAATTTATCTTGTGTCCTCAATACCTGTCG 1080
 Db 1021 GAGCCATTTAATTCGAGGACATCGGCCCAAAATTTATCTTGTGTCCTCAATACCTGTCG 1080
 Qy 1081 AATTTTCTCTTTAGTAAAGTAACCAATGATGCGCCATGTTGCAAAAAAGGCTGATAGT 1140
 Db 1081 AATTTTCTCTTTAGTAAAGTAACCAATGATGCGCCATGTTGCAAAAAAGGCTGATAGT 1140
 Qy 1141 ATGATCTTTGGAGTTGTTGGTGCATTTGCAAGCTGACGATGGCCCTCAGGCAAAATTA 1200
 Db 1141 ATGATCTTTGGAGTTGTTGGTGCATTTGCAAGCTGACGATGGCCCTCAGGCAAAATTA 1200
 Qy 1201 GSGCGCAACCCAGATGTCAAAGAGACAAAGAGACAGCCCAACCTTTCTTAAACAGAT 1260
 Db 1201 GSGCGCAACCCAGATGTCAAAGAGACAAAGAGACAGCCCAACCTTTCTTAAACAGAT 1260
 Qy 1261 CATCACAGATCGGCGAGTAAAGGTAAATTAATTTAAACAAATAGCTCTTGACCGGAA 1320
 Db 1261 CATCACAGATCGGCGAGTAAAGGTAAATTAATTTAAACAAATAGCTCTTGACCGGAA 1320
 Qy 1321 CTCCGTATTTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCAA 1380
 Db 1321 CTCCGTATTTCTCACTTCCATAAACCCCTGATTAATTTGGTGGAAAGCGACAGCAA 1380
 Qy 1381 CCCACAAAAGTCCAGATGTCATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTT 1440
 Db 1381 CCCACAAAAGTCCAGATGTCATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTT 1440
 Qy 1441 TTCTCTCTATATTTCTGGTTCACCGTTGGAGTCAATGGCATGCGTGAAGATGTACATAT 1500
 Db 1441 TTCTCTCTATATTTCTGGTTCACCGTTGGAGTCAATGGCATGCGTGAAGATGTACATAT 1500
 Qy 1501 TGGTGTAGGTTCCAAATATTTTGGGAGGTTGGTGAACCGCAAGTTCTCTATATATCGA 1560
 Db 1501 TGGTGTAGGTTCCAAATATTTTGGGAGGTTGGTGAACCGCAAGTTCTCTATATATCGA 1560
 Qy 1561 ACCTTCCACCAATACCTCTCAATCCCACTTTATCCGTTTATTTCTCTGCTT 1620
 Db 1561 ACCTTCCACCAATACCTCTCAATCCCACTTTATCCGTTTATTTCTCTGCTT 1620
 Qy 1621 TCCCTTCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTGCTGACC 1680
 Db 1621 TCCCTTCTCGAGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTGCTGACC 1680
 Qy 1681 GGCCTCGAGACCCAGATGACCCGACCCCAAGTCTCGGACGACGAGGCACTCTTCGCG 1740
 Db 1681 GGCCTCGAGACCCAGATGACCCGACCCCAAGTCTCGGACGACGAGGCACTCTTCGCG 1740

Qy 1741 ATGAGCTGGCGAGCCCTCCGTGCTCCCATGTGCTTAAAGCGCGCCATCGAGATCGAC 1800
 Db 1741 ATGAGCTGGCGAGCCCTCCGTGCTCCCATGTGCTTAAAGCGCGCCATCGAGATCGAC 1800
 Qy 1801 CTCTCTCGAGATCATGCGCCAAAGGACGCGCGCGGCTTCTCTCCACCGGGGAAATCGCG 1860
 Db 1801 CTCTCTCGAGATCATGCGCCAAAGGACGCGCGCGGCTTCTCTCCACCGGGGAAATCGCG 1860
 Qy 1861 GCAAGCTCCGACCCAGAAACCCCGAGGACCCCGTCACTGCTCGACCGGATCTTCGGGCTG 1920
 Db 1861 GCAAGCTCCGACCCAGAAACCCCGAGGACCCCGTCACTGCTCGACCGGATCTTCGGGCTG 1920
 Qy 1921 CTGGCCAGCTTACTCCGTGCTCAGTGCACCTCCGCGACCTCCCGATGCGCAAGGTTCGAG 1980
 Db 1921 CTGGCCAGCTTACTCCGTGCTCAGTGCACCTCCGCGACCTCCCGATGCGCAAGGTTCGAG 1980
 Qy 1981 CGGCTCTACCGCTTAGCGCGGTGTCAGATTTCTTGGTCAAGAACGAGAGACGGGTCTCC 2040
 Db 1981 CGGCTCTACCGCTTAGCGCGGTGTCAGATTTCTTGGTCAAGAACGAGAGACGGGTCTCC 2040
 Qy 2041 ATCCGCCACTCAACTTTGATGAACCCAGGACAAATCTCTATGGAAGCTGGTATTACCTG 2100
 Db 2041 ATCCGCCACTCAACTTTGATGAACCCAGGACAAATCTCTATGGAAGCTGGTATTACCTG 2100
 Qy 2101 AAAGATCGGTCTTGAAGCGGGAATCCCATTCACAAAGCGGTACGGGATGACCGGTTTC 2160
 Db 2101 AAAGATCGGTCTTGAAGCGGGAATCCCATTCACAAAGCGGTACGGGATGACCGGTTTC 2160
 Qy 2161 GAGTATCATGGCACCGACCCGCGATTCAACAAGATCTTTAAACCGGGGAATGTCTGATCAC 2220
 Db 2161 GAGTATCATGGCACCGACCCGCGATTCAACAAGATCTTTAAACCGGGGAATGTCTGATCAC 2220
 Qy 2221 TCCACCATTAATGAGAGAGATCTCGAAACATACAAAGGCTTCGAGGCGCTCGAGACC 2280
 Db 2221 TCCACCATTAATGAGAGAGATCTCGAAACATACAAAGGCTTCGAGGCGCTCGAGACC 2280
 Qy 2281 GTGGTTCGATGTGCGAGGCGGCACTGGGGCGGTGCTCAGCATGATCGTTGCCAAATACCCA 2340
 Db 2281 GTGGTTCGATGTGCGAGGCGGCACTGGGGCGGTGCTCAGCATGATCGTTGCCAAATACCCA 2340
 Qy 2341 TCAATGAAAGGATCAACTTCGACCGCCCAAGGATGGAAGACGCGCCACCCCTTCCTG 2400
 Db 2341 TCAATGAAAGGATCAACTTCGACCGCCCAAGGATGGAAGACGCGCCACCCCTTCCTG 2400
 Qy 2401 GTGTCAAGCACGTCGAGGCGGACATGTTGTCAGGCTTCCAAAGGAGATGCCATTTTCA 2460
 Db 2401 GTGTCAAGCACGTCGAGGCGGACATGTTGTCAGGCTTCCAAAGGAGATGCCATTTTCA 2460
 Qy 2461 TGAAGTGGATATGCCATGATGAGTGAAGGATGATCGTTGCGAGTGCCTTCCCTGTGTACC 2520
 Db 2461 TGAAGTGGATATGCCATGATGAGTGAAGGATGATCGTTGCGAGTGCCTTCCCTGTGTACC 2520
 Qy 2521 ACCATCGCTTCCCAACAAATGAAAGGTGATCGTTGCGAGTGCCTTCCCTGTGTACC 2580
 Db 2521 ACCATCGCTTCCCAACAAATGAAAGGTGATCGTTGCGAGTGCCTTCCCTGTGTACC 2580
 Qy 2581 CAGACACGAGCTTAGCGACCAAGATATGATCCATCGACTGATCATGTTGGGCCACA 2640
 Db 2581 CAGACACGAGCTTAGCGACCAAGATATGATCCATCGACTGATCATGTTGGGCCACA 2640
 Qy 2641 ACCGAGCGGAAAGAGAGACACAGAGGATTCGAGGCAATGGCCAAAGGGGCGGAT 2700
 Db 2641 ACCGAGCGGAAAGAGAGACACAGAGGATTCGAGGCAATGGCCAAAGGGGCGGAT 2700
 Qy 2701 TTCAAGGCTTCCAAAGTCAATGCTGGCTTTCGGCACTCACGTCAAGGATTCCTCAAGA 2760
 Db 2701 TTCAAGGCTTCCAAAGTCAATGCTGGCTTTCGGCACTCACGTCAAGGATTCCTCAAGA 2760
 Qy 2761 CCGCTTCAATCTGCTCTCTGTTGATGTTCAATGTTCTTGGATTTGAAAGGTCGTGAAG 2820
 Db 2761 CCGCTTCAATCTGCTCTCTGTTGATGTTCAATGTTCTTGGATTTGAAAGGTCGTGAAG 2820

Qy	2821	GAGCCCTTTTCTC	CACAGTTGGCTTC	GGCATACCAAGTTC	TCTCATATAAAGGAACAATA	2880
Db	2821	GAGCCCTTTTCTC	CACAGTTGGCTTC	GGCATACCAAGTTC	TCTCATATAAAGGAACAATA	2880
Qy	2881	AGAAGCACCTGTAT	GTATGATGGCGCAAGT	TACAAGATTGTTGTTTATGTCATAAA	2940	
Db	2881	AGAAGCACCTGTAT	GTATGATGGCGCAAGT	TACAAGATTGTTGTTTATGTCATAAA	2940	
Qy	2941	AGTTTTCAGTCTTCT	GCATCTGATTTTC	CACAGATGTGTACGAAACGGCGTATATCGAT	3000	
Db	2941	AGTTTTCAGTCTTCT	GCATCTGATTTTC	CACAGATGTGTACGAAACGGCGTATATCGAT	3000	
Qy	3001	GTGCCTGAATGATG	GGAATTGTGATATCT	TGTCCTTTCTTTTTTCAGTAAATCACCTTCGAAACA	3060	
Db	3001	GTGCCTGAATGATG	GGAATTGTGATATCT	TGTCCTTTCTTTTTTCAGTAAATCACCTTCGAAACA	3060	
Qy	3061	AAAAAAAAAA	3070			
Db	3061	AAAAAAAAAA	3070			

RESULT 3

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US-10-927-641-113
; Sequence 113, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleston, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-113

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	Query Match	100.0%;	Score 3070;	DB 10;	Length 3070;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 3070;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AGCACCATCAGCAAAAATAGATGGGATAGAGTGGGACACACCTGTTTCAGTTTGATTC	60		
Db	1	AGCACCATCAGCAAAAATAGATGGGATAGAGTGGGACACACCTGTTTCAGTTTGATTC	60		
Qy	61	CTTGAGATGACCTACAGTGTAGCTTGATGAATAAGATGGGATTAATAGATTCACACAGG	120		
Db	61	CTTGAGATGACCTACAGTGTAGCTTGATGAATAAGATGGGATTAATAGATTCACACAGG	120		
Qy	121	GATAAAAAGGTAGGAGATAGGGGATCTCCCGTCTGATCGCTCGGGTAGGTTGAAAATA	180		

Db	121	GATAAAGATGAGGAGATAGGGGATCTCCCGTCTGATGCTCGGTGAGTGGTGAATAAATA	180
Qy	181	AGCCAAAGTTCCCGTGTGAATTTGACAGCAAAAGACACCGTCTGTTATGCAATTCGCATGAT	240
Db	181	AGCCAAAGTTCCCGTGTGAATTTGACAGCAAAAGACACCGTCTGTTATGCAATTCGCATGAT	240
Qy	241	CCATTGTACCCATGTAGGGTGAATCCTAGAGTGAGGAGATAGTCTCTTTTAGAAGTCCCA	300
Db	241	CCATTGTACCCATGTAGGGTGAATCCTAGAGTGAGGAGATAGTCTCTTTTAGAAGTCCCA	300
Qy	301	TTCCACCCTATCATAGGCTTTCTGCAATATCCATTTTAAAGAAACAGCCGGAAATTCACGTCT	360
Db	301	TTCCACCCTATCATAGGCTTTCTGCAATATCCATTTTAAAGAAACAGCCGGAAATTCACGTCT	360
Qy	361	ACATTTTCTGCATTTAAATTTGATGTAGAACCTCTTAGACTATTTAAAAATAATGCTCTGAAT	420
Db	361	ACATTTTCTGCATTTAAATTTGATGTAGAACCTCTTAGACTATTTAAAAATAATGCTCTGAAT	420
Qy	421	TTGAGCTCAGTACAAAAGCGCTTTGCTCCTCGAAAAAATGCTACAGGACAGGTAGGGCTT	480
Db	421	TTGAGCTCAGTACAAAAGCGCTTTGCTCCTCGAAAAAATGCTACAGGACAGGTAGGGCTT	480
Qy	481	AAGCGATTTGGCAATCACCTTTAGAAATGATCTTATATGCGTAAATTAACAAGACTGATGGG	540
Db	481	AAGCGATTTGGCAATCACCTTTAGAAATGATCTTATATGCGTAAATTAACAAGACTGATGGG	540
Qy	541	GCGGTATTTGCTTAAATTTGTTTCCAGGATGTGGTACCTTTGGGTATTTAGGGCTATGATGTTTCG	600
Db	541	GCGGTATTTGCTTAAATTTGTTTCCAGGATGTGGTACCTTTGGGTATTTAGGGCTATGATGTTTCG	600
Qy	601	ATTGAGATTCGGTGGTATGATGACCAAAATTAATAAAGTGTGCACTGATGAGAAATAGTTTC	660
Db	601	ATTGAGATTCGGTGGTATGATGACCAAAATTAATAAAGTGTGCACTGATGAGAAATAGTTTC	660
Qy	661	ATCCTCGAGTATATCCCAATGATCTGGTGAAGAGTCCATTCAGGCCATCTCGACCGGG	720
Db	661	ATCCTCGAGTATATCCCAATGATCTGGTGAAGAGTCCATTCAGGCCATCTCGACCGGG	720
Qy	721	GGCCTTTGGTAAAGTCCAGTTGGAAAGTAGCCCTCTCTAACTTCTCTTGGTAAACAGGAGC	780
Db	721	GGCCTTTGGTAAAGTCCAGTTGGAAAGTAGCCCTCTCTAACTTCTCTTGGTAAACAGGAGC	780
Qy	781	TATTAGGACATATTCATCTCATTTAGTAAACAACTTAAGGACACTGGTTTCAAGATAGGCCAA	840
Db	781	TATTAGGACATATTCATCTCATTTAGTAAACAACTTAAGGACACTGGTTTCAAGATAGGCCAA	840
Qy	841	GTAGTCTCGATGTCCCACTGTCTGAAATAGATGTGAAGTAACCTATCGTCATCATCTT	900
Db	841	GTAGTCTCGATGTCCCACTGTCTGAAATAGATGTGAAGTAACCTATCGTCATCATCTT	900
Qy	901	CAAAATTTCAGGATCGCGACCCCAAGCTTGATTTGTCACTCTCGAAACATACTAATCTTGTT	960
Db	901	CAAAATTTCAGGATCGCGACCCCAAGCTTGATTTGTCACTCTCGAAACATACTAATCTTGTT	960
Qy	961	TCGTTGTGTCCTTTGTATAGTTGTCATGAAAAAATTTTAGTATTTTGTCTCCCCAGCT	1020
Db	961	TCGTTGTGTCCTTTGTATAGTTGTCATGAAAAAATTTTAGTATTTTGTCTCCCCAGCT	1020
Qy	1021	GAGCCATTTAAATTCGAGAGCAGATCGCCCAAAATTTATCTTCTGTGCGCAATACCTGTCG	1080
Db	1021	GAGCCATTTAAATTCGAGAGCAGATCGCCCAAAATTTATCTTCTGTGCGCAATACCTGTCG	1080
Qy	1081	AATTTTCTCTTTTAGGTAAAGTAAACCAATGATGCCATGTTTGACAAAAAGGCTGATTAGT	1140
Db	1081	AATTTTCTCTTTTAGGTAAAGTAAACCAATGATGCCATGTTTGACAAAAAGGCTGATTAGT	1140
Qy	1141	ATGATCTTGAGTGTGTTGGTGCAAAATTTGCAAGCTGACATGCGCCCTCAGGGAAATTA	1200
Db	1141	ATGATCTTGAGTGTGTTGGTGCAAAATTTGCAAGCTGACATGCGCCCTCAGGGAAATTA	1200
Qy	1201	GGCGCCAAACCGATTTGCAAGAGACAAAGAGCAGACCCACCTTCTTAAACAAGAT	1260
Db	1201	GGCGCCAAACCGATTTGCAAGAGACAAAGAGCAGACCCACCTTCTTAAACAAGAT	1260

QY	1261	CATCACCAGATCGGCCAGTAAGGGTAATTAATTTAA	1320	QY	2341	TCATGAAGAGGATCACTTCGACCGCCCAACG	2400
Db	1261	CATCACCAGATCGGCCAGTAAGGGTAATTAATTTAA	1320	Db	2341	TCATGAAGAGGATCACTTCGACCGCCCAACG	2400
QY	1321	CTCCGATTTCTCTCACTTCCATTAACCCCTGATTA	1380	QY	2401	GTGTCAAGCAGCTCGGAGCGGACATGTTGTC	2460
Db	1321	CTCCGATTTCTCTCACTTCCATTAACCCCTGATTA	1380	Db	2401	GTGTCAAGCAGCTCGGAGCGGACATGTTGTC	2460
QY	1381	CCACAAAAGGTGAGATGTCATCCACGAGAGAGAG	1440	QY	2461	TGAAGTGGATATGCCATGATCGAGTGCAGCAT	2520
Db	1381	CCACAAAAGGTGAGATGTCATCCACGAGAGAGAG	1440	Db	2461	TGAAGTGGATATGCCATGATCGAGTGCAGCAT	2520
QY	1441	TTCTCTATATTTCTGGTTACCGGTTGAGTCAATG	1500	QY	2521	ACGATCGGCTTCCCAACAATGGAAGGTGATCG	2580
Db	1441	TTCTCTATATTTCTGGTTACCGGTTGAGTCAATG	1500	Db	2521	ACGATCGGCTTCCCAACAATGGAAGGTGATCG	2580
QY	1501	TGGTGTAGGTCCTCAATATTTTGGGAGGGTGGT	1560	QY	2581	CAGACACGAGCCTAGCGACCAAGAATGTGATC	2640
Db	1501	TGGTGTAGGTCCTCAATATTTTGGGAGGGTGGT	1560	Db	2581	CAGACACGAGCCTAGCGACCAAGAATGTGATC	2640
QY	1561	ACCTCCACCACTCACTCAATCCCAATTTATCCG	1620	QY	2641	ACCCAGCGGGAAAGAGAGGACACAGAAGGTT	2700
Db	1561	ACCTCCACCACTCACTCAATCCCAATTTATCCG	1620	Db	2641	ACCCAGCGGGAAAGAGAGGACACAGAAGGTT	2700
QY	1621	TCCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAG	1680	QY	2701	TTCAAGGCTTCCCAAGTCAATGCTGCGCTTT	2760
Db	1621	TCCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAG	1680	Db	2701	TTCAAGGCTTCCCAAGTCAATGCTGCGCTTT	2760
QY	1681	GGCTCCGAGACCCAGATGACCCCAAGTCTCGGA	1740	QY	2761	CCGCTTGATCTGCTCCTCTGCTGCTGCTGCT	2820
Db	1681	GGCTCCGAGACCCAGATGACCCCAAGTCTCGGA	1740	Db	2761	CCGCTTGATCTGCTCCTCTGCTGCTGCTGCT	2820
QY	1741	ATGAGCTGGGAGGCTCGTCTCCCAATGCTTAA	1800	QY	2821	GAGCCCTTTCTCAGCTTGGCTTCGGCATACCA	2880
Db	1741	ATGAGCTGGGAGGCTCGTCTCCCAATGCTTAA	1800	Db	2821	GAGCCCTTTCTCAGCTTGGCTTCGGCATACCA	2880
QY	1801	CTCTCTGAGATCATGGCCAGGACGGGCGGGCG	1860	QY	2881	AGAAGCGACTGATGATGGCGCAAGTGGAA	2940
Db	1801	CTCTCTGAGATCATGGCCAGGACGGGCGGGCG	1860	Db	2881	AGAAGCGACTGATGATGGCGCAAGTGGAA	2940
QY	1861	GCACAGCTCCCGACCCAGAACCCCGAGCACCC	1920	QY	2941	AGTTTGTAGTCTTCTGCTGCTGCTGCTGCT	3000
Db	1861	GCACAGCTCCCGACCCAGAACCCCGAGCACCC	1920	Db	2941	AGTTTGTAGTCTTCTGCTGCTGCTGCTGCT	3000
QY	1921	CTGGCCAGTCTCTGCTGCTGCTGCTGCTGCT	1980	QY	3001	GTGCTCTGAATGATGAAATTTGATGATGAT	3060
Db	1921	CTGGCCAGTCTCTGCTGCTGCTGCTGCTGCT	1980	Db	3001	GTGCTCTGAATGATGAAATTTGATGATGAT	3060
QY	1981	CGGCTCTACGGTTAGCGCGGTGTGCAAGTCTT	2040	QY	3061	AAAAAATAA 3070	
Db	1981	CGGCTCTACGGTTAGCGCGGTGTGCAAGTCTT	2040	Db	3061	AAAAAATAA 3070	
QY	2041	ATCGCCGCACTCACTGATGAACAGGACAAATCC	2100	RESULT 4			
Db	2041	ATCGCCGCACTCACTGATGAACAGGACAAATCC	2100	US-10-137-036-60			
QY	2101	AAAGATGCGGTCTTGAAGGCGGAATCCCATTT	2160	; Sequence 60, Application US/10137036			
Db	2101	AAAGATGCGGTCTTGAAGGCGGAATCCCATTT	2160	; Publication No. US20030101478A1			
QY	2161	GAGTATCATGGACCGACCGGATTTAAACGGGA	2220	; GENERAL INFORMATION:			
Db	2161	GAGTATCATGGACCGACCGGATTTAAACGGGA	2220	; APPLICANT: Perera, Ranjan			
QY	2221	TCCACCACTTACTATGAAGAGATGACTGGAACA	2280	; APPLICANT: Rice, Stephen			
Db	2221	TCCACCACTTACTATGAAGAGATGACTGGAACA	2280	; APPLICANT: Bagleton, Clare			
QY	2281	GTGGTCGATGTCGAGGCGGACATGGGGCGGCT	2340	; APPLICANT: Lasham, Annette			
Db	2281	GTGGTCGATGTCGAGGCGGACATGGGGCGGCT	2340	; APPLICANT: Wood, Marion			
				; APPLICANT: Visser, Elizabeth			
				; TITLE OF INVENTION: Compositions and Methods for the			
				; TITLE OF INVENTION: Modification of Gene Expression			
				; FILE REFERENCE: 11000.1036c4			
				; CURRENT APPLICATION NUMBER: US/10137, 036			
				; CURRENT FILING DATE: 2002-04-30			
				; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115			
				; PRIOR FILING DATE: 2001-06-20			
				; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724, 624			
				; PRIOR FILING DATE: 2000-11-28			

;; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
;; PRIOR FILING DATE: 2000-06-20
;; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
;; PRIOR FILING DATE: 1999-07-30
;; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
;; PRIOR FILING DATE: 1999-03-25
;; NUMBER OF SEQ ID NOS: 143
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 60
;; LENGTH: 2096
;; TYPE: DNA
;; ORGANISM: Eucalyptus grandis
US-10-137-036-60

Query Match 65.8%; Score 2020.4; DB 6; Length 2096;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;

QY 1019 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTTATTTCTTCTGTCGCCATAACTGT 1078
DB 41 CTGAGCCATTAAATTCGAGAGCACATCGCCCAAAATTTATTTCTTCTGTCGCCATAACTGT 100

QY 1079 CGAATTTTCTCTTTAGGTAAAGTAAACCAATGATCGGCATGTTGACAAAAGGCTGATTA 1138
DB 101 CGAATTTTCTCTTTAGGTAAAGTAAACCAATGATCGCATCATGTTGACAAAAGGCTGATTA 160

QY 1139 GTATGATCTTGGAGTTGTTGTCGCAATTTGCAAGCTGACGATGGCCCTCAGGGAATTT 1198
DB 161 GTATGATCTTGGAGTTGTTGTCGCAATTTGCAAGCTGACGATGGCCCTCAGGGAATTT 220

QY 1199 AAGCGCCCAACCCAGATTGCAAGAGCACAAAGAGCAGCCCAACCTTTCTTAAACAAG 1258
DB 221 AAGCGCCCAACCCAGATTGCAAGAGCACAAAGAGCAGCATCCAACTTTCTTAAACAAG 280

QY 1259 ATCATACACAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGTCTTTGTACCGGG 1318
DB 281 ATCATACACAGATCGGCCAGTAAGGGTAATTAATTTAAACAATAGTCTTTGTACCGGG 340

QY 1319 AACTCCGTAATTTCTCACTTCCATAAACCCCTGATTAATTTGTTGGGAAAGCAGACC 1378
DB 341 AACTCCGTAATTTCTCACTTCCATAAACCCCTGATTAATTTGTTGGGAAAGCAGACC 400

QY 1379 AACCCCAAAAGTGCAGATGTCATCCAC----GAGAGAGAGAGAGAGAGAGAGAG 1434
DB 401 AACCCCAAAAGTGCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460

QY 1435 AGAGTTTCTCTCTATATTTCTGTTTCAACCGTTGGAGTCAATGGCATGCGTGCAGAAATGT 1494
DB 461 AGAGTTTCTCTCTATATTTCTGTTTCAACCGTTGGAGTCAATGGCATGCGTGCAGAAATGT 520

QY 1495 ACATATTTGGTGAAGGTCCTAATTTTTCGGGAGGGTTGGTGAACCCGAAAGTTCTTATA 1554
DB 521 ACATATTTGGTGAAGGTCCTAATTTTTCGGGAGGGTTGGTGAACCCGAAAGTTCTTATA 580

QY 1555 TATCGAACCCTCCACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTTCT 1614
DB 581 TATCGAACCCTCCACCATACCTCACTTCAATCCCAACCAATTTATCCGTTTATTTCTTCT 640

QY 1615 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT 1674
DB 641 CTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGGT 700

QY 1675 TCGACCGGCTCCGAGACCCAGATGACCCGACCCCAAGCTCTCGGACGAGAGGCGAACTTC 1734
DB 701 TCGACCGGATCCGAGACCCAGATGACCCGACCCCAAGCTCTCGGACGAGAGGCGAACTTC 760

QY 1735 TTGCGCATGACGTGGGAGGCGCTCCGTGCTCCCATGTTCTTAAAGGCGCGCATCGAG 1794
DB 761 TTGCGCATGACGTGGGAGGCGCTCCGTGCTCCCATGTTCTTAAAGGCGCGCATCGAG 820

QY 1795 ATCGACCTCTCTCGAGATCATGGCCCAAGGACGGGCGCGGCTTCTCTCCACGGGGAA 1854

DB 821 CTGACCTCTCTCGAGATCATGGCCCAAGGCGGGCGGTCCTCTCTCCCGGGGAA 880
QY 1855 ATGCGGCGACAGTCTCCGAGCCCGAGAACCCCGAGGACCCCGTCATGCTCGACCGATCTTC 1914
DB 881 GTGCGGCGGCGAGTCCCGAGCCCGAGAACCCCGAGGACCCCGTCATGCTCGACCGGATCTTC 940
QY 1915 CGGCTGTGCGCCAGCTACTCTCGGTCTCACGCTGACCCCTCGCGACCTCCCGATGCGCAAG 1974
DB 941 CGGCTGTGCGCCAGCTACTCTCGGTCTCACGCTGACCCCTCGCGACCTCCCGATGCGCAAG 1000
QY 1975 GTGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGTGTCAAGAACGAGGACGG 2034
DB 1001 GTGAGCGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGTGTCAAGAACGAGGACGG 1060
QY 2035 GTCTTCATCGCGCACCTCAACTTGTGAACGAGGACCAAAATCTCTCATGGAAGCTGTAT 2094
DB 1061 GTCTTCATCGCGCACCTCAACTTGTGAACGAGGACCAAAATCTCTCATGGAAGCTGTAT 1120
QY 2095 TACTGAAAGATCGGTCCTTGAAGCGGAATCCCATTTCAACGAGGCTACGGGATGACC 2154
DB 1121 TACTGAAAGATCGGTCCTTGAAGCGGAATCCCATTTCAACGAGGCTACGGGATGACC 1180
QY 2155 GCGTTGAGTATCATGCGCACCGACCCCGCATTTCAACAAGATCTTTAAACCGGGAAATGTCT 2214
DB 1181 GCGTTGAGTATCATGCGCACCGACCCCGCATTTCAACAAGATCTTTAAACCGGGAAATGTCT 1240
QY 2215 GATCACTCCACCATTAATTAAGAGAGATGCTGGNAACATACAAGGCTTCGAGGGCTC 2274
DB 1241 GATCACTCCACCATTAATTAAGAGAGATGCTGGNAACATACAAGGCTTCGAGGGCTC 1300
QY 2275 GAGACGCTGTGCTGATGCGGAGCGGCACCTGGGCGCTGCTCAGCATGATCTTGGCCAAA 2334
DB 1301 GAGACGCTGTGCTGATGCGGAGCGGCACCTGGGCGCTGCTCAGCATGATCTTGGCCAAA 1360
QY 2335 TACCCCATCAATGAAGGATCAACTTGCACCGCCCAACGGAATGAAGAGCCGCCACCCC 2394
DB 1361 TACCCCATCAATGAAGGATCAACTTGCACCGCCCAACGGAATGAAGAGCCGCCACCCC 1420
QY 2395 TTCTGTGTCAAGCAGCTCGGAGGCGACATGTTGTCAGCGGTCGAGGATGATGCTTCC 2454
DB 1421 TTCTGTGTCAAGCAGCTCGGAGGCGACATGTTGTCAGCGGTCGAGGATGATGCTTCC 1480
QY 2455 TTTTTCATGAAGTGCATGCTGAGTGCAGACCATTTGCGCGAAGTTCTCTCAAGA 2514
DB 1481 TTTTTCATGAAGTGCATGCTGAGTGCAGACCATTTGCGCGAAGTTCTCTCAAGA 1540
QY 2515 ACTGCTACGATGCGCTTCCCAACAATGGAAGGTGATCGTTGCGAGAGTGCCTACTCCCTG 2574
DB 1541 ACTGCTACGATGCGCTTCCCAACAATGGAAGGTGATCGTTGCGAGAGTGCCTACTCCCTG 1600
QY 2575 TGTACCCAGACAGGCGCTAGCCACCAAGATGATGATCCCATCATGATGATGTTGG 2634
DB 1601 TGTACCCAGACAGGCGCTAGCCACCAAGATGATGATCCCATCATGATGATGTTGG 1660
QY 2635 CCCACAACCCAGCGGGAAGAGAGAGACACAGAGGAGTTTCGAGGCAATTCGCCAAAGGG 2694
DB 1661 CCCACAACCCAGCGGGAAGAGAGAGACACAGAGGAGTTTCGAGGCAATTCGCCAAAGGG 1720
QY 2695 CCGGATTTTCAGGCGCTTCCCAAGTCAATGTCGCGCTTTTCGGCACTCACGTCATGAGTTC 2754
DB 1721 CCGGATTTTCAGGCGCTTCCCAAGTCAATGTCGCGCTTTTCGGCACTCACGTCATGAGTTC 1780
QY 2755 TGAAGACCGCTTCAATGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2814
DB 1781 TGAAGACCGCTTCAATGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1840
QY 2815 GTCAAGGAGCCCTTTCTCACAGTTGCGCATACCAAGTTCTTCTCATAAAGGAA 2874
DB 1841 GTCAAGGAGCCCTTTCTCACAGTTGCGCATACCAAGTTCTTCTCATAAAGGAA 1900
QY 2875 ACATAAGAGGAGGAGTGTATGATGGGCGCAAGTGAAGTTCTTCTCATAAAGGAA 2934

Db 1901 ACATTAAGAAGCGACTGTATGATGGCGCAAGTGAAGTTTACAAGATTGTTGTTTATGT 1960

Qy 2935 CTATATAAGTTTGAAGTCTTCTGCATCTGATTTTACAGATGTGTAAACGAAACGGCGTAT 2994

Db 1961 CTATATAAGTTTGAAGTCTTCTGCATCTGATTTTACAGATGTGTAAACGAAACGGCGTAT 2020

Qy 2995 ATCGATGTGCTCAATGATGGAATTTGATATTTCTGCTCTTTTTCAGTAAATCACTT 3054

Db 2021 ATCGATGTGCTCAATGATGGAATTTGATATTTCTGCTCTTTTTCAGTAAATCACTT 2080

Qy 3055 CGAACAAAAA 3070

Db 2081 CGAACAAAAA 2096

RESULT 5

US-10-702-319A-60

; Sequence 60, Application US/10702319A

; Publication No. US20050026162A1

; GENERAL INFORMATION:

; APPLICANT: Perera, Ranjan

; APPLICANT: Rice, Stephen

; APPLICANT: Eagleton, Clare

; TITLE OF INVENTION: Compositions and Methods for the

; TITLE OF INVENTION: Modification of Gene Expression

; FILE REFERENCE: 11000.1036c5

; CURRENT APPLICATION NUMBER: US/10702.319A

; CURRENT FILING DATE: 2003-11-06

; PRIOR APPLICATION NUMBER: U.S. No. 10/291,447

; PRIOR FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: U.S. No. 60/425,087

; PRIOR FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: U.S. No. 10/137,036

; PRIOR FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401

; PRIOR FILING DATE: 2000-06-20

; PRIOR APPLICATION NUMBER: PCT/NZ00/00018

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599

; PRIOR FILING DATE: 1999-03-25

; NUMBER OF SEQ ID NOS: 129

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 60

; LENGTH: 2096

; TYPE: DNA

; ORGANISM: Eucalyptus grandis

US-10-702-319A-60

Query Match 65.8%; Score 2020.4; DB 9; Length 2096;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 2041; Conservative 0; Mismatches 11; Indels 4; Gaps 1;

Qy 1019 CTGAGCCATTAAATTCGAGACACATCGCCAAAATTATTTCTTCTGCTGCAATACTGT 1078

Db 41 CTGAGCCATTAAATTCGAGACACATCGCCAAAATTATTTCTTCTGCTGCAATACTGT 100

Qy 1079 CGAATTTCTTTTAGGTAACTAACCAATGATGCCCATGTTGACAAAAGGCTGATTA 1138

Db 101 CGAATTTCTTTTAGGTAACTAACCAATGATGATCATGTTGACAAAAGGCTGATTA 160

Qy 1139 GTATGATCTTGGAGTTTGGTGCAAAATTTGCAAGTGAAGTGCCTCTCAGGAAATTT 1198

Db 161 GTATGATCTTGGAGTTTGGTGCAAAATTTGCAAGTGAAGTGCCTCTCAGGAAATTT 220

Qy 1199 AAGCGCCAAACCCAGATTTGCAAGACACAAAGACACCAACCTTTCCCTTAAACAAG 1258

Db 221 AAGCGCCAAACCCAGATTTGCAAGACACAAAGACACCAACCTTTCCCTTAAACAAG 280

Qy 1259 ATCATCACCAGATCGGCCAGTAAGGGTAAATTAATTTAAACAATAGTCTTTGTACCGGG 1318

Db 281 ATCATCACCAGATCGGCCAGTAAGGGTAAATTAATTTAAACAATAGTCTTTGTACCGGG 340

Qy 1319 AACTCCGATTTTCTCTCATCTCCATAAACCCCTGATTAATTTGGTGGGAAGCGAGACC 1378

Db 341 AACTCCGATTTTCTCTCATCTCCATAAACCCCTGATTAATTTGGTGGGAAGCGAGACC 400

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Db 401 AACCCAAAAGGTTCAGATCTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460

Qy 1435 AGAGTTTCTCTCTATATTTCTGGTTTACCGTTGGAGTCAATGGCATGCTGAGCATGT 1494

Db 461 AGAGTTTCTCTCTATATTTCTGGTTTACCGTTGGAGTCAATGGCATGCTGAGCATGT 520

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Qy 1555 TATCGAACCTCCACACCATACCTCACTTCAATCCCAACCATTTATCCGTTTATTTTCT 1614

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Qy 1615 CTGCTTTCTTTTGTCTCGAGTCTCGGAAAGAGAGAGAGAGAGAGAGAGAGAGATGGT 1674

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Db 701 TCGACCGGATCGAGACCCAGATGACCCCAAGTCTCGGACGAGAGAGAGAGAGAGAGAG 760

Qy 1735 TTGCGCATGAGCTGGCGAGCGCTTCCGTGCTCCCATGCTTAAAGCGCCATCGAG 1794

Db 761 TTGCGCATGAGCTGGCGAGCGCTTCCGTGCTCCCATGCTTAAAGCGCCATCGAG 820

Qy 1795 ATCGACCTCTCTGAGATCATGGCCHAAGACGGCGGGGGGCTCTCCACGGGGGAA 1854

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Db 1001 GTGAGCGGCTCTACGGCTTAGCGCGGTGTCAGAGTTCTTGGTCAAGAACGAGACGGG 1060

Qy 2035 GTCTCCATCGCGCACTCAACTTTGATGAACGAGGACAAATCTCATGAAAGCTGGTAT 2094

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Qy 2155 GCGTTGAGTATCATGCGACCGACCCGATTCACAGATCTTTAAACCGGGGAAATGTCT 2214

Db 1181 GCGTTGAGTATCATGCGACCGACCCGATTCACAGATCTTTAAACCGGGGAAATGTCT 1240

Qy 2215 GATCAGTCCACCATTAATGAAAGAGATCTGAAACATACAGGGCTTCGAGGGGCTC 2274

Db 1241 GATCAGTCCACCATTAATGAAAGAGATCTGAAACATACAGGGCTTCGAGGGGCTC 1300

Qy 2275 GAGACCGTGTGATGTCGAGGGGCGCTGCTCAGCATGATGCTGTTGCCAA 2334

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Qy 2335 TACCACCAATGAAAGGAGTCAACTTCGACCGCCCAACCGGATGTAAGAGACGCCACCC 2394

1361	Db	TACCCATCAATGAAAGGATCAACTTCGACGCGCCCAACGAGTTGAAGACGCCCCACCCC	1420
2395	Qy	TTCTGTGTCAAGCAGCGTCGGAGCGACATGTTGTCAGCGTTCCAAAGGGAGATGCCA	2454
1421	Db	TTCTGTGTCAAGCAGCGTCGGAGCGACATGTTGTCAGCGTTCCAAAGGGAGATGCCA	1480
2455	Qy	TTTTCATGAGTGGATATGCCATGACTTGGAGTGAAGCAACATTTGCGCGAAGTTTCCTCAAGA	2514
1481	Db	TTTTCATGAGTGGATATGCCATGACTTGGAGTGAAGCAACATTTGCGCGAAGTTTCCTCAAGA	1540
2515	Qy	ACTGCTACGATCGCTTCCCAACAATCGAAAGGTGATCGTTGCAGAGTGGGTACTCCCTG	2574
1541	Db	ACTGCTACGATCGCTTCCCAACAATCGAAAGGTGATCGTTGCAGAGTGGGTACTCCCTG	1600
2575	Qy	TGTACCCACAGACGAGCGCTAGCGACCAAGAAATGTGATCCACATCGACTGCATCATGTTGG	2634
1601	Db	TGTACCCACAGACGAGCGCTAGCGACCAAGAAATGTGATCCACATCGACTGCATCATGTTGG	1660
2635	Qy	CCCAACAACCCAGCGCGGAAAGAGAGGACACAGAAGGAGTTTCGAGGCATTTGGCCAAAGGGG	2694
1661	Db	CCCAACAACCCAGCGCGGAAAGAGAGGACACAGAAGGAGTTTCGAGGCATTTGGCCAAAGGGG	1720
2695	Qy	CCGATTTTCAGGGCTTCCAAAGTCATGCTGCGCTTTCGCGACATCGATCGAGTTCC	2754
1721	Db	CCGATTTTCAGGGCTTCCAAAGTCATGCTGCGCTTTCGCGACATCGATCGAGTTCC	1780
2755	Qy	TGAAGACCGCTTGATCTGCTCCTCTGTGGTGATGTTTCATGGTCTTCGATTTTGAAGGTC	2814
1781	Db	TGAAGACCGCTTGATCTGCTCCTCTGTGGTGATGTTTCATGGTCTTCGATTTTGAAGGTC	1840
2815	Qy	GTGAAGGAGCCCTTTTCTCAAGTTGGCTTCGGCATACCAAGTTCTTCTCATAAAGGAA	2874
1841	Db	GTGAAGGAGCCCTTTTCTCAAGTTGGCTTCGGCATACCAAGTTCTTCTCATAAAGGAA	1900
2875	Qy	ACAATAAGACCGACTGTATGATGCGCGCAAGTGAAGTTTCAAGATTTGTTTATGT	2934
1901	Db	ACAATAAGACCGACTGTATGATGCGCGCAAGTGAAGTTTCAAGATTTGTTTATGT	1960
2935	Qy	CTATAAGTTTTGAGTCTTCTGCAATCTGATTTTCCACAGAATGCTGAACGAACGCGGTAT	2994
1961	Db	CTATAAGTTTTGAGTCTTCTGCAATCTGATTTTCCACAGAATGCTGAACGAACGCGGTAT	2020
2995	Qy	ATGATGTGCTGAAATGATGAAATTTGTGATTTCTGCTCTTTTTTCAGTAAATCACTT	3054
2021	Db	ATGATGTGCTGAAATGATGAAATTTGTGATTTCTGCTCTTTTTTCAGTAAATCACTT	2080
3055	Qy	CGAACAAAAA	3070
2081	Db	CGAACAAAAA	2096

RESULT 6

QY	ACATATTGGTGTAGGGTCCCAATATTTTCGGGAGGGTGGTGAACCCGAAAGTTCCTTATA	1555
QY	ACATATTGGTGTAGGGTCCCAATATTTTCGGGAGGGTGGTGAACCCGAAAGTTCCTTATA	1555
Db	ACATATTGGTGTAGGGTCCCAATATTTTCGGGAGGGTGGTGAACCCGAAAGTTCCTTATA	580
QY	TATCGAACCTCCACCAACCATTCTCAATCCCCACCAATTTATCCGTTTATTTCTCT	1614
Db	TATCGAACCTCCACCAACCATTCTCAATCCCCACCAATTTATCCGTTTATTTCTCT	640
QY	CTGCTTTTCCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGATGGGT	1674
Db	CTGCTTTTCCTTTGCTCGAGTCTCGCGGAAGAGAGAGAGAGAGAGAGAGATGGGT	700
QY	TCGACCGGCTCCGAGACCCAGATGATCCCGACCCCAAGTCTCGGACGACGAGCGCAACCTC	1734
Db	TCGACCGGATCCGAGACCCAGATGATCCCGACCCCAAGTCTCGGACGAGCGCAACCTC	760
QY	TTGCGCATGCAGCTGCGGAGCGCCTCGTGTCCCGATGGTCTCTAAAGCGCGCATCGAG	1794
Db	TTGCGCATGCAGCTGCGGAGCGCCTCGTGTCCCGATGGTCTCTAAAGCGCGCATCGAG	820
QY	ATCGACCTCTCTCGATCATGCGCAAGACGCGGCGCGGTTCCTCTCCACGCGGGGAA	1854

1901 ACATTAAGACGACTGTATGATGCGCAAGTGAAGTATCAAGATTGTTGTTTATGT 1960
2935 CTATAAGTTTGAAGTCTTCTGCATCTGATTTACAGAACTGTAAAGAAACGGGTAT 2994
1961 CTATAAGTTTGAAGTCTTCTGCATCTGATTTACAGAACTGTAAAGAAACGGGTAT 2020
2995 ATGAGTGTGCTGAAATGATGAAATTTGATATTTCTGTTCTTTTCAAGTAAATCATT 3054
2021 ATGAGTGTGCTGAAATGATGAAATTTGATATTTCTGTTCTTTTCAAGTAAATCATT 2080
3055 CGAACAATAAAAAA 3070
2081 CGAACAATAAAAAA 2096
RESULT 7
US-10-174-693-107
; Sequence 107, Application US/10174693
; Publication No. US2003013173A1
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; TITLE OF INVENTION: Materials and Methods for the
; FILE OF INVENTION: Modification of Plant Lignin Content
; FILE OF INVENTION: 11000.1003cs
; CURRENT APPLICATION NUMBER: US/10174,693
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 09/615,192
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 407
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-174-693-107
Query Match 46.6%; Score 1429.6; DB 7; Length 1630;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 1601 CCGTTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAG 1660
Db 1 CCGTTTATTTCTCTGCTTTCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAG 60
QY 1661 AGGAGAGATGGTTCGACCGGCTCGAGACCCAGATGATGATGATGATGATGATGAT 1720
Db 61 AGGAGAGATGGTTCGACCGGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAG 120
QY 1721 ACAGAGCACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1780
Db 121 AGGAGCACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 1781 AGGCGGCACTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840
Db 181 AGGCGGCACTCGAGTCTGATCTCTCGAGATCTCGAGATCTCGAGATCTCGAGAT 240
QY 1841 TCTTCAAGGGGGAATTCGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1900
Db 241 TCTTCAAGGGGGAATTCGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 1901 TCGAGCCGATCTTCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1960
Db 301 TCGAGCCGATCTTCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 1961 TCCCGGATGGCAAGGTTCGAGGCTCTACGGCTTAGCGGCTGCTGCTGCTGCTGCTGCT 2020

821 CTCGACCTCTCGAGATCATGCGCAAGCGCGCGCGGCTCTCTCCCGGGGAA 880
1855 ATCGCGGACAGCTCCCGGACCCAGAACCCCGAGGCAACCGGTATGCTCGACGGATCTTC 1914
881 GTCGCGGCCAGCTCCCGGACCCAGAACCCCGAGGCAACCGGTATGCTCGACGGATCTTC 940
1915 CGGCTGTGGCAGCTACTCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1974
941 CGGCTGTGGCAGCTACTCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
1975 GTCGAGCGGCTCTACGGCTTAGCGCGGTGCTGCAAGTCTTCTGCTCAAGAACGAGACGG 2034
1001 GTCGAGCGGCTCTACGGCTTAGCGCGGTGCTGCAAGTCTTCTGCTCAAGAACGAGACGG 1060
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1061 GTCTCCATCCCGCACTCAACTTGTATGATGACAGGACCAAAATCTCATGGAAGCTGTAT 1120
2095 TACCTGAAGATCGGCTCTTGAAGCGGAAATCCCAATCAACAAAGCGGTACGGGATGACC 2154
1121 TACCTGAAGATCGGCTCTTGAAGCGGAAATCCCAATCAACAAAGCGGTACGGGATGACC 1180
2155 GCGTTCGAGTATCATGACCGGACCGGCACTCAAGATCTTTAACCGGGGAATGCTCT 2214
1181 GCGTTCGAGTATCATGACCGGACCGGCACTCAAGATCTTTAACCGGGGAATGCTCT 1240
2215 GATCTCCACCATTAATGACAGGATGATGACAGGATGATGACAGGATGATGACAGGATG 2274
1241 GATCTCCACCATTAATGACAGGATGATGACAGGATGATGACAGGATGATGACAGGATG 1300
2275 GAGACCGTGTGCTGATGTCGAGGCGGCACTGGGCGGCTGCTGCTGCTGCTGCTGCTG 2334
1301 GAGACCGTGTGCTGATGTCGAGGCGGCACTGGGCGGCTGCTGCTGCTGCTGCTGCTG 1360
2335 TACCATCAATGAAGGATCACTTCGACCGGCACTGGGCGGCTGCTGCTGCTGCTGCTG 2394
1361 TACCATCAATGAAGGATCACTTCGACCGGCACTGGGCGGCTGCTGCTGCTGCTGCTG 1420
2395 TTCTGCTGCTCAAGACGCTCGAGGCGGCACTGTTGCTGCTGCTGCTGCTGCTGCTGCT 2454
1421 TTCTGCTGCTCAAGACGCTCGAGGCGGCACTGTTGCTGCTGCTGCTGCTGCTGCTGCT 1480
2455 TTTTTCATGAAGTGGATATGCCATGATGATGATGATGATGATGATGATGATGATGATG 2514
1481 TTTTTCATGAAGTGGATATGCCATGATGATGATGATGATGATGATGATGATGATGATG 1540
2515 ACTGCTACGATGCTGCTTCCCAATGGAAGGATGATGCTGCTGCTGCTGCTGCTGCTG 2574
1541 ACTGCTACGATGCTGCTTCCCAATGGAAGGATGATGCTGCTGCTGCTGCTGCTGCTG 1600
2575 TGTACCCAGACAGGCTTAGCGACCAAGATGATGATGATGATGATGATGATGATGATG 2634
1601 TGTACCCAGACAGGCTTAGCGACCAAGATGATGATGATGATGATGATGATGATGATG 1660
2635 CCAACAACCCAGCGGGAAGAGAGACAGAGAGGTTTCAGGATGATGATGATGATGATG 2694
1661 CCAACAACCCAGCGGGAAGAGAGACAGAGAGGTTTCAGGATGATGATGATGATGATG 1720
2695 CCGGATTTACGGGCTTCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2754
1721 CCGGATTTACGGGCTTCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1780
2755 TGAAGACCGTGTGATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2814
1781 TGAAGACCGTGTGATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1840
2815 GTGAAGAGCGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2874
1841 GTGAAGAGCGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1900
2875 ACAATAAGAGCGACTGTATGATGCGCAAGTGAAGTTTCAAGATTTGTTTATGCT 2934

Db 361 TCCCGATGCGAAGGTCGAGCGGCTCTACGCGCTAGCGCGGTGTGCAAGTCTCTGTGTC 420

Qy 2021 AGAAGAGGAGCGGGTCTCCATCGCGCACTCAACTTGATGAACCGAGCAAAATCCTCA 2080

Db 421 AGAAGAGGAGCGGGTCTCCATCGCGCACTCAACTTGATGAACCGAGCAAAATCCTCA 480

Qy 2081 TGAAGAGCTGGTATTACCTGAAAGATCGCGTCTCTTGAAGCGGGAATCCCAATCAACAAGG 2140

Db 481 TGAAGAGCTGGTATTACCTGAAAGATCGCGTCTCTTGAAGCGGGAATCCCAATCAACAAGG 540

Qy 2141 CGTACGGGATGACCGGCTTCGAGTATCATGCGACCGGACCGCGGATTCACAAAGATCTTTA 2200

Db 541 CGTACGGGATGACCGGCTTCGAGTATCATGCGACCGGACCGCGGATTCACAAAGATCTTTA 600

Qy 2201 ACCGGGAATGCTGATCACTCCACCACTTACTGAAGAGATACCTGGAACATACAAGG 2260

Db 601 ACCGGGAATGCTGATCACTCCACCACTTACTGAAGAGATACCTGGAACATACAAGG 660

Qy 2261 GCTTCGAGGCGCTCGAGACCGTGTGATGTCGAGGCGGCACTGGGGCGGTGCTCAGCA 2320

Db 661 GCTTCGAGGCGCTCGAGACCGTGTGATGTCGAGGCGGCACTGGGGCGGTGCTCAGCA 720

Qy 2321 TGATCGTTGCCAATACCCATCAATGAAGAGGATCACTTCGACC-GCCCAACGGATTG 2379

Db 721 TGATCGTTGCCAATACCCATCAATGAAGAGGATCACTTCGACCCTGCTCAGGTGATTG 780

Qy 2380 AAGACGCCCCACCCCTTCTGTTGTCAGACGCTCGGAGGCGGACATGTTGCTCAGCGTTC 2439

Db 781 AAGACGCTCCACCCCTTCTGTTGTCAGACGCTCGGAGGCGGACATGTTGCTCAGCGTTC 840

Qy 2440 CAAAGGAGATGCGATTTTCATGAAGTGATATGCCATGCTGGAGTGACGACCATTCGG 2499

Db 841 CAAAGGAGATGCGATTTTCATGAAGTGATATGCCATGCTGGAGTGACGACCATTCGG 900

Qy 2500 CGAAGTTCCTCAAGAACTGCTACGATCGCTTCCCAACAATGAAAGGTGATCCTGACG 2559

Db 901 CGAAGTTCCTCAAGAACTGCTACGATCGCTTCCCAACAATGAAAGGTGATCCTGACG 960

Qy 2560 AGTGGCTACTCCTGTGTACCCAGACAGGACCTAGCGACCAAGATGTGATCCACATCG 2619

Db 961 AGTGGCTACTCCTGTGTACCCAGACAGGACCTAGCGACCAAGATGTGATCCACATCG 1020

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Db 1021 ACTGCAATCATGTTGGGCCCAACCCAGGCGGGAAGAGAGGACACAGAAGGATTCGAGG 1080

Qy 2680 CATGGCCAAAGGGCGCGGATTTTCAAGGCTTCCAAAGTCATGTGCTGCGCTTTCGGCACTC 2739

Db 1081 CATGGCCAAAGGGCGCGGATTTTCAAGGCTTCCAAAGTCATGTGCTGCGCTTTCGGCACTC 1140

Qy 2740 ACCTCATGGAGTTCCTGAAGACCGCTTGATCTGCTCTCTGTGGTATGTTCAATGTTCT 2799

Db 1141 ACCTCATGGAGTTCCTGAAGACCGCTTGATCTGCTCTCTGTGGTATGTTCAATGTTCT 1200

Qy 2800 TGAATTTGAAGGTCGTGAAGGAGCCCTTTTCTCACAAGTTGGCTTCGGCATACCAAGTTC 2859

Db 1201 TGAATTTGAAGGTCGTGAAGGAGCCCTTTTCTCACAAGTTGGCTTCGGCATACCAAGTTC 1260

Qy 2860 TTCTCAATAAAGGAAACAATAAGAGCGACTGTATGATGCGCAAGTGAAGTGTACAAGA 2919

Db 1261 TTCTCAATAAAGGAAACAATAAGAGCGACTGTATGATGCGCAAGTGAAGTGTACAAGA 1320

Qy 2920 TTTGTTGTTTATGTCTATAAAGTTTGTAGTCTTCTGCACTCTGCAATTTTCAAGAATGTGT 2979

Db 1321 TTTGTTGTTTATGTCTATAAAGTTTGTAGTCTTCTGCACTCTGCAATTTTCAAGAATGTGT 1380

Qy 2980 AACGAACCGCGTATATGAGTGTGCTGAATGATGGAATTTGATATTTCTGCTCTCTTT 3039

Db 1381 AACGAACCGCGTATATGAGTGTGCTGAATGATGGAATTTGATATTTCTGCTCTCTTT 1440

Qy 3040 TTCAGTAAATCACTTCGAACAAA 3063

Db 1441 TTCAGTAAATCACTTCGAACAAA 1464

RESULT 8

US-10-137-036-12
; Sequence 12, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-12

Query Match 20.8%; Score 638.2; DB 6; Length 661;
Best Local Similarity 98.9%; Pred. No. 5.6e-185;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
Qy 1019 CTGAGCCATTATTCGAGAGCACATCGGCCCAAAATTTATTTCTTGTGCTGCAATACTGT 1078
Db 1 CTGAGCCATTATTCGAGAGCACATCGGCCCAAAATTTATTTCTTGTGCTGCAATACTGT 60
Qy 1079 CGAATTTTCTTTTAAAGTAAGTAACCAATGATGATCATGTTGACAAAAGGCTGATTA 1138
Db 61 CGAATTTTCTTTTAAAGTAAGTAACCAATGATGATCATGTTGACAAAAGGCTGATTA 120
Qy 1139 GTATGATCTGGAGTTGTTGGTGCRAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 1198
Db 121 GTATGATCTGGAGTTGTTGGTGCRAATTTGCAAGCTGACGATGGCCCTCAGGGAAAT 180
Qy 1199 AAGGCCCAACCCAGATTGCAAGAGCACAAAGAGACACGACCAACCTTTTCTTTAAACAAG 1258
Db 181 AAGGCCCAACCCAGATTGCAAGAGCACAAAGAGACACGATCCAACTTTCTTTAAACAAG 240
Qy 1259 ATCATCACAGATCGGCCAGTAAGGTAATTTAAATTTAAACAATAGCTCTTGTACCGGG 1318
Db 241 ATCATCACAGATCGGCCAGTAAGGTAATTTAAATTTAAACAATAGCTCTTGTACCGGG 300
Qy 1319 AACTCGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGTTGGTGGAAAGCGACGCC 1378
Db 301 AACTCGTATTTCTCTCACTTCATTAACCCCTGATTAATTTGTTGGTGGAAAGCGACGCC 360
Qy 1379 AACCCCAAAAAGTCAAGTGTCTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1434
Db 361 AACCCCAAAAAGTCAAGTGTCTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 1435 AGAGTTTTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCATCGGTGACGAATGT 1494
Db 421 AGAGTTTTCTCTATATTTCTGTTTACCGGTTGGAGTCAATGGCATCGGTGACGAATGT 480


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Query Match      20.8%; Score 638.2; DB 10; Length 661;
Best Local Similarity 98.9%; Pred. No. 5.6e-185;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 1019 CTGAGCCATTAAATTCAGAGCAGCATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 1078
Db 1 CTGAGCCATTAAATTCAGAGCAGCATCGCCCAAAATTAATCTTCTGCTGCCATAACTGT 60

Qy 1079 CGAATTTTCTCTTTTAGTAAAGCAATGATCGCGCATGTTTGCACAAAAGGCTGATTA 1138
Db 61 CGAATTTTCTCTTTTAGTAAAGCAATGATCGCATGTTTGCACAAAAGGCTGATTA 120

Qy 1139 GTATGATCTTGGAGTGTGTGTCAAATTTGCAAGCTGACGATGCGCCCTCAGSGAAAT 1198
Db 121 GTATGATCTTGGAGTGTGTGTCAAATTTGCAAGCTGACGATGCGCCCTCAGSGAAAT 180

Qy 1199 AAGCGCCCAACCCAGATTCGAAGAGCACAAGAGCAGCAGCCAACTTTCCTTAACAAG 1258
Db 181 AAGCGCCCAACCCAGATTCGAAGAGCACAAGAGCAGCAGTCCAACTTTCCTTAACAAG 240

Qy 1259 ATCATACCCAGATCGCGCAGTAAGGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 1318
Db 241 ATCATACCCAGATCGCGCAGTAAGGGTAATTAATTTAAACAATAGCTCTTGTACCGGG 300

Qy 1319 AACTCCGATTTCTCTCACTTCCATAAAACCCCTGATTAATTTGGTGGGAAAGCGACAGCC 1378
Db 301 AACTCCGATTTCTCTCACTTCCATAAAACCCCTGATTAATTTGGTGGGAAAGCGACAGCC 360

Qy 1379 AACCACAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1434
Db 361 AACCACAAGGTCAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 1435 AGAGTTTCTCTATATTTCTGTTTCCCGGTTGAGTCAATGCGATGCGTGCAGATGT 1494
Db 421 AGAGTTTCTCTATATTTCTGTTTCCCGGTTGAGTCAATGCGATGCGTGCAGATGT 480

Qy 1495 ACATATTTGGTGTAGGGTCCAAATTTTGGCGGGGGTGGTGAACCGCAAAAGTTCTCTATA 1554
Db 481 ACATATTTGGTGTAGGGTCCAAATTTTGGCGGGGGTGGTGAACCGCAAAAGTTCTCTATA 540

Qy 1555 TATCGAACCTCCACACATACCTCACTTCAATCCCAACCAATTAATCCGTTTATTTTCT 1614
Db 541 TATCGAACCTCCACACATACCTCACTTCAATCCCAACCAATTAATCCGTTTATTTTCT 600

Qy 1615 CTGCTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1674
Db 601 CTGCTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

Qy 1675 T 1675
Db 661 T 661

RESULT 11
US-09-947-027-5
; Sequence 5, Application US/09947027
; Patent No. US20020124281A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIO
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/09/947,027
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: aspen populus tremuloides

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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: AldomT; GenBank accession number: X62096
US-09-947-027-5

Query Match      20.8%; Score 631; DB 3; Length 1503;
Best Local Similarity 74.5%; Pred. No. 1.6e-182;
Matches 807; Conservative 0; Mismatches 275; Indels 1; Gaps 1;

Qy 1687 GAGACCCAGATGACCCCGACCCCAAGTCTCGGAGCAGGCGCAACCTCTTCGCCATGCGAG 1746
Db 80 GAAACTCAGATGACTCAACTCAGGTATCAGATGAAGAGCAGACCTCTTTTGGCATGCAA 139

Qy 1747 CTGGCAGAGCCCTCCCGTGTCTCCCATGCTCTAAAGCGCGCCATCGAGATCGACCTCCTC 1806
Db 140 CTAGCCAGTGTCTTCACTTCTACCAATGATCTCTCAAAACAGCCATTGAACCTCGACCTCT 199

Qy 1807 GAGATCATGGCCAAAGACGCGCGCGGGCGGTCTCTCTCAACGGGGAAATTCGGGCGACAG 1866
Db 200 GAAATCATGGCTAAAGCTGGCCCTGTGCTTCTTGTCCACATCTGAGATAGCTTCTCAC 259

Qy 1867 CTCGCCACCCAGAACCCCGAGGCGACCGCTCATGCTCGACCGGATCTTCGGGCTGTGGCC 1926
Db 260 CTCCTTACCAAAACCCCTGATGCGCTGTATGATGAGCCGTATCTTGGCCCTCTCTGGCT 319

Qy 1927 AGCTACTCTCGTGTCTCACGTGCACTCCGCGACCTCCCGATGCGCAAGGTTCGAGCGGCTC 1986
Db 320 AGCTACTCTCACTTCTTACTGCTCTCTGAAAGATCTTCTGATGGGAAGGTTCGAGACTG 379

Qy 1987 TAGCGTTTAGCGCGGTGTGCAAGTCTTGGTCAAGAACGAGGACGCGGTCTCCATCGCC 2046
Db 380 TATGGCTCGCTCTCTGTTGTAATTTCTTGACCAAGAACGAGGACGCTGTCTCTGTGAGC 439

Qy 2047 GCATCTCACTTGTATGACGAGGACCAAAATCTCTCATGGAAGCTGTATTTACCTGAAAGAT 2106
Db 440 CCTCTCTGTCTATGAACCAAGGCAAGGTCTCTATGGAAGCTGTATTTTGAAGAT 499

Qy 2107 GCGGTCTTGAAGCGGGAATCCCATTTCAACAAAGCGGTACGGGATGACCGGTTTCGAGTAT 2166
Db 500 GCATTTCTTGTATGAGGGAATTCATTTTAAAGGCTATGGGATGACTGCAATTTGAATAT 559

Qy 2167 CATGGCACCGACCCCGGATTCACAAAGATCTTTTAAACGGGGAATGTCTGATCATCTCCACC 2226
Db 560 CATGGCACGGATCCAAAGATTCACAAAGGTCTTCAACAAAGGAATGTCTGACCACTCTAC 619

Qy 2227 ATTACTATGAGAGATATCTGNAACATACAGGGCTTCGAGGGCTTCGAGAGCGGTGTC 2286
Db 620 ATTACCATGAAGAAGATTTCTTGAGACCTTCAAAAGGCTTTGAAGGCTCTACGTCTCTGGTG 679

Qy 2287 GATGTCGAGGCGGACCTGGGCGGTGCTCAGCATGATCGTTGCCAAATACCCATCAATG 2346
Db 680 GATGTTGGTGGGACTGGAGCGGTCTGTTTACACCATCGTCTCTTAAATACCTTCAATC 739

Qy 2347 AAAGGATCAACTTGA - CGGCCCCAAACGGATTTGAAGACCGCCCAACCTTCTCTGTGTC 2405
Db 740 AAGGCAATTAATCTGATCTGCCCCACGTCAATGAGGATGCCCATCTTATCCCGGAGTG 799

Qy 2406 AAGCAGCTCGAGGCGACATGTTCTGTCAGGTTCCAAAGGGAGATGCCATTTTCATGAAG 2465
Db 800 GAGCATGTTGGTGGGACATGTTGTTGTTAGTGGCCCCAAAGCAGATGCCGTTTTCATGAAG 859

Qy 2466 TGGATATGCCATGACTGAGTACGACCACTTGGCGGAAGTTCTCTAAGAACTGCTACGAT 2525
Db 860 TGGATATGCCATGATTTGGAGCGACGCCACTGCTTAAATTTCTTGAAGATTCGTATGAC 919

Qy 2526 GCGCTTCCCAACAATGAAGAGTGTGTTGTCAGAGTGGGTACTCCCTGTGTACCCAGAC 2585
Db 920 GCGTTCGCGAAAACGGCAAGGTGATCTTGTGTTGAGTGCATTTCTCCCGTGGCTCTGAC 979

Qy 2586 ACAGGCTTAGCGACCAAGAAATGTGATCCACATCGATGCTGATGTTGGCCCAACCCCA 2645
Db 980 ACAAGCCTTGGCCCAAGGAGTGTGTCGAGTGTGTCATCATGCTGCGGCGCAACCC 1039

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QY 2646 GCGGGAAGAGAGGACACAGAAGGATTCGAGGCATTTGGCCAAAGGGCCGGATTCAG 2705
Db 1040 GGTGGGAAGAGAGGACCCGAGAAGGAATTTGAGGGCTTAGCTAAGGGAGCTGGCTTCCAA 1099
QY 2706 GGCTTCCAAAGTCAATGCTGCGGTTTCGGCACTCAGTCATGAGTTCCTGAAGACCGCT 2765
Db 1100 GGTTTTGAAGTAAATGCTGTGCAATTCAAACACATGTCATTGAATTCGCAAGAAGGCC 1159
QY 2766 TGA 2768
Db 1160 TAA 1162

RESULT 12
US-10-091-009-5
; Sequence 5, Application US/10091009
; Publication No. US20020138870A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND
; TITLE OF INVENTION: COMPOSITION, AND
; FILE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/10/091,009
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; NAME/KEY: misc feature
; OTHER INFORMATION: AldomT; GenBank accession number: X62096
US-10-091-009-5

Query Match 20.6%; Score 631; DB 6; Length 1503;
Best Local Similarity 74.5%; Pred. No. 1.6e-182; Indels 1; Gaps 1;
Matches 807; Conservative 0; Mismatches 275;

QY 1687 GAGACCCAGATGACCCCGACCCCAAGTCTCGGACGAGGCGAACCCTTCGCGCATGCG 1746
Db 80 GAACTCAGATGACTCCCAACTCAGGTATCAGATGAAGAGGCACACCTCTTTGGCCATGCAA 139
QY 1747 GTGGGAGGCGCTCGGTGCTCCCATGTCCTTAAGGCGCGCATCGAGATCGACCTCCTC 1806
Db 140 CTAGCCAGTGTCTAGTTCTACCAATGATCTCTCAAAACAGCCATTAAGTCACTGACCTTCTT 199
QY 1807 GAGATCATGGCCAAAGAGCGGCGCGGCGGCTTCCTCTCCACGGGGGAAATCGCGGCACAG 1866
Db 200 GAAATCATGGCTTAAGCTGGCCCTGGTCTCTTCTTGTCACATCTGAGATAGCTTCTCAC 259
QY 1867 CTCGCGACCCAGAACCCCGAGGACCCGTATGCTGTCGACCGGATCTTCGGCTCTGGCC 1926
Db 260 CTCCTTACCAAAACCCCTGATCGCGCTGTCTATGTTAGACCGTATCTCTCGGCTCTCGCT 319
QY 1927 AGCTACTCGGTCTCAGTCGACCTCTCCGACCTCCCGATGGCAAGTTCGAGCGGCTC 1986
Db 320 AGCTACTCATTCTTACCTGCTCTCTGAAGATCTTCTGATGGAGGTTGAGAGACTG 379
QY 1987 TACGGCTTAGCGCCGGTGTGCAAGTTCTTTGGTCAAGAACGAGGACGGGTTCTCCATGCC 2046
Db 380 TATGGCTCGCTCCTGTTTGTAAATCTTGACCAAGAACGAGGACGGTGTCTCTGTCAGC 439
QY 2047 GCATCAACTTGAATGACGACGACAAATCCTCATGGAAGCTGTTACTTACTGAAAGAT 2106
Db 440 CCTCTCTGCTCATGAACAGGACCAAGGCTCTCATGGAAGCTGTTATTTTGAAGAT 499
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QY 2107 GCGTCTCTGAAGCGCGAATCCCATTCACAAAGCGTACGGGATGACCGCGTTTCGAGTAT 2166
Db 500 GCAATCTTGTATGAGGAATTCATTTTAAACAAGCCCTATGGGATGACTGCATTTGAATAT 559
QY 2167 CATGGCACCCGACCCCGGATTCACAAAGATCTTTAAACGGGGAATGTCTGATCACTCCACC 2226
Db 560 CATGGCAGCGATCCAAGATTCACAAAGGCTTCTCAACAAGGGAATGTCTGACCACTCTACC 619
QY 2227 ATTACTATGAAGAAGATGACTGGAACATACAAGGGCTTCGAGGGCTTCGAGACCGTGGTC 2286
Db 620 ATTACCATGAAGAGATTTCTTGAGACCTCAAAAGGCTTTTGAAGCCCTCAGCTCTTGGTG 679
QY 2287 GATGTCGAGCGCGCACTGGGCGCTGCTCAGCATGATCGTTGCAAAATACCCATCAATG 2346
Db 680 GATGTTGGTGGGACTGGAGCGCTGTTAAACCATGCTCTCTAAATACCCCTTCAATC 739
QY 2347 AAAGGATCAACTTTCGA-CCGCCCCAACGGATTTGAAGACGCCCCACCCCTTCCTGGTGC 2405
Db 740 AAGGCAATTAATTCGATCTGCCCACTCATTTGAGGATGCCCATCTTATCCGGAGTG 799
QY 2406 AAGCAGCTCGAGGCGGACATGTTGTCAGCGTTTCCAAAGGAGATGCCATTTTCATGAAG 2465
Db 800 GAGCATGTTGGTGGGACATGTTTGTAGTGTGCCAAAGCAGATGCGGTTTTCATGAAG 859
QY 2466 TGGATATGCCATGACTGGAGTGACGACCATTTGCCGGAAGTTCTCAAGAACTGCTACGAT 2525
Db 860 TGGATATGCCATGATTTGAGCGCGCCACTGCTTAAATTTCTTGAAGAATTTGCTATGAC 919
QY 2526 GCGTTTCCCAACATGGAAGGATGATGTTGTCAGAGTGGCTACTCCCTGTGTACCCAGAC 2585
Db 920 GCGTTGCGCGAAACGGCAAGGTGATCTTTGTGAGTGCACTCTCCGCTGGCTCTGAC 979
QY 2586 ACGAGCCTTAGCGACCAAGAATGTGATCCACATCGACTGCATCATGTTGGCCCCACAACCCA 2645
Db 980 ACAAGCCTTGCCACCAAGGAGTCTGTGACCGTTGATGTCATCATGCTGCGCGCACAAACCCC 1039
QY 2646 GCGCGGAAAGAGAGACACAGAAGGATTCGAGGATTTGGCCAAAGGGCCGGATTTTCAG 2705
Db 1040 GGTGGGAAAGAGAGACCGGAAAGGAAATTTGAGGGCTTAGCTAAGGGAGCTGGCTTCCAA 1099
QY 2706 GCGTTCCAAAGTCACTGCTGCGCTTCGGCACTCAGTCATGGAGTTCTCTGAAGACCGCT 2765
Db 1100 GGTTTTGAAGTAAATGCTGTGTCATTCACACACATGTCATGATTCGCGAAGAGGCC 1159
QY 2766 TGA 2768
Db 1160 TAA 1162

RESULT 13
US-11-057-518-5
; Sequence 5, Application US/11057518
; Publication No. US20050166283A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; FILE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/11/057,518
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; NAME/KEY: misc_feature
;
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; OTHER INFORMATION: AldomT; GenBank accession number: X62096
US-11-057-518-5

Query Match 20.6%; Score 631; DB 13; Length 1503;
Best Local Similarity 74.5%; Pred. No. 1.6e-182;
Matches 807; Conservative 0; Mismatches 275; Indels 1; Gaps 1;

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QY 1687 GAGACCCAGATGACCCCGACCCAGTCTCGAGCAGCAGGAGCAACCTCTTCGCGCATGACG 1746
DB 80 GAACTCAGATGACTCAACTCAGTATCAGATCAGATGAGAGGACACCTCTTGGCATGCAA 139
QY 1747 CTGCGAGCGCTCTCGTCTCCCATCGTCTTAAAGCCCGCCATCGAGATCGACCTCTC 1806
DB 140 CTAGCCAGTCTCAGTCTTACCAATGATCTCTAAACAGCAGCAATGAACTCGACCTCTT 199
QY 1807 GAGATCATGCGCAAGGAGCGCGCGCTCTCTCCACGCGGGAATCGCGGCACAG 1866
DB 200 GAAATCATGCTAAAGCTGCGCTCTCTGCTCTTCTGCTCCACATCTGAGATAGCTTCTC 259
QY 1867 CTCCGAGCCAGAACCCCGAGGACCGCTCATGCTCGACCGGATCTTCGCGCTCTGGCC 1926
DB 260 CTCCCTACCAAAACCTGATGCGCTCTCATGTTAGACCGTATCTCGCGCTCTGGCT 319
QY 1927 AGCTACTCCGTCTCAGTGCACCTCTCGGACCTCCCGATGCGCAAGGTCGAGCGCTC 1986
DB 320 AGCTACTCCATCTTACTCTCTCTGAAAGATCTTCTGATGGAAGGTTGAGAGACTG 379
QY 1987 TAGCGCTTAGCGCGGTGTGAGTCTTCTGTTGTAAGAACGAGAGCGGGTCTCATCGCC 2046
DB 380 TATGGCTCGCTCTGTTGTTAAATCTTGACCAAGAACGAGAGCGGTCTCTGTGACG 439
QY 2047 GCCTCAACTGTATGACACGAGCAAAATCTCTATGGAAGCTGTATTAACCTGGAAGAT 2106
DB 440 CCTCTCTGTCTATGACACGAGCAAGGCTCTATGGAAGCTGTATTAATTTGAAAGAT 499
QY 2107 GCGTCTCTTGAAGCGGAAATCCCATCAACAGCGGTACGCGGATGACCGGTTTCGAGTAT 2166
DB 500 GCAATCTCTGATGAGGAAATCCATTTAAACAGGCTATGGGATGACTGCAATTTGAATAT 559
QY 2167 CATGGACCGACCGCGGATTTCAACAGATCTTTAAACCGGGGATGTCTGATCATCTCACC 2226
DB 560 CATGGACCGATCCAGATTTCAACAGGCTTTCAACAGGGAATGTCTGACCACTCTTACC 619
QY 2227 ATTACTATGAGAGTACTGGAACATACAAGGCTTCGAGGCGCTCGAGACCGTGGTC 2286
DB 620 ATTACCATGAGAGATTTCTTGAGACCTTCAAGGCTTTTGAAGGCTTCACGCTCTCGGTG 679
QY 2287 GATGTCGAGCGGCACTGGGCGGTGCTCAGCATGATCTGTGCAATATCCCATCAATG 2346
DB 680 GATGTTGGTGGTGGGACTGGAGCGTCTGTTAAACCATCTCTCTAATATCCCTTCAATC 739
QY 2347 AAGGGATCACTTCGA - CGCGCCCAACGAGATTGAAGACCGCCACCCCTTCTCTGGTGC 2405
DB 740 AAGGCAATTAATCTCGATCTGCGCCACGTCATTGAGGATGCCCATCTTATCCCGGAGTG 799
QY 2406 AAGCACTCGGAGCGCATGTTGCTCAGGTTTCCAAAGGAGATGCGCATTTTCATGAAG 2465
DB 800 GAGCATGTTGGTGGCGACATGTTGTTAGTGTGCGCCAAAGACAGATGCCGTTTCATGAAG 859
QY 2466 TGGATATGCCATGACTGGAGTGACGACATTTGCGGAAAGTTCTTCAAGAACTGCTACGAT 2525
DB 860 TGGATATGCCATGATTGGAGGACGCCACATGCTTAAATTTCTTGAAGAAATGCTATGAC 919
QY 2526 GCGCTTCCCAACAAATGAAAGGTGATCGTTGCGAGTGCCTGCTCTCTGTGTATCCACGAC 2585
DB 920 GCGTTGCGGAAACGCAAGGTGATCTTGTGAGTGCAATCTTCTCCGTTGGCTCTCTGAC 979
QY 2586 ACAGGCTTAGCGACCAAGATGATCCATCGACTGCAATCATGTTGGCCCAACACCA 2645
DB 980 ACAAGCCTTCCCAACAAAGGAGTGTGTCAGCTTGTATCATGCTGGCGGCAACCC 1039
QY 2646 GCGGGAAAGAGAGGACACAGAGAGTTCGAGGCAATGGCCAAAGGGCGGATTTTCAG 2705
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DB 1040 GGTGGAAAGAGAGAGGACCGAGAAAGAAATTTAGGGCTTAGCTAAGGAGATGGCTTCCAA 1099
QY 2706 GGTTCCTCAAGTCAATGCTGCGCTTTTCGGCACTTCAGTCAATGAGTTCTCTGAAGACGCT 2765
DB 1100 GGTTCCTCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1159
QY 2766 TGA 2768
DB 1160 TAA 1162
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RESULT 14

US-10-424-599-20299
; Sequence 20299, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 20299
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118334C.1
US-10-424-599-20299

Query Match 20.0%; Score 613.4; DB 8; Length 2037;
Best Local Similarity 72.5%; Pred. No. 5.4e-177;
Matches 808; Conservative 0; Mismatches 306; Indels 1; Gaps 1;

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QY 1687 GAGACCCAGATGACCCCGACCCAGTCTCGAGCAGCAGGAGCAACCTCTTCGCGCATGACG 1746
DB 593 GAGACTCAGATGACTCTCAACCCCATGATCTGATGAGAGGCAACCTTTTCGCGCATGCAA 652
QY 1747 CTGCGCAGCGCTCTCCGTGCTCCCATGCTCTTAAAGCGCGCCATCGAGATCGACCTCTC 1806
DB 653 CTAGCAGGTCCTCAGTCTCCTATGTTCTCAATCAGCTCTTGAAGCTTGTATCTGTTG 712
QY 1807 GAGATCATGCGCAAGGAGCGCGCGGTCTCTTCAACGCGGGAATTCGCGGCACAG 1866
DB 713 GAAATCATAGCCAAAGGCTGCGCTGCTGCTTCACTTTCCCGCTCCGACATTTGCTTCGG 772
QY 1867 CTCCGACCCAGAACCCCGAGGACCGCTCATGCTCGACCGGATCTTCGCGCTCTGGCC 1926
DB 773 CTCCCAACACACACCCCTGATGACCCCTGATGTTGAGACCGTATATGCGCCTCTTGGCT 832
QY 1927 AGTACTCTCGTCTCAGCTGACCTCTCCGACCTCCCGATCGCAAGGTCGAGCGGCTC 1986
DB 833 TGCTAATATCTCTCTTTCTCTCGCACTCTCCCTCATGCGAAGGTTGAGAGGCTC 892
QY 1987 TAGCGCTTAGCGCGGTGTGCAAGTCTTTGGTCAAGAAACGAGGACGCGGTTCTCATCGCC 2046
DB 893 TATGGTCTCGCCCTCTGCTGTAAGTACTTTGGTTCAGGAAACGAGATGCTGCTCCTCATGCT 952
QY 2047 GCATCACTTGTATGATGACCAAGCAAAATCTCTCATGAAAGCTGTTATTAACCTGGAAGAT 2106
DB 953 GCTCTCAACCTCATGAAACGAGGCAAAATCTCTCATGAAAGCTGTTATTTTGAAGAT 1012
QY 2107 GCGCTCTTGAAGGCGGAATCCCATTCACAGCGGTACGCGGATGACCGGTTTCGAGTAT 2166
DB 1013 GCATCTTGAAGGGGTTATTCATTTAACAAGCATATGATGACAGCCTTTGATATC 1072
QY 2167 CATGGACCGACCGCGGATTTCAACAGATCTTTTAAACCGGGGAATGTCTGATCACTCCAC 2226
DB 1073 CATGGAACGATCCAAAGGTTTAAAGGTTTCAACAGGGGATGCTGATCACTCTTACC 1132
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QY	2227	ATTACTATGAAGAAGTACTGGAACATACAAAGGCTTCAGGGCTCGAGACCGTGGTC	2286	Db	182	TTGAGATCATGGCCAAAGTCCGTCCCTCCAGCGGTACATCTCTCCGGCGGAGATTGCGG	241
Db	1133	ATTACAAATGAAGAAATTTTGAGACCTACACAGGCTTTGAGGACTTAAATCCCTGGTT	1192	QY	1862	CACAGTCCCGAACCCAGAACCCCGAGGACCCCGTCAATGCTCGACCGGATCTTCGGGCTGC	1921
QY	2287	GATGTCCGAGCGGCACTCGGGCGGTGTCAGCATGATCGTTGCCAAATACCCATCAATG	2346	Db	242	CGAGCTTCTACACCAACCCCTGAAGCTCCGGTGATGTGTGACCGGTGCTCCCGGCTCC	301
Db	1193	GATGTTGGTGAGAGAACTCGAGCTGTAGTCAACATGATTTGTCTCAAGTATCCCACTATT	1252	QY	1922	TGGCCAGCTACTCCGTGCTCACTGACGCTCCGCGACCTCCCGATGGCAAGTGCAGC	1981
QY	2347	AAAGGATCACTTCCA-CGGCCCAACGGAATGAAGACCCGCCCTTCCTGGTGC	2405	Db	302	TAGCCAGCTACTCCGTGTAACATACACTCTCCGGNACTTCCAGCGGCAAGTGGAGA	361
Db	1253	AAGGCAATTAATTTGATTTGCCCATGATTCATTGAAGATGCCCATCTTATCCAGAGTG	1312	QY	1982	GGCTCTACGGCTTAGCGCCGGTGTGCAAGTCTTGTGTCAAGAACGAGGCGGCTCTCCA	2041
QY	2406	AAGCAGCTCGAGGCGACATGTTGCTCAGCGTTTCAAAGGAGATGCCATTTTCATGAAG	2465	Db	362	GGCTGTACGGCTCGCCCTGTCTGCAAGTCTTGACCCAGAACGAGGATGAGTGTCTC	421
Db	1313	GAACATGTTGGTGAGATATGTTGTGAGTGTTCCTCAAAAGCTGATGCTATTTTATGAAG	1372	QY	2042	TGCGCGCACTCACTTGATGAACACGAGCAAAATCCCTCATGGAAAGCTGTGTATTAACCTGA	2101
QY	2466	TGATATGCCATGACTGGAGTAGCAGCACTTGGCGAAGTCTCAAGAACTGCTACAGAT	2525	Db	422	TTGCTCTCTTTTGTCTCACGGCTACCGACAAGGTCTTTTGGAGCCCTGGTTTACTTGA	481
Db	1373	TGGATTTGCCACGATTGGAGTGATGAGCACTGCTTGAAGTTTGTGAAGTATTTTGAAGT	1432	QY	2102	AAGATCGGCTCTTGAAGCGGGAATCCCATTTCAACAGGCGTACGGGATCACCGGTTTCG	2161
QY	2526	GCGTTCCTCCACATGAGAAAGGTGATCGTTGACAGTGGCTACTCCCTGTGTACCCAGAC	2585	Db	482	AAGATGCGATTTCTGAAGGAGGAATCCATTTCAATAAGCGTATGGAATGAATGAATTCG	541
Db	1433	GCACTACAGATTAATGGAAGGTGATTTGGCGGAATGCATTTCTCGGTGGCTCCAGAC	1492	QY	2162	AGTATCATGGCACCGACCCCGGATTTCAACAGATCTTTAAACCGGGGATCTCTGATCACT	2221
QY	2586	ACGAGCCTAGCGACCAAGAAATGTATCCACATCGACTGCATCATGTTGGCCGCAACCCA	2645	Db	542	ATTACCATGGAAACAGACACACAGATTTCAACAAAGGTGTTCAAACAGGGAATGTCCAGCACT	601
Db	1493	TCTAGCTTGGCCACAAAGGTGTGTTTCAATCGATGATCATGTTGGTCTATAATCCA	1552	QY	2222	CCACCATTTACTATCAAGNAGATCTGGAACATACAAAGGCTTCGAGGGCTTCGAGACCG	2281
QY	2646	GCGGGAAAGAGAGACACAGAGGAGTTGAGGCATTTGCCAAAGGGCGGATTTTCAG	2705	Db	602	CTACCATCACCATTGAAGAAGATCTTGAATGTACACAGGATTCGAGGGGCTTAACACGA	661
Db	1553	GGTGGAAAGAGAGACAGAGAAAGTTTGGAGCTCTGGCCAAAGGGCTGGAATTTCCA	1612	QY	2282	TGCTCGATGTCCGAGGGGCGCACTGGGGCGGTGCTCAGCATGATCGTTGCGCAATACCCAT	2341
QY	2706	GGCTTCCAAGTCATGTCTGGCTTTTCGGCACTCACCTCATGAGTTTCTTGAAGACCGCT	2765	Db	662	TTGTGATGTTGGGGCGGTACAGGTGCGGTGGCTAGCATGATTTGTGCTAAGTATCCTT	721
Db	1613	GTTTCCGAGTCTGTCTGTGCTTTCAATACCTACCTCATGGAATTTCTCAAAAAGGTT	1672	QY	2342	CAATGAAAGGAGATCACTTCGACC-GCCCCAAGGATGGAAGCGCCCCACCCCTTCCTG	2400
QY	2766	TGATCTGCTCTCTGTGTGTGATGTTTCATGTTCTT 2800		Db	722	CCATCAAGCCCATCAACTTCGACCTCGCTCATGTTTTCAGGATGCTCCAGCTTTTCTG	781
Db	1673	TAAAGTTCTTTGGCGTGGATTCTATATCAAGTTGCAT 1707		QY	2401	GTGTCAGCAGCTCGAGGCGACATGTTGCTCAGCGTTTCCAAAGGAGATGCCATTTTCA	2460
RESULT 15							
US-10-469-993-11							
; Sequence 11, Application US/10469993							
; Publication No. US20040078847A1							
; GENERAL INFORMATION:							
; APPLICANT: Paldi, Nitzan							
; TITLE OF INVENTION: METHOD OF ENHANCING ENTOMOPHILOUS							
; FILE REFERENCE: 26678							
; CURRENT APPLICATION NUMBER: US/10/469,993							
; CURRENT FILING DATE: 2003-09-16							
; NUMBER OF SEQ ID NOS: 22							
; SOFTWARE: PatentIn version 3.1							
; SEQ ID NO 11							
; LENGTH: 1486							
; TYPE: DNA							
; ORGANISM: Clarkia breweri							
US-10-469-993-11							
Query Match							
Best Local Similarity 73.9%; Pred. No. 5.8e-177; Indels 4; Gaps 2;							
Matches 804; Conservative 0; Mismatches 280; Indels 4; Gaps 2;							
QY	1685	CCGAGACCAGATGACCCCGACCCCAAGTCTCGAGCAGAGCGGAACCTCTTCGCCATGC	1744	Db	962	CTGACCCCGAGTATCGCCACCAAGGTAGTATCATCCATACCGACGCCCTCATGTTGGGCTACA	1021
Db	62	CAGAGATCCAGATATATCCCCACCCACTCTCCGAGGAGGACCAACCTCTTCGCCATGC	121	QY	2641	ACCCAGCGGGAAGAGAGGACACAGAGGAGTTCGAGGCATTGGCCAAAGGGCGCGGAT	2700
QY	1745	AGTGGCGAGCGCTCCGTGCTCCCATGTTCTTAAAGCGCCCATCGAGATCGACCTCC	1804	Db	1022	ACCCAGCGGCAAGAAAGGAGTTCGAGGAGTTCGAGGCTTTGGCTATGCGCTTCGGAT	1081
Db	122	AGTGGCGAGCGCGCGGTCTCCCATGTTCTCCCATGTTCTTAAAGCGCCCATCGAGCTCGACGTC	181	QY	2701	TTTCAGGGCTTCCAAAGTCATGTCTGCGCTTTTCGGCACTCACGTCATGGAGTTCCTGAAGA	2760
QY	1805	TCGAGATCATGGCCAAAG---GACGGGCGGGCGCGTTCCTCTCCACGGGGGAATCGCGG	1861	Db	1082	TCAGGGGTTTCAAAAGTAGCATCTTGTGCTTCAACACTTACGTCATGGAGTTCCTCAAAA	1141

Db 121 AGGAGCGAAACCTCTTCGCGATGACAGTGGCGAGCGCTCGTGTGCCCATGGTCCTCA 180
QY 1781 AGCGCGCATCGAGATCGACCTCTCGAGATCATGSCCAAGGACGGCGCGCGGTTC 1840
Db 181 AGCGCGCATCGAGCTCGACCTCTCGAGATCATGGCCAAAGCGCGCGCGGTTC 240
QY 1841 TCTCCACGGGGGAAATCGGGGACAGCTCCCGACCCAGAACCCGAGGACCCGTCATGC 1900
Db 241 TCTCCCGGGGAAGTCGGGGCCAGCTCCCGAACCCAGAACCCGAGGACCCGTCATGC 300
QY 1901 TCGACCGGATCTTCGGGCTGTGGCGAGCTACTCGGTGCTCAGTGCACCCCTCCGAGC 1960
Db 301 TCGACCGGATCTTCGGGCTGTGGCGAGCTACTCGGTGCTCAGTGCACCCCTCCGAGC 360
QY 1961 TCCCGGATGCAAGGTGCGAGCGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTTGGTCA 2020
Db 361 TCCCGGATGCAAGGTGCGAGCGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTTGGTCA 420
QY 2021 AGAACGAGGAGCGGGTCTCCATCCCGCACTCACTTGATGAACCAAGGACAAATCCTCA 2080
Db 421 AGAACGAGGAGCGGGTCTCCATCCCGCACTCACTTGATGAACCAAGGACAAATCCTCA 480
QY 2081 TGGAAAGCTGGTATTACTGAAGATCGGTCTTGAAGCGGAATCCCATCAACAAG 2140
Db 481 TGGAAAGCTGGTATTACTGAAGATCGGTCTTGAAGCGGAATCCCATCAACAAG 540
QY 2141 CGTACGGGATGACCGCGTTCGAGTATCATGGCACCGACCGCGGATTCACAGATCTTTA 2200
Db 541 CGTACGGGATGACCGCGTTCGAGTATCATGGCACCGACCGCGGATTCACAGATCTTTA 600
QY 2201 ACCGGGGAATGTGTATCATCTCAACATTAATGAAGAAGTACTGGAACATCAAGG 2260
Db 601 ACCGGGGAATGTGTATCATCTCAACATTAATGAAGAAGTACTGGAACATCAAGG 660
QY 2261 GCTTCGAGGGCTCGAGACCGTGTGATGTCGAGGCGGCACTGGGCGGCTGCAGCA 2320
Db 661 GCTTCGAGGGCTCGAGACCGTGTGATGTCGAGGCGGCACTGGGCGGCTGCAGCA 720
QY 2321 TGATGTTGCCAAATACCCATCAATGAAGGATCAACTTCGACC-CCCCAACGGATTG 2379
Db 721 TGATGTTGCCAAATACCCATCGATGAAGGATCAACTTCGACCCTGCCTCAGGTATTG 780
QY 2380 AAGCGCCCAACCCCTTCGTGTGATGACGACGTGAGGCGGACATGTCGTGAGCGTTC 2439
Db 781 AAGCGCTCCACCCCTTCGTGTGATGACGACGTGAGGCGGACATGTCGTGAGCGTTC 840
QY 2440 CAAAGGGAGATGCCATTTTCATGAAGTGGATATGCCATGACTGGAGTGACACCATTCG 2499
Db 841 CAAAGGGAGATGCCATTTTCATGAAGTGGATATGCCATGACTGGAGTGACACCATTCG 900
QY 2500 CGAAGTTCCTCAAGAACTGCTACGATGCGCTTCCCAACATGGAAGAGTGATCGTCAG 2559
Db 901 CGAAGTTCCTCAAGAACTGCTACGATGCGCTTCCCAACATGGAAGAGTGATCGTCAG 960
QY 2560 AGTGGTACTCCTGTGTACCCAGACGACGCTAGCCACCAAGAAATGTGATCCACATCG 2619
Db 961 AGTGGTACTCCTGTGTACCCAGACGACGCTAGCCACCAAGAAATGTGATCCACATCG 1020
QY 2620 ACTGCATCATGTGGCCCAACACCCAGCGGGAAGAGAGGACACAGAAGAGTTCGAGG 2679
Db 1021 ACTGCATCATGTGGCCCAACACCCAGCGGGAAGAGAGGACACAGAAGAGTTCGAGG 1080
QY 2680 CATTTGSCCAAGGGCGGATTTCAAGGCTTCCAAAGTATGTGCTGCGCTTTCGCACTC 2739
Db 1081 CATTTGSCCAAGGGCGGATTTCAAGGCTTCCAAAGTATGTGCTGCGCTTTCGCACTC 1140
QY 2740 AGCTCATGAGTTCCTGGAAGCGCTTGATCTGCTCTGTGATGATGTTTCATGTTCT 2799
Db 1141 AGCTCATGAGTTCCTGGAAGCGCTTGATCTGCTCTGTGATGATGTTTCATGTTCT 1200
QY 2800 TGGATTTGAAGGTTCGTGAAGGAGCCCTTTTCTCAGTTCGCTTCGCAATCAAGTTC 2859
Db 1201 TGGATTTGAAGGTTCGTGAAGGAGCCCTTTTCTCAGTTCGCTTCGCAATCAAGTTC 1260

QY 2860 TTCTCATAAAGGAAACAATAAGACGACTGTATGATGGCGCAAGTGAAGTTTCAAGA 2919
Db 1261 TTCTCATAAAGGAAACAATAAGACGACTGTATGATGGCGCAAGTGAAGTTTCAAGA 1320
QY 2920 TTTTGTCTTTTATGTCTATAAAGTTTTTGAAGTCTTCTGCATCTGATTTACAGAATGTGT 2979
Db 1321 TTTTGTCTTTTATGTCTATAAAGTTTTTGAAGTCTTCTGCATCTGATTTACAGAATGTGT 1380
QY 2980 AACGAAACCGGATATATGATGTGCTGATGATGGAATTTGATATTTCTTCTTTT 3039
Db 1381 AACGAAACCGGATATATGATGTGCTGATGATGGAATTTGATATTTCTTCTTTT 1440
QY 3040 TTCTAGTAAATCACTTCGAAACAAA 3063
Db 1441 TTCTAGTAAATCACTTCGAAACAAA 1464

RESULT 2
US-11-216-545-7471
; Sequence 7471, Application US/11216545
; Publication No. US20060135758A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO Technology, LLC
; APPLICANT: McLaird, Paul L
; APPLICANT: Tao, Nengheng
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Soybeans.
; FILE REFERENCE: 38-21 (53659)B
; CURRENT APPLICATION NUMBER: US/11/216,545
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: US 60/606,062
; PRIOR FILING DATE: 2004-08-31
; NUMBER OF SEQ ID NOS: 8783
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7471
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Glycine max
US-11-216-545-7471

Query Match 19.9%; Score 610.6; DB 8; Length 1410;
Best Local Similarity 72.0%; Pred. No. 1.8e-166;
Matches 810; Conservative 0; Mismatches 314; Indels 1; Gaps 1;
QY 1685 CCGAGACCCAGATGACCCGACCCCAAGTCTGGACGACGAGCGAAACCTCTTCGCCATGC 1744
Db 73 CTGAGACTCAGATTAATCTCCACCCATGATCTGATGAAGAGCAACCTTTTGGCATGC 132
QY 1745 AGCTGGCGAGCGCTCCGTCCTCCCATGGTCTTAAAGCGCGCATCGAGATCGACCTCC 1804
Db 133 AACTAGCAGTGGCTCTGTACTCCCTATGTTCTCAAAATCAGCTCTTGAAGTGTATCTGT 192
QY 1805 TCGAGATCATGGCCAAAGGACGGCGCGGTCTCTCCACGGGGAAATCGCGGAC 1864
Db 193 TGGAAATCATAGCAAGGCTGGCCCTTGTGTTTCATCTTTCCCCCACTGACATTTCTTCTC 252
QY 1865 AGCTCCGACCCAGAACCCCGAGGACCCGTCATGCTCGACCGGATCTTTCGGCTGCTGG 1924
Db 253 AGCTTCCAAACAGAACCCCTGATGACCCGTTATGTTGACCGCATTTTTCGGCTCTTGG 312
QY 1925 CCAAGTACTCCGTCGTCTCAGTGCACCTCCGCGACCTCCCGATGGCAAGTTCGAGCGC 1984
Db 313 CTTCGTACAATATCCCTTTCTTCTCCGTACTCTCCCTGATGACCAAGTTCGAGAGGC 372
QY 1985 TCTACGGCTTAGCGCGGTGTGCAAGTCTTGTGTAAGAACCGAGGACGGGCTCTCCATCG 2044
Db 373 TCTATGCTCTCGCCCCCGTTGTGTAAGTACTGCTCAAGACCCGAGATGTTGTTCTTCCATTG 432
QY 2045 CCGCACTCAACTTGTGTAAGAACCGAGCAAAATCTCTATGGAAGAGTCTGTTTACCTGAAAG 2104
Db 433 CTGCTCTTAACCTCATGAAACCGAGCAAAAGTCTCATGGAAGAGTCTGTTTACCTGAAAG 492

1865 AGTCCCGACCCAGAACCCGAGGACCCGTCATCTCGACCGGATCTTCGGGTCTGG 1924
266 AACTCCGACCCAAACCCCTGAGCTCCGTCATCTCGACCGTATCTCCGCTCTCTTA 325
1925 CCAGCTACTCCGTCGTCACTGTCACCCCTCCGCGACCTCCCGATGGCAAGTTCGAGCGC 1984
326 CGTCTTACTCCGTCGTAACTCTGCTCAACCGTAACTTTCCGGTGATGGCGTGTGAACGA 385
1985 TCTACGGCTTAGCGCGGTGTCAGAGTCTTCTGTCAGAAACGAGGACCGGGTCTCCATCG 2044
386 TTTACGGGCTTGGTCCGGTTTTCAGATATTGACCAAGAACCAAGATGGTGTTCATTTG 445
2045 CCGCACTCAACTTGTATGAACACGAGCAAAATCCTCATGAAAGCTGTGTATTAACCTGAAG 2104
446 CTGCTCTTTGCTTATGAACCAAGCAAGTCTCATGAAAGCTGTGTATTAACCTGAAG 505
2105 ATGGGCTTCTTGAAGCGGATCCCAATTCACCAAGGCTACCGGATGACCGGTTCGAGT 2164
506 ATGCAATTTCTTGATGGTGGATTCATTCACCAAGGCTTATGGAATGAGGGGTTCGAGT 565
2165 ATCATGCGACCGACCGCGATTCACCAAGATCTTTAAACCGGGGAATGTCTGATCACTCCA 2224
566 ACCACGGGACTGACCTTAGATTCACCAAGTCTTTAAACCAATGATGTCTAACCAATCCA 625
2225 CCATTACTATGAAGAAGATACCTGAAACATACAAAGGCTTCGAGGCTTCGACCGCTGG 2284
626 CAATCACCATGAAGAAGATTTCTGAGACCTATAAGGGTTTTTGAAGGATTCGATCTTTTGG 685
2285 TCGATGTCGAGGCGGCACTGGGCGCGTCTCAGCATGATCGTTGCCAAATACCCATCAA 2344
686 TTGATGTTGGTGGTGGCATTTGGTCTACCTCACTCAAAATGATGTCTCAAGTACCTTAATC 745
2345 TGAAGGATCAACTTTCGACCGCCC-CAACGAGTTGAAGACGCGCCCAACCCCTTCCTGTTG 2403
746 TTAAGGCAATCACTTTGATCTCCACATGTCATTGAAGATGCTCTCTTCATCTCGGTA 805
2404 TCAAGCAGTCGAGGCGACATGTTGTCAGCGTTCCAAAGGAGATGCCATTTTCATGA 2463
806 TTGAGCATTTGGAGGAGATGATTTGTAAGTGTCCTTAAAGGTGATGCCATATTCATGA 865
2464 AGTGATATGCCATGACTGGAGTGACGACCACTTCGGGAAAGTTCCTCAAGAACTGCTACG 2523
866 AGTGATATGTCATGACTGGAGTGACGAACTTCGGTGAATTTCTGAAAAAAGTCTACG 925
2524 ATGCGCTTCCCAACAAATGGAAGGATCGTTGACAGTGGTCTACTCCCTGTGTACCCAG 2583
926 AGTCACTTCCAGAGGATGGAAGGATGATTTAGCAGAGTGTATCTTCCAGAGACCCAG 985
2584 ACACGAGCCTAGCGACCAAGATGTGATCCATCGACTCATGTCATGTTGGCCCAACACC 2643
986 ACTCAAGCCTCTCAACCAACAAAGTAGTCCATGTCGATTGATTTGTTGGCTCAACAATC 1045
2644 CAGCGGGAAAGAGAGGACACAGAAAGGATTCGAGGCAATGGCCAAAGGGCGGATTTTC 2703
1046 CCGAGGCAAGAAACGAAACCGAGAAAGAGTTTGAAGGCAATAGCCAAAGATCAGGCTTCA 1105
2704 AGGGCTTCCAAAGTCATGCTCGCTTCGGGCTTCAGCTACAGTCAAGTGTCTTGAAGACCG 2763
1106 AGGCAATCAAGTGTCTCGGACGCTTTTGGTGTAACTTATGAGTTACTCAAGAGC 1165
2764 CTTGATCTGCTCTCTGTGGTGATGTTTCATGGTT 2797
1166 TCTAATAACAAACAATGTTCTTATGAAGATGATT 1199

RESULT 4
US-11-056-355B-22559
; Sequence 22559, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 22559
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1266)
; OTHER INFORMATION: as cited in SEQ ID NO 12338255
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1266)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14304148
; OTHER INFORMATION: as cited in SEQ ID NO 57313
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1266)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598513
; OTHER INFORMATION: as cited in SEQ ID NO 64102
US-11-056-355B-22559

Query Match 18.4%; Score 566.4; DB 9; Length 1266;
Best Local Similarity 70.6%; Pred. No. 1.2e-153;
Matches 786; Conservative 0; Mismatches 321; Indels 7; Gaps 2;

1685 CCGAGACCCAGATGACCCCGACCCAGTCTCGAGCAGCAGGAGCAACCTTTCGGCATGC 1744
92 CCGAGACACAAATAACTCCGGTCAAGTCAACGACGAGAGTGCCTCTTCGGCATGC 151
1745 AGCTGGGAGCGCTCCGTCCTCCCATGGTCTCTAAAGCGCGCATCGAGATCGACCTCC 1804
152 AACTAGCAGTGTCTTCGTTCTTCGATGCTTTAAATCCGCTTTAGAGCTTGACCTTC 211
1805 TCGAGATCATGCGCAAGGACGGCGCGTCTCTTCCACGGGGAAATCGCGGCAC 1864
212 TTGAGATTATGGCCAAAGTGGTTCTCCCATGTCCTTACC-----GAGATCGCTTCTA 265

1865 AGTCCCGACCCAGAACCCGAGGACCCGTCATCTCGACCGGATCTTCGGGTCTGG 1924
266 AACTCCGACCCAAACCCCTGAGCTCCGTCATCTCGACCGTATCTCCGCTCTCTTA 325
1925 CCAGCTACTCCGTCGTCACTGTCACCCCTCCGCGACCTCCCGATGGCAAGTTCGAGCGC 1984
326 CGTCTTACTCCGTCGTAACTCTGCTCAACCGTAACTTTCCGGTGATGGCGTGTGAACGA 385
1985 TCTACGGCTTAGCGCGGTGTCAGAGTCTTCTGTCAGAAACGAGGACCGGGTCTCCATCG 2044
386 TTTACGGGCTTGGTCCGGTTTTCAGATATTGACCAAGAACCAAGATGGTGTTCATTTG 445
2045 CCGCACTCAACTTGTATGAACACGAGCAAAATCCTCATGAAAGCTGTGTATTAACCTGAAG 2104
446 CTGCTCTTTGCTTATGAACCAAGCAAGTCTCATGAAAGCTGTGTATTAACCTGAAG 505
2105 ATGGGCTTCTTGAAGCGGATCCCAATTCACCAAGGCTACCGGATGACCGGTTCGAGT 2164
506 ATGCAATTTCTTGATGGTGGATTCATTCACCAAGGCTTATGGAATGAGGGGTTCGAGT 565
2165 ATCATGCGACCGACCGCGATTCACCAAGATCTTTAAACCGGGGAATGTCTGATCACTCCA 2224
566 ACCACGGGACTGACCTTAGATTCACCAAGTCTTTAAACCAATGATGTCTAACCAATCCA 625
2225 CCATTACTATGAAGAAGATACCTGAAACATACAAAGGCTTCGAGGCTTCGACCGCTGG 2284
626 CAATCACCATGAAGAAGATTTCTGAGACCTATAAGGGTTTTTGAAGGATTCGATCTTTTGG 685
2285 TCGATGTCGAGGCGGCACTGGGCGCGTCTCAGCATGATCGTTGCCAAATACCCATCAA 2344
686 TTGATGTTGGTGGTGGCATTTGGTCTACCTCACTCAAAATGATGTCTCAAGTACCTTAATC 745
2345 TGAAGGATCAACTTTCGACCGCCC-CAACGAGTTGAAGACGCGCCCAACCCCTTCCTGTTG 2403
746 TTAAGGCAATCACTTTGATCTCCACATGTCATTGAAGATGCTCTCTTCATCTCGGTA 805
2404 TCAAGCAGTCGAGGCGACATGTTGTCAGCGTTCCAAAGGAGATGCCATTTTCATGA 2463
806 TTGAGCATTTGGAGGAGATGATTTGTAAGTGTCCTTAAAGGTGATGCCATATTCATGA 865
2464 AGTGATATGCCATGACTGGAGTGACGACCACTTCGGGAAAGTTCCTCAAGAACTGCTACG 2523
866 AGTGATATGTCATGACTGGAGTGACGAACTTCGGTGAATTTCTGAAAAAAGTCTACG 925
2524 ATGCGCTTCCCAACAAATGGAAGGATCGTTGACAGTGGTCTACTCCCTGTGTACCCAG 2583
926 AGTCACTTCCAGAGGATGGAAGGATGATTTAGCAGAGTGTATCTTCCAGAGACCCAG 985
2584 ACACGAGCCTAGCGACCAAGATGTGATCCATCGACTCATGTCATGTTGGCCCAACACC 2643
986 ACTCAAGCCTCTCAACCAACAAAGTAGTCCATGTCGATTGATTTGTTGGCTCAACAATC 1045
2644 CAGCGGGAAAGAGAGGACACAGAAAGGATTCGAGGCAATGGCCAAAGGGCGGATTTTC 2703
1046 CCGAGGCAAGAAACGAAACCGAGAAAGAGTTTGAAGGCAATAGCCAAAGATCAGGCTTCA 1105
2704 AGGGCTTCCAAAGTCATGCTCGCTTCGGGCTTCAGCTACAGTCAAGTGTCTTGAAGACCG 2763
1106 AGGCAATCAAGTGTCTCGGACGCTTTTGGTGTAACTTATGAGTTACTCAAGAGC 1165
2764 CTTGATCTGCTCTCTGTGGTGATGTTTCATGGTT 2797
1166 TCTAATAACAAACAATGTTCTTATGAAGATGATT 1199

RESULT 5
US-10-953-349-3948
; Sequence 3948, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al
; TITLE OF INVENTION: SEQUENCES-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY

FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953.349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3948
LENGTH: 1394
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-953-349-3948

Query Match 18.4%; Score 564.8; DB 6; Length 1394;
Best Local Similarity 70.5%; Pred. No. 3.6e-153;
Matches 785; Conservative 0; Mismatches 322; Indels 7; Gaps 2;

1685 CCAGACCCAGATGACCCCGACCCAGTCTCGGACGAGGCGGAACCTCTTCGCCATGC 1744
134 CAGAGACACAATTAACATCCCGGTGCAAGTCCAGGACGAGCTGCCCTCTTCGCCATGC 193

1745 AGCTGGGAGCGCTCCCGTCTCCCATGTCTCTAAAGGCGCCATCGAGATCGACCTCC 1804
194 AACTAGGCAATGCTTCGGTCTTCGGATGGCTTTAAATCGGCTTAGAGCTTGACCTTC 253

1805 TCAGATCATGGCCAGGACGCGGCGCGGTCTCTCCACGCGGGAATCGCGCAC 1864
254 TTGAGATTATGGCCAGAAATGTTCTCCCATGTCTCTACC-----GAGATCGCTCTA 307

1865 AGCTCCGACGACGACCCGAGGACCGGTCTGATGCTCGACGCGATCTTCGGGTGGTG 1924
308 AACTTCGACGACAAATTCCTGAAGTCCGGTCTGATGCTCGACCGGTATCTCCGTCTTCTA 367

1925 CCAGTACTCCGCTCAGCTGACCTCCGCGACCTCCCGATGCGAAGTGGAGCGGC 1984
368 CGTCTTACTCCGCTTAACTGCTTCAACCGTAACTTTCGGTGATGGGTGAACGGA 427

1985 TCTACGCTTATAGCGCGGTGTCAAGTCTTGTGTCAAGACGAGGAGCGGTCTCCATCG 2044
428 TTTACGGGCTTGTGTCGGTGTCAAGTATTGACCAAGACGAGATGGTGTTCATTG 487

2045 CCGCACTCAATGATGAACGAGACAAATCTCTATGGAAGAGTGTGTATACCTGAAG 2104
488 CTGCTCTTGTCTTATGAACCAAGACAAAGTCTCTATGGAAGAGTGTGTATACCTGAAG 547

2105 ATCGGCTCTTGAAGCGGATCCATTCACAGGCGTACGAGTACCGCGTTCAGT 2164
548 ATGCAATCTTGTGTTGGATTCATTCACAGGCGTATGGAATGAGCGGTTCAGT 607

2165 ATCATGCGACCGCCCGGATTCACCAAGATCTTTAACCGGGGAATCTCTGATCACTCCA 2224
508 ACCAGGGAATGACCTTAGATTCACCAAGGTCTTTACATGGAATGTTTACCAATCCA 667

2225 CCATTATATGAAGAGATCTGGAACATACAGGCGTTCGAGGCGCTCGAGACCGTGG 2284
668 CAATCACCATGAAGAGATCTTGAGACCTATAGGGTCTTGAAGGATGACCTCTTTGG 727

2285 TCGATGTCGAGGCGGACCTGGGCGGTCTGATGATGCTGCAATGATGCTGCAATGATCA 2344
728 TTGATGTTGGTGGGATGTTGCTACCTCAAAATGATGTTCTCAAGTACCTTAATC 787

2345 TGAAGGGAATCACTTCGACCGCC-CAACGGAATGAAGACGCGCCACCCCTCTCTGGTG 2403
788 TTAAGGCAATCACTTTGATCTCCACATGATCGAAGATGCTCTCTCATCTGTA 847

2404 TCAAGCAGCTGGAGGCGACATGTTGTCAGCTGTTCAAGGGGAGATGCCATTTTCA 2463
848 TTGAGCATGTTGGAGGAGATGTTGTAAGTGTCCCTAAAGGTGATGCCATATTCATGA 907

2464 AGTGGATGCGCATGATGAGTGAACCAATTCGCGGAAGTCTCAAGACCTGCTACG 2523
908 AGTGGATGATGATGATGAGTGAACCAATTCGCGGAAGTCTCAAGACCTGCTACG 967

2524 ATGCGCTTCCCAACATGGAAGGTGATGTTGAGAGTGTGCTCTCCCTGTGTACCCAG 2583

968 AGTCACTTCCAGAGGATGGAAGTGTATATTAGCAGAGTGTATATTCCAGAGACACAG 1027

2584 ACAGAGAGCTAGCGACCAAGAAATGTGATCCACATCGACTGCATCATGTTGGGCCCAAC 2643

1028 ACTAAGCCTCTCAACCAACAAAGTAGTCAATGTCGATTGCAATGTTGGCTCACATC 1087

2644 CAGGCGGAAAGAGAGGACACAGAGGAGTTCGAGCATTTGGCCAAAGGGCGGATTC 2703

1088 CCGAGGCAAGAAAGAACGACGAGAAAGAGTTTGAGGCAATTAGCCAAAGCATCAGGCTTCA 1147

2704 AGGGCTTCAAGTCAATGCTGCGCTTTCGGCACTCAGCTCATGAGGTTCTTCAAGACCG 2763

1148 AGGGCATCAAGTGTCTGCGCGCTTTGGTGTAACTTATTGAGTTACTCAAGAAGC 1207

2764 CTGTGATCTGCTCTGCTGTGTGATGTTTCATGTT 2797

1208 TCTAAACCAACATGTTCTTATGAAGATGATT 1241

RESULT 6
US-11-174-307B-2145
; Sequence 2145, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2145
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1394)
; OTHER INFORMATION: Ceres cdna ID no. 13491017
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1394)
; OTHER INFORMATION: Ceres CLONE ID no. 253173
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1394)
; OTHER INFORMATION: Also known as Ceres CDNA ID no. 23370749
US-11-174-307B-2145

Query Match 18.4%; Score 564.8; DB 9; Length 1394;
Best Local Similarity 70.5%; Pred. No. 3.6e-153;
Matches 785; Conservative 0; Mismatches 322; Indels 7; Gaps 2;

1685 CCAGACCCAGATGACCCCGACCCAGTCTCGGACGAGGCGGAACCTCTTCGCCATGC 1744
134 CAGAGACACAATTAATCTCCGTTGCAAGTCAACGACGAGGCTGCCCTCTTCGCCATGC 193

1745 AGCTGGGAGCGCTCCCGTCTCCCATGTCTCTAAAGGCGCCATCGAGATCGACCTCC 1804
194 AACTAGGCAATGCTTCGGTCTTCGGATGGCTTTAAATCGGCTTAGAGCTTGACCTTC 253

1805 TCAGATCATGGCCAGGACGCGGCGCGGTCTCTCCACGCGGGAATCGCGCAC 1864
254 TTGAGATTATGGCCAGAAATGTTCTCCCATGTCTCTACC-----GAGATCGCTCTA 307

1925 CCAGTACTCCGCTCAGCTGACCTCCGCGACCTCCCGATGCGAAGTGGAGCGGC 1984
368 CGTCTTACTCCGCTTAACTGCTTCAACCGTAACTTTCGGTGATGGGTGAACGGA 427

1985 TCTACGCTTATAGCGCGGTGTCAAGTCTTGTGTCAAGACGAGGAGCGGTCTCCATCG 2044
428 TTTACGGGCTTGTGTCGGTGTCAAGTATTGACCAAGACGAGATGGTGTTCATTG 487

2045 CCGCACTCAATGATGAACGAGACAAATCTCTATGGAAGAGTGTGTATACCTGAAG 2104
488 CTGCTCTTGTCTTATGAACCAAGACAAAGTCTCTATGGAAGAGTGTGTATACCTGAAG 547

2105 ATCGGCTCTTGAAGCGGATCCATTCACAGGCGTACGAGTACCGCGTTCAGT 2164
548 ATGCAATCTTGTGTTGGATTCATTCACAGGCGTATGGAATGAGCGGTTCAGT 607

2165 ATCATGCGACCGCCCGGATTCACCAAGATCTTTAACCGGGGAATCTCTGATCACTCCA 2224
508 ACCAGGGAATGACCTTAGATTCACCAAGGTCTTTACATGGAATGTTTACCAATCCA 667

2225 CCATTATATGAAGAGATCTGGAACATACAGGCGTTCGAGGCGCTCGAGACCGTGG 2284
668 CAATCACCATGAAGAGATCTTGAGACCTATAGGGTCTTGAAGGATGACCTCTTTGG 727

2285 TCGATGTCGAGGCGGACCTGGGCGGTCTGATGATGCTGCAATGATGCTGCAATGATCA 2344
728 TTGATGTTGGTGGGATGTTGCTACCTCAAAATGATGTTCTCAAGTACCTTAATC 787

2345 TGAAGGGAATCACTTCGACCGCC-CAACGGAATGAAGACGCGCCACCCCTCTCTGGTG 2403
788 TTAAGGCAATCACTTTGATCTCCACATGATCGAAGATGCTCTCTCATCTGTA 847

2404 TCAAGCAGCTGGAGGCGACATGTTGTCAGCTGTTCAAGGGGAGATGCCATTTTCA 2463
848 TTGAGCATGTTGGAGGAGATGTTGTAAGTGTCCCTAAAGGTGATGCCATATTCATGA 907

2464 AGTGGATGCGCATGATGAGTGAACCAATTCGCGGAAGTCTCAAGACCTGCTACG 2523
908 AGTGGATGATGATGATGAGTGAACCAATTCGCGGAAGTCTCAAGACCTGCTACG 967

2524 ATGCGCTTCCCAACATGGAAGGTGATGTTGAGAGTGTGCTCTCCCTGTGTACCCAG 2583

308 AACTTCGACCAAAATCTGAAGTCCGGTCAATGCTCGACCGTATCTCCGTCTCTTA 367
1925 CCAGCTACTCCGTGCTCAGTGCACCTCCGACCTCCCGATGGCAAGTTCGAGCGC 1984
368 CGTCTTACTCCGTCTTAACCTGCTCCACCGTAAACTTTCCGGTATGGCGTTGACCGA 427
1985 TCTACGGCTTAGCGCGGTGTCAAGTCTTGGTCAAGAACGAGGACGGGTCTCCATCG 2044
428 TTATCGGGCTTGTCCGGTTTGCAGTATTTGACCAAGAACGAGATGGTGTTCATTTG 487
2045 CCGCACTCAACTTGTATGAACCAAGGACAAATCTCTATGAAAGCTGGTATACCTGAAG 2104
488 CTGCTCTTGTCTTATGAACCAAGGATTTCTCATGGAAGCTGGTACCAATTTGAAG 547
2105 ATGGGCTTCTGAAGCGGATCCCAATCAAGAGGCTTCAAGGATGACCGGTTTCGAGT 2164
548 ATGCAATTTCTTGTATGGTGGGATTTCCATTTCAACAGGCTTATGGAATGAGCGGTTG 607
2165 ATCATGGCACCGACCCCGGATTCAAAGATCTTTAAACCGGGAATGTCTGATCACTCA 2224
608 ACCAGGGATCTGACCTTAGATTCAAAGAGTCTTTAAACATGGAATGTCTAACCAATTC 667
2225 CCATTAATGAGAGATGACTGGAACATACAGGCTTCGAGGCTTCGAGACCGTGG 2284
668 CAATCAGCATGAGAGATTTCTTGAACCTTATAGGCTTTTGAAGGATGACTTCTTTGG 727
2285 TCGATGTCGAGGCGGACCTGGGCGCTGCTCAGCATGATCGTTGCCAATACCCATCA 2344
728 TTGATGTTGGTGGGATTTGCTGCTACACTCAAAATGATTTCTCAAGTACCTTAATC 787
2345 TGAAGGATCAACTTCGACCGCCC - CAACGGATTTGAAGAGCGCCACCCCTTCCTGGTG 2403
788 TTAAGGATCAACTTTGATCTCCACATGTCATCGAAGATGCTCTCTCATCTCGGTA 847
2404 TCAAGCAGCTCGGAGGCGACATGTTGTCAGCGTTCCAAAGGAGATGCCATTTTCATGA 2463
848 TTGAGCATGTTGGAGGAGATATGTTGTAAGTGTCCTTAAGTGATGCCATTTTCATGA 907
2464 AGTGATATGCTGACTGAGTGAACGACCAATTCGCGGAAGTTCCCTCAAGATGCTACG 2523
908 AGTGATATGCTGACTGAGTGAACGACCAATTCGCGTAAATTTCTGAAGAACTGCTACG 967
2524 ATGCGCTTCCCAACATGAGGATGATCGTTGACAGTGGTACTCCCTGTGACCCAG 2583
968 AGTCACTTCCAGAGGATGGAAGATGATTTAGAGTGCCTTAAGTGATGCCATTTTCATGA 1027
2584 ACACGAGCTAGCGACCAAGATGTGATCCACATGCTGATCATGATGTTGGCCCAAC 2643
1028 ACTCAAGCTCTCAACCAACAAAGTAGTCCATGTCGATTTGATGATTTGGCTCACAATC 1087
2644 CAGCGGGAAAGAGAGACAGAGAGGATTCGAGGCAATTCGCCAAGGGCGCGATTC 2703
1088 CCGAGGCAAGAAACGACCGGAAAGAGTTTGAAGCATTTAGCCAAAGCATCAGGCTTCA 1147
2704 AGGCTTCAAGTCAATGCTGCTCGCTTCGCGCACTCAGTCAATGAGTTCCTGAAGACCG 2763
1148 AGGCGATCAAGTGTGCTCGACGCTTTTGGTGTAACTTATGAGTTACTCAAGAGC 1207
2764 CTGATCTGCTCTCTGTGGTGTGATGTTTCATGGTT 2797
1208 TCTAAAACAAACAAATGTTTCTTGAAGATGATT 1241

RESULT 7
US-11-056-355B-36626
; Sequence 36626, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 36626
LENGTH: 1394
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1394)
OTHER INFORMATION: Ceres Seq. ID no. 13491017
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(1394)
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 14304148
OTHER INFORMATION: as cited in SEQ ID NO 57313
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1394)
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13598513
OTHER INFORMATION: as cited in SEQ ID NO 64102
US-11-056-355B-36626

Query Match 18.4%; Score 564.8; DB 9; Length 1394;
Best Local Similarity 70.5%; Pred. No. 3.6e-153;
Matches 785; Conservative 0; Mismatches 322; Indels 7; Gaps 2;
QY 1685 CCGAGACCCAGATGACCCCGACCCAGTCTCGGACGAGGAGGAACTCTTGCCCATGC 1744
Db 134 CAGAGACAAATTAATCCGGTCAAGTCAACCGACGAGAGCTGCCCTCTTCCGCATGC 193
QY 1745 AGCTGGGAGCGCTCCGTGCTCCCATGGTCTTAAAGGCCGCGCATCGAGATCGACCTCC 1804
Db 194 AACTAGCAGTGTCTCCGTCTTTCGATGGCTTTAAATCGCTTAGAGCTTGACCTTC 253
QY 1805 TCGAGATCATGCCAAGGACGGGCGGGCGGCTCTCTCCACGGGGAAATCGGGCAC 1864
Db 254 TTGAGATTTATGCCAAGAAATGTTCTCCCATGTCTCTTACC-----GAGATCGCTCTA 307
QY 1865 AGCTCCGACCCAGAACCCCGACCCGACCCGTCATGCTCGACGGATCTTCGGGTGTCTGG 1924
Db 308 AACTTCGACCAAAATCTGAAAGTCCGGTCAAGTCTCGACGCTATCTCCGTCTCTTA 367
QY 1925 CCAGCTACTCCGTCTCAGTGCACCTCCCGCACCTCCCGATGGCAAGTTCGAGCGC 1984
Db 368 CGTCTTACTCCGTCTTAACCTGCTCAACCGTAAACTTTCCGGTGTATGGCGTTGAACGGA 427
QY 1985 TCTACGGCTTAGCGCGGTGTCAAGTCTTGGTCAAGAACGAGGACGGGTCTCCATCG 2044
Db 428 TTATCGGGCTTGTTCGGTTCGAAATTTGACCAAGGCTTATGGAATGAGCGGTTGAGT 487
QY 2045 CCGCACTCAACTTGTATGAACCAAGGACAAATCTCATGGAAGCTGGTATACCTGAAAG 2104
Db 488 CTGCTCTTGTCTTATGAACCAAGGATTTCTCATGGAAGCTGGTACCAATTTGAAG 547
QY 2105 ATCGGCTCTTGAAGCGGAATCCCAATTCAAAGCGTACGGATGACCGGTTGAGT 2164
Db 548 ATGCAATTTCTGATGGTGGATTTCCATTCAAAGGCTTATGGAATGAGCGGTTGAGT 607
QY 2165 ATCATGGCACCGGACCGGATTCAAAGATCTTTAAACCGGGGAATGTCTGATCACTCA 2224
Db 608 ACCAGGGACTGACCTTAGATTCAAAGGCTTTCGAGACCTTAAAGGTTTGAAGGATTTG 667
QY 2225 CCATTAATGAGAGATGACTGGAACATACAGGCTTCGAGGCTTCGAGACCGTGG 2284
Db 668 CAATCAGCATGAGAGATTTCTTGAACCTTATAGGCTTTTGAAGGATTTGACTTCTTTGG 727
QY 2285 TCGATGTCGAGGCGGACCTGGGCGGCTGCTCAGCATGATCGTTGCCAATACCCATCA 2344
Db 728 TTGATGTTGGTGGGATTTGCTGCTACACTCAAAATGATTTCTCAAGTACCTTAATC 787


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QY 1877 A---GAACCCGAGGACCCGTCATCTCGACCGGATCTTCGGCGTCTGGCCAGTACT 1933
Db 297 AGCGGAACCCGGCGGCGGACATGGTGACCGCATGCTCCGCTCTGCTCGCTCTCTACA 356
QY 1934 CCGTGTCTCAGTGCACCCCTCCGCGACCTCCCGATGCGAAGGTTCGAGCGGCTCTACGGCT 1993
Db 357 ACCTCTCAGTTCGAGATGGAGAGGGCGCGACGCAAGCTCTCCGCGCTACGCCG 416
QY 1994 TAGCGCGGTGTCAAGTCTTGGTCAAGAACGAGGACGGGTCTCCATCGCGCACTCA 2053
Db 417 CCGCGCGGTGTCAAGTGTGACGCCCAACGAGGACGGGTCTCCATGGCGCGCTCG 476
QY 2054 ACTTGATGAACACGAGCAAAATCTCATGGAAGCTGTATTACCTGAAAGATCGGCTCC 2113
Db 477 CCCTCATGAACACGAGCAAGGTCTCATGAGAGCTGGTACTACCTTAAGGACGAGTCC 536
QY 2114 TTGAAGCGCGAATCCCAITTCACAAAGCGGTACGCGGTTCGAGTATCATGGCA 2173
Db 537 TGGACCGCGCATCCCGTTCAACAAGCGGTACGCGGTTCGAGTACCAACGGCA 596
QY 2174 CGACCCGCGATTCACAGATCTTTAAACGGGGATGTCTGATCACTCAACCATTTACTA 2233
Db 597 CGGACCGCGCTTCAACCGCGTCTTCAACGAGGCGCATGAAGAACCACTCCGTCAATCA 656
QY 2234 TGAAGAGATACCTGGAACAATACAAAGGCTTCGAGGCGCTCGAGACCGGTGCGATGTCG 2293
Db 657 CCAAGAAGCTGCTCGACCTCTACCGCGCTTCACCGCGCTTCACCGCGGTGAGCGTGG 716
QY 2294 GAGCGCGCACTGGGCGCGTCTCAGATGATCGTTCGCAAAATACCCATCAATGAAGGGA 2353
Db 717 GCGCGCGGTGGGCGCACTGTGGCGCGCTCTCTCCGCGCACCGCACATCCGGGGGA 776
QY 2354 TCAACTTCGACCGCCCAAGC-GATTGAAGACGCCCAACCCCTTCTCTGTGTCAAGACG 2412
Db 777 TCAACTACGACCTCCCGCACTCATCTCCGAGGCGCGCGTTCGCCGCGGTGGAGCAG 836
QY 2413 TCGGAGCGCATGTTGTCAGGTTC---AAAGGAGATGCCATTTTCATGAAGTGA 2469
Db 837 TCGGCGCGCATGTTGCTGCTGCTGCGCGCGCGCGCGCGCATCTCTGATGAAGTGA 896
QY 2470 TATGCGCATGCTGAGTGACGACCATTTGCGCGAAGTTCCTCAAGAACTGTCTAGATGCGC 2529
Db 897 TCCTCAAGACTGGAGCGACGACATGCGCGCGGTGCTCAAGAACTGTCTAGACGCGC 956
QY 2530 TTCCCAACAATGAAGAGTGATCGTTGACAGATGCGTATCTCTCTGTGTACCCAGACGA 2589
Db 957 TGGCGGAGCACGGGAAGTGGTGTGTGAGTGCCTGTGCGGAGAGCTCCGACGCGGA 1016
QY 2590 GCCTAGCGACCAAGATGTGATCCATCGACTGCATCATGTTGGCCCAACCCAGGCG 2649
Db 1017 CGGCGAGGAGCGGGGGTGTTCACGTGCATGATGATCATGCTCGGCCCAACCCCGGCG 1076
QY 2650 GGAAGAGAGACACAGAAGAGTTCGAGGCATTTGGCCAAAGGGCGCGGATTTTCAGGGCT 2709
Db 1077 GCAAGGAGAGTACGAGAGGAGTTCAGGAGCTTCGCGCGCGCGCGCGGATTCACCGGCT 1136
QY 2710 TCCAAGTCATGTGTCGCGCTTCGCGCACTCAGCTCATGGAGTTCCTGAAG 2759
Db 1137 TCAAGGCCACCTATCATCTACGCCAACCGCTGGGCCATCGAGTTCAACAAG 1186
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RESULT 10

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US-11-056-355B-5836
; Sequence 5836, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
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; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 5836
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1522)
; OTHER INFORMATION: Ceres Seq. ID no. 12369443
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1522)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14304148
; OTHER INFORMATION: as cited in SEQ ID NO 57313
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1522)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598513
; OTHER INFORMATION: as cited in SEQ ID NO 64102
US-11-056-355B-5836
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Query Match 13.7%; Score 419.6; DB 9; Length 1522;

Best Local Similarity 64.7%; Pred. No. 6.3e-111;

Matches 694; Conservative 0; Mismatches 359; Indels 19; Gaps 4;

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QY 1704 GACCAAGTCTCGAGCGAGCGGAACTCTTCCGCCATGAGCTGGCGAGCGCTCCGT 1763
Db 143 GCGCGGTGTGGACGAGGAGCGTGCATGTACGCGATGCGCTGGCGTCTCGTCCAT 202
QY 1764 GTTCCCATGCTTAAAGCGCGCATCGAGATCACCTCTCGAGATCATGCCAAGGA 1823
Db 203 CTGCCCCATGACGTGAAGAACGCCATCGAGCTGGGCTCTGAGAGTCTCTCAAGAAG 262
QY 1824 CGGCGCGGCG-----GGTTCCTCTCCACGGGGGAAATCGCGGCACAGCTCCCGAC--- 1874
Db 263 GCGCGCGCGCGCAAGGCGCGCTGGCGCCCGAGAGGTGGTGGCGGATGCCCGCGC 322
QY 1875 -----CCAGAACCCCGAGGACCGCTCATGCTCGACCGGATCTTCGGGCTCTGGCCAG 1928
Db 323 GCGCGCGGACCGCGCGCGCGCATGTGTGACCGCATGCTCCGCTCTCGCCTC 382
QY 1929 CTACTCCGTGCTCAGTGCACCTCGGACCTCCCGATGCGAAGTTCGAGCGCTCTA 1988
Db 383 CTACGACGTGCTCCGGT---CCAGATGAGACCGGACCGCGGTACGAGCGCGCTA 439
QY 1989 CGGCTTAGCGCGCGGTGTCAAGTCTTGGTCAAGAACGAGGACGGGCTCTCCATCGCGC 2048
Db 440 CTCGCGCGCGCGCTGCAAGTGGCTCACCCCAACGAGGACGGCTGTCATGCGCGC 499
QY 2049 ACTCAATTGATGAACCGAGCAAAATCTCATGAAAGCTGGTATTACTGAAGATGC 2108
Db 500 CCTCGCGCTCATGAACACGAGCAAGTCTCTCATGAGAGCTGGTACTATCTCAAGGACGC 559
QY 2109 GGTCTTGAAGCGGAAATCCCATTCAAAGCGGTACGGGATGACCGCTTCGAGTATCA 2168
Db 560 GGTGTGGAAGCGCGCATCCCGTTCAACAAAGCGGTACGGGATGACGGCGTTCGAGTACCA 619
QY 2169 TGGCACCGACCGCGGATTCACAAAGATCTTTAAACGGGGAAATGTCTGATCACTCCACCAT 2228
Db 620 CGGACGGAATCGCGCTTCAACCGCGTGTTCACGAGGGCATGAAGAACCACTCGGTGAT 679
QY 2229 TACTATGAAGAAGATATCTGAAACATACAAAGGGCTTCGAGGGCTTCGAGACCGTGTGCA 2288
Db 680 CATCAACCAAGAGTGTCTGACTTCTACACGGGCTTCGAGGGCGTGTGACGCTGTGGA 739
QY 2289 TGTGAGGCGGCACTGGGGCGCTGCTCAGCATGATCGTTGCAAAATACCCATCAATGA 2348
Db 740 CGTGGCGCGCGGTGGGCGCCACGCTGCACGCCATCACGTCCCGCCACCCGACATCTC 799
QY 2349 AGGATCAACTTCGACC-GCCCCAACGGATTGAAGACGCGCCACCCACCCCTTCTCTGGTCA 2407
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[illegible]

RESULT 11

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US-10-449-902-4559
; Sequence 4559, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCES: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIORITY APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIORITY APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4559
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK061859
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-4559

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	Query Match	13.6%	Score 418;	DB 6;	Length 1227;
	Best Local Similarity	67.4%;	Pred. No. 1.6e-110;		
	Matches 635;	Conservative 0;	Mismatches 300;	Indels 7;	Gaps 3;
Qy	1825	GGGCGGGCGTTCCTCTCACGGGGGAAATCGCGCACAGTCCCGACCCCA--CAAC	1881		
Db	43	GGGAGCGGCGTGTCTGACGCCCGCGAGGTGGCCGACAGCTGCCGTCTCAGGCGAAC	102		
Qy	1882	CCCGAGCACCCCGTCACTGCTCGACCCGATCTTCGGGTGTGGCCAGCTACTCCGTGCTC	1941		
Db	103	CCGCGCGCGCCACATGTTGGACCGCATGTCTCGCTGTCTGCGCTCTCTACCAAGTCTGTC	162		
Qy	1942	ACGTGCACCTTCGCGACCTTCCCCGATGGCAAGTTCAGCGGCTCTACGGCTTTAGCGCCG	2001		
Db	163	AGTTCGAGATGGAGGAGGCGCGGACGCGCAAGCTCTCCGCGCGCTACGCGCGCGCGCG	222		
Qy	2002	GTGTGCAAGTTCTTGGTCAAGAACGAGACGGGGTCTTCCATCGCGCGACCTCAACTTGATG	2061		

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; TYPE: DNA
; ORGANISM: Vanilla planifolia
US-10-532-464-1

Query Match      13.2%; Score 404; DB 6; Length 1219;
Best Local Similarity 59.5%; Pred. No. 1.9e-106; Indels 1; Gaps 1;
Matches 700; Conservative 0; Mismatches 475;

QY 1706 CCAAGTCTCGACGACGAGGCGAACTCTTGGCCATGACGTGGCGAGCGCTCCGTGC 1765
DB 44 CCAAGACGTGGACGAGGAGCGTGCATGTACGCCATGAGTGTGCGAGCATGGTCTGCC 103
QY 1766 TCCCATGTCCTAAAGCGCGCATCGAGATGACCTCTCGAGATCATGCGCAAGGACG 1825
DB 104 TCCGATGACGCTTAGGCTAGCGCTCGAGCTCGGCATCTCGAACAAATCCAGGCGGGG 163
QY 1826 GCGCGGGCGGTCTCTCCACGGGGGAATCGCGCACAGTCCCGACCCAGAACCCCG 1885
DB 164 GCCAGATTCTGTACTTACTGCGGAGGATTTGGCGGAGGCTCGGCACTCCNACCCCT 223
QY 1886 AGGCACCGCTCATGCTCGACCGGATCTTCGGGTGCTGGCCAGCTACTCGGTCTCACGT 1945
DB 224 TAGCTCGGTTCATGATCGAGCGATCTCGGCTGTCTCACAGCTACTCCATCTTAACT 283
QY 1946 GCACCTTCGGGACCTCCCGATGGGAGTTCGAGCGGCTCTACGCTTAGCGCGGTCT 2005
DB 284 TCACCGACACCGTTCGACGGGAGGCTAGGACCGTTCGGAGCTACGGCGGCGCATGTCT 343
QY 2006 GCAATGTTCTTGGTCAAGAACGAGACGGGTCTCCATCGCGGCACTCAACTTGATGAAC 2065
DB 344 GCAAGTACCTGACTCCCAACGAGACGGCTCTCCATGGCGCTCTCGTCTCATGAACA 403
QY 2066 AGGACAAATCTCATGAAAGTGTGTTATCTGTGAAGATCGGTCTTGAAGCGGAA 2125
DB 404 CGGATAAGTCTTATGGAGAGCTGTGTAACACATGAAGGATGAGTACAAATGGTGGAA 463
QY 2126 TCCATTCAACAGCGCTACGGGATGACCGGTTCGAGTATCATGACCGGACCGCGAT 2185
DB 464 TACCATTCATCTAGCATATGGGATGACGCTTTGAGTATCATGGGAAGATCTAAGT 523
QY 2186 TCAACAGATCTTTAAACGGGGAATGTCTGATCACTCCACCATTTACTATGAAGAATAC 2245
DB 524 TTAATAGGTCTTCAACGAGGCGATGAAGAACACTCGATCATTTATAACGAAGATTT 583
QY 2246 TGGAAACATACAGGGCTTCAGGCGCTCGAGACCGTGTGTCATGTCGGAGCGGCACTG 2305
DB 584 TAGAGAGATACAAAGGTTTGAAGATGTCAATGTTTAAATGATGTTGGTGGTGAATG 643
QY 2306 GGGCGTCTCAGCATGATCGTTCCAAATACCCATCAATGAAGGATCAACTTCGACC 2365
DB 644 GTGGAACCTATCAGTATGATTAAGTGAAGTATCCATATACATGAGATTAATTTGACC 703
QY 2366 -GCCCCAAACGGATGAAGACGCCACCCCTTCCTGTTGTCAAGCACGTGGAGGCGACA 2424
DB 704 TTCCTCATGTTCTTCTGAAGCTCCACCTTTCCAAAGGGGTAGAACATGTGGTGGAAACA 763
QY 2425 TGTTCGTGAGGCTTCCAAAGGAGATGCCATTTTCAAGATGATGATGATGATGATGATG 2484
DB 764 GTTTTGAAGTGTCCCGCATGTTGATGCAATCTTTATAAAGTGAATCTTCATGATGGA 823
QY 2485 GTGACGACATTTGCGGAGGATTTCTTCAAGAACTGTACGATGCGCTTCCCAACAAATGAA 2544
DB 824 GTGATGAGCATTTGTTGAAGTCTTGAAGATTTGCAAAATTTGCAAAATCTTTACCTGACAAAGAA 883
QY 2545 AGGTGATCGTTGACAGAGTGGTACTCTCTGTGTATCCAGACACGAGCTTACGACCAAGA 2604
DB 884 AAGTCATAGTTGTGAAATGCAATCTTCCCGATGACCTTTGTTGTCGACGAGAGTGAAG 943
QY 2605 ATGTGATCCACATGCACTGCATGATGTTGGCCCAACACCGAGGCGGGAAGAGAGGACAC 2664
DB 944 GTGTCTTTTATTTGGACATGATTAATGTTGGCTTCAATCTTGGGGGAAGAGAGAACAA 1003
QY 2665 AGAAGGAGTTTCGAGGCAATTTGGCCAAAGGGCGCGGATTTTCAGGGCTTCCAAATCATGTGCT 2724

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RESULT 13
US-11-056-355B-5315
; Sequence 5315, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 5315
; LENGTH: 1531
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: Ceres Seq. ID no. 12435048
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: Ortholog of Ceres Seq. ID NO 14304148
; OTHER INFORMATION: as cited in SEQ ID NO 57313
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: Ortholog of Ceres Seq. ID NO 13598513
; OTHER INFORMATION: as cited in SEQ ID NO 64102
US-11-056-355B-5315

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Query Match      13.0%; Score 398.2; DB 9; Length 1531;
Best Local Similarity 64.2%; Pred. No. 1.1e-104;
Matches 688; Conservative 0; Mismatches 358; Indels 25; Gaps 5;

QY 1704 GACCCAAAGTCTCGGACGACGAGCGGAACTCTTGGCCATGACGTGGCGAGCGCTCCGT 1763
DB 141 GCGCGCGGTGGTGGACGAGGAGCGGTGATGTACGCGATGCGAGTGGCGTCTCGTCCAT 200
QY 1764 GCTCCCATGTTCTTAAGCGCGCATCGAGATCGACCTCTCGAGATCATGGCCAAAGGA 1823
DB 201 CCT-----GCCCTGAAGAACGCCATCGATGGCCCTGCTGGAGGTCTCGAGAGGA 253
QY 1824 CG-----GGCGGGCGCGTCTCTCTCCACGGGGGAAATCGGCGACAGCTCCGAC 1875
DB 254 GGCGGGCGGGCAAGCGCGGTGGCGGAGGAGTGGTGGCGGATGCCCGGGG 313
QY 1876 CAGAACCCGAGGACCCCGT-----ATGCTCGACCGATCTTCCGGCTGTGGCCAGC 1929
DB 314 CCAGAGGACCCCGCGCGCGCGNCAATGGTGGACCGCATGCTCCGCTCTCGCTCC 373
QY 1930 TACTCGTGTCTACGTGGACACCTCTCCCGGACCTCCCGGATGGCAAGGTCTGAGCGGCTCTAC 1989

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; SEQ ID NO 106
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-106

Query Match      12.7%; Score 391; DB 7; Length 407;
Best Local Similarity 97.5%; Pred. No. 5.5e-103;
Matches 397; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1601 CCGTTTATTTCCTCTGCTTTCTTTCGAGTCTCGGGAAGAGAGAGAGAGAGAG 1660
Db      |||||||
Qy 1661 AGGAGAGAATGGGTTCGACCCGGCTCCGAGACCCAGATGACCCCGACCCCAAGTCTCGGACG 1720
Db      |||||||
Qy 1721 ACAGGCGAACCTTTCGCCATGCGCTGGGAGCGCCTCCGTGCTCCCATGGTCTCTAA 1780
Db      |||||||
Qy 181 AGGAGCGAACCTTTCGCCATGCGCTGGGAGCGCCTCCGTGCTCCCATGGTCTCTCA 180
Db      |||||||
Qy 1781 AGGCGGCATCGAGATCGACCTCTCGAGATCATGSCAAGGACGGGCGGCGCTTCC 1840
Db      |||||||
Qy 181 AGGCGGCATCGAGCTCGACCTCTCGAGATCATGSCAAGGACGGGCGGCGCTTCC 240
Db      |||||||
Qy 1841 TCTCCACGGGGGAATCGCGGCAAGCTCCCGACCCAGAACCCCGAGGACCCCGTCATGC 1900
Db      |||||||
Qy 241 TCTCCCGGGGGAAGTCCGCGCCAGCTCCCGACCCAGAACCCCGAGGACCCCGTAATGC 300
Db      |||||||
Qy 1901 TCGACCGGATCTTCGGGCTGCTGGCCAGCTACTCCGTGCTCAGTGCACTCCCGGACC 1960
Db      |||||||
Qy 301 TCGACCGGATCTTCGGGCTGCTGGCCAGCTACTCCGTGCTCAGTGCACTCCCGGACC 360
Db      |||||||
Qy 1961 TCCCGGATGGCAAGTTCGAGCGGCTCTACGGCTTAGCGCGGTGTGC 2007
Db      |||||||
Qy 361 TCCCGATGGCAAGTTCGAGCGGCTCTACGGCTTAGCGCGGTGTGC 407
Db      |||||||
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Search completed: November 1, 2006, 14:52:51
Job time : 666.818 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:00:22 ; Search time 2754 Seconds
(without alignments)
7772.260 Million cell updates/sec

Title: US-10-702-319A-113

Perfect score: 3070

Sequence: 1 agcaccatcagcaaaaaata.....acttcgacacaaaaaaaaa 3070

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 20

Total number of hits satisfying chosen parameters: 10136

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
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- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3070	100.0	3070	6	ABK17109
2	3070	100.0	3070	10	ADH75529
3	3070	100.0	3070	14	ADH80563
4	1255	40.9	2096	3	AAC62810
5	1255	40.9	2096	6	ABK17075
6	1255	40.9	2096	10	ADH75476
7	1255	40.9	2096	14	ADH80510
8	774	25.2	1630	3	AAA68014
9	774	25.2	1630	10	ADB41764
10	534	17.4	534	13	ADQ88319
11	485	15.8	485	13	ADQ88320
12	306	10.0	306	13	ADQ88321
13	293	9.5	293	13	ADQ88322
14	272	8.9	661	3	AAC62762
15	272	8.9	661	6	ABK17027
16	272	8.9	661	10	ADH75428
17	272	8.9	661	14	ADW80462
18	119	3.9	119	13	ADQ88323

19	111	3.6	407	3	AAA68013	Aaa68013 Eucalyptu
20	111	3.6	407	10	ADD41763	ADD41763 O-methyl
21	111	3.6	421	2	AAV23844	AAV23844 Plant OMT
22	111	3.6	421	2	AAZ06845	Aaz06845 Eucalyptu
23	111	3.6	421	3	AAA69595	Aaa69595 Eucalyptu
24	111	3.6	421	3	AAA67931	Aaa67931 Eucalyptu
25	111	3.6	421	10	ADD41681	ADD41681 O-methyl
26	111	3.6	421	14	AED59781	Aed59781 Eucalyptu
27	98	3.2	98	13	AQ88324	Adq88324 Eucalyptu
28	66	2.1	66	13	AQ88325	Adq88325 Eucalyptu
29	41	1.3	354	5	AAF64869	Aaf64869 Novel hum
30	36	1.2	60	13	ADS53019	Ads53019 Eucalyptu
31	36	1.2	96599	10	ADC85298	Adc85298 Human Egr
32	36	1.2	96599	9	ADA02819	Ada02819 Mouse Sos
33	36	1.2	96600	10	ADB72557	Adb72557 Mouse Sos
34	36	1.2	96600	12	ADM74414	Adm74414 Murine ca
35	36	1.2	123192	13	ADV34995	Adv34995 Murine CD
c	36	1.2	157875	6	ABK99972	Abk99972 Human CAD
37	35	1.1	308	4	AAI82105	Aai82105 Human pol
38	35	1.1	350	4	AAI83240	Aai83240 Human pol
c	35	1.1	353	12	ADP04958	Adp04958 Chinese c
39	35	1.1	356	3	AAA31195	Aaa31195 Plant mic
40	35	1.1	402	3	AAA31117	Aaa31117 Plant mic
41	35	1.1	404	5	AAF64250	Aaf64250 Novel hum
42	35	1.1	529	10	ACC55509	Acc55509 Rice endo
43	35	1.1	537	3	AAA79498	Aaa79498 Eucalyptu
44	35	1.1	1262	13	ADS54768	Ads54768 Bacterial
c	45	1.1				

ALIGNMENTS

RESULT 1

ABK17109

ID ABK17109 standard; cDNA; 3070 BP.

XX AC ABK17109;

XX DT 26-MAR-2002 (first entry)

XX DE Eucalyptus grandis promoter polynucleotide #51.

XX KW Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis;
temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
PCR primer.

XX OS Eucalyptus grandis.

XX PN WO200198485-A1.

XX PD 27-DEC-2001.

XX PF 20-JUN-2001; 2001WO-NZ000115.

XX PR 20-JUN-2000; 2000US-00598401.

XX PR 28-NOV-2000; 2000US-00724624.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PA (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.

XX PI Perera R, Rice S, Eagleton C, Lasham A;

XX XX WPI; 2002-114593/15.

XX XX Novel polynucleotide promoter sequences from Pine and Eucalyptus useful
for modifying expression of endogenous and/or heterologous
polynucleotides in transgenic plants.

XX PS Claim 1; Page 103-104; 121pp; English.

XX CC The invention relates to isolated promoter sequences from Pinus radiata
and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,
flower-, pollen-, bud-, meristem-specific promoters or temporally

CC regulated promoters such as xylogenesis-specific promoters. The promoter
 CC polypeptides and their related polynucleotides are useful in the
 CC production of genetic constructs, used for modifying gene expression in a
 CC target organism, in particular a plant. The method is useful for
 CC modifying expression of a polynucleotide that comprises an intron
 CC sequence, through removal of the intron sequence. The method is useful
 CC for modifying growth and development of plants, and cellular responses to
 CC external stimulus, such as environmental factors and disease pathogens.
 CC The sequences are useful in genome and physical mapping, in positional
 CC cloning of genes, in various assays to determine biological activity, to
 CC raise antibodies, to isolate corresponding interacting proteins and other
 CC compounds, and to quantitatively determine levels of interacting proteins
 CC or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata
 CC and Eucalyptus grandis polynucleotides and PCR primers used in the method
 CC of the invention

XX
 SQ Sequence 3070 BP; 829 A; 718 C; 755 G; 768 T; 0 U; 0 Other;

Query Match 100.0%; Score 3070; DB 6; Length 3070;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGCACCATGACCAAAATAGATGGGATAGGAGTGGGACACCACTCTTCAGTTTGATCC	60
Dd	1	AGCACCATGACCAAAATAGATGGGATAGGAGTGGGACACCACTCTTCAGTTTGATCC	60
Qy	61	CTTGAGATGACCTACAGTACAGTCTTGATGAATAAGATGGGATTAATAGATTACACAGAGG	120
Dd	61	CTTGAGATGACCTACAGTACAGTCTTGATGAATAAGATGGGATTAATAGATTACACAGAGG	120
Qy	121	GATAAAAAGGTAGGGAGATAGGGATCTCCCGTCTGATGCTCGGCTAGGTGGAANA	180
Dd	121	GATAAAAAGGTAGGGAGATAGGGATCTCCCGTCTGATGCTCGGCTAGGTGGAANA	180
Qy	181	AGGCAAAAGTTCGCGCTTGATTTGACAGCAAAAGACACCGTCTGATGCAATGCAATGAT	240
Dd	181	AGGCAAAAGTTCGCGCTTGATTTGACAGCAAAAGACACCGTCTGATGCAATGCAATGAT	240
Qy	241	CCATTGTACCATGTAGGGTGAAATCCTAGAGTGAGGAGATAGTCTTTAGAAAGTCCCA	300
Dd	241	CCATTGTACCATGTAGGGTGAAATCCTAGAGTGAGGAGATAGTCTTTAGAAAGTCCCA	300
Qy	301	TTCCACCCATCATAGGCTTCTGCATATCCATTTTAAAGAACACCGCGAATGACGTCT	360
Dd	301	TTCCACCCATCATAGGCTTCTGCATATCCATTTTAAAGAACACCGCGAATGACGTCT	360
Qy	361	ACATTTTCTGACTTAAATGATGTAGAACCTCTTAGACTATTAAATAATTGCTCTGAAT	420
Dd	361	ACATTTTCTGACTTAAATGATGTAGAACCTCTTAGACTATTAAATAATTGCTCTGAAT	420
Qy	421	TTGACGTCACCTGACAAAGCGCTTGTCTCTGGAAATAGTACAGGAGGTAGGCTT	480
Dd	421	TTGACGTCACCTGACAAAGCGCTTGTCTCTGGAAATAGTACAGGAGGTAGGCTT	480
Qy	481	AAGCGGATGGCAATCACCTTAGAAATGATCTTATGCGTAATTAACAAGACTGATGGG	540
Dd	481	AAGCGGATGGCAATCACCTTAGAAATGATCTTATGCGTAATTAACAAGACTGATGGG	540
Qy	541	CGGCTATTGGTCTAAATTGTCAGGATGTGGTACCTTGGGTAATTAGGGCTATGATGGTTCG	600
Dd	541	CGGCTATTGGTCTAAATTGTCAGGATGTGGTACCTTGGGTAATTAGGGCTATGATGGTTCG	600
Qy	601	ATTGAGATTCGGTGGTATGATGCCAGAAATTAAGAAGTGTGCACTGATGAGATAGTTC	660
Dd	601	ATTGAGATTCGGTGGTATGATGCCAGAAATTAAGAAGTGTGCACTGATGAGATAGTTC	660
Qy	661	ATCTCGGATATATCCCAATGATGCTGGTAGAAGAGTCCATTAAGCCATCTGGACCGGG	720
Dd	661	ATCTCGGATATATCCCAATGATGCTGGTAGAAGAGTCCATTAAGCCATCTGGACCGGG	720
Qy	721	GGCTTTGGTAAAGTCCAGTTGAAAGTAGGCTCTCTAACTTCTTCTTGGTTAAACAGGAGC	780
Dd	721	GGCTTTGGTAAAGTCCAGTTGAAAGTAGGCTCTCTAACTTCTTCTTGGTTAAACAGGAGC	780

Qy	781	TATTAGGACATATTCATCTCTATTAGTAACAACCTAAGGACACTGGTTTCAGAAATAGGCAA	840
Dd	781	TATTAGGACATATTCATCTCTATTAGTAACAACCTAAGGACACTGGTTTCAGAAATAGGCAA	840
Qy	841	GTAGTCTCGATGTCCCACTGTCTGAAATAGATGTGAAAGTAGTAACCTATCGTCATCATCTT	900
Dd	841	GTAGTCTCGATGTCCCACTGTCTGAAATAGATGTGAAAGTAGTAACCTATCGTCATCATCTT	900
Qy	901	CAAAATTTAGGATCGCGACCCCAAGCTTGATCTCATCTCTGCAACATATACTATCTTGT	960
Dd	901	CAAAATTTAGGATCGCGACCCCAAGCTTGATCTCATCTCTGCAACATATACTATCTTGT	960
Qy	961	TCGTTGTGTTCTTGTATAGTGTGTCATGAAAAATTTAGTATTTTGTCTCCCGCCAGCT	1020
Dd	961	TCGTTGTGTTCTTGTATAGTGTGTCATGAAAAATTTAGTATTTTGTCTCCCGCCAGCT	1020
Qy	1021	GAGCCATTTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTTGTGCAATTAATCTGCG	1080
Dd	1021	GAGCCATTTAAATTCGAGAGCACATCGCCCAAAATTAATCTTCTTGTGCAATTAATCTGCG	1080
Qy	1081	AATTTTCTCTTTAGGTAAGTAACCAATGATGCGCCATTTGACAAAAAGCTGATTAGT	1140
Dd	1081	AATTTTCTCTTTAGGTAAGTAACCAATGATGCGCCATTTGACAAAAAGCTGATTAGT	1140
Qy	1141	ATGATCTTGGAGTTGTTGTCGAAATTTGCAAGCTGACGATGGCCCTCAGGGAAATTA	1200
Dd	1141	ATGATCTTGGAGTTGTTGTCGAAATTTGCAAGCTGACGATGGCCCTCAGGGAAATTA	1200
Qy	1201	GGCGCCAAACCCAGATGTCGAAAGGACACAAAGAGACACCAACCTTTCCTTAACAAGAT	1260
Dd	1201	GGCGCCAAACCCAGATGTCGAAAGGACACAAAGAGACACCAACCTTTCCTTAACAAGAT	1260
Qy	1261	CATCACAGATGCGCGAGTAAGGTAATATTAATTTAAACAAATAGCTCTTGTACCGGAA	1320
Dd	1261	CATCACAGATGCGCGAGTAAGGTAATATTAATTTAAACAAATAGCTCTTGTACCGGAA	1320
Qy	1321	CTCCGTATTTCTCTCACCTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGCAA	1380
Dd	1321	CTCCGTATTTCTCTCACCTTCCATTAACCCCTGATTAATTTGGTGGGAAAGCGACGCAA	1380
Qy	1381	CCCAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGATG	1440
Dd	1381	CCCAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGATG	1440
Qy	1441	TTCTCTCTATATTTCTGTTTCAACCGGTTGAGTCAATGGCATGCGTACGAAATGTACATAT	1500
Dd	1441	TTCTCTCTATATTTCTGTTTCAACCGGTTGAGTCAATGGCATGCGTACGAAATGTACATAT	1500
Qy	1501	TGGTGTAGGTCCTAATATTTTGGCGGAGGTTGGTGAACCCGAAAGTTCTTATATATCGA	1560
Dd	1501	TGGTGTAGGTCCTAATATTTTGGCGGAGGTTGGTGAACCCGAAAGTTCTTATATATCGA	1560
Qy	1561	ACCTCCACCATACCTCCTCAATCCCAACCAATTTATCCGTTTATTTCTCTCTGCTT	1620
Dd	1561	ACCTCCACCATACCTCCTCAATCCCAACCAATTTATCCGTTTATTTCTCTCTGCTT	1620
Qy	1621	TGCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTTCGACC	1680
Dd	1621	TGCTTTGCTCGAGTCTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGGTTCGACC	1680
Qy	1681	GGCTCCGAGACCCAGATGACCCCGACCCAGTCTCGGACGAGCGGACCTCTTCGCGC	1740
Dd	1681	GGCTCCGAGACCCAGATGACCCCGACCCAGTCTCGGACGAGCGGACCTCTTCGCGC	1740
Qy	1741	ATGCACTCGGAGCGCTCTCGTCTCCCAATGGTCTTAAAGCGCCCATCGAGATCGAC	1800
Dd	1741	ATGCACTCGGAGCGCTCTCGTCTCCCAATGGTCTTAAAGCGCCCATCGAGATCGAC	1800
Qy	1801	CTCCTCGAGATCATGCGCAAGGACGCGCGCGGCGGTCTCTCCACGCGGGGAAATCGCG	1860
Dd	1801	CTCCTCGAGATCATGCGCAAGGACGCGCGCGGCGGTCTCTCTCCACGCGGGGAAATCGCG	1860

181 AGGCAAAAGTTGCGCGTTGAAATTTGACAGCAAAAGACACCGTCTGTTATGCAATGTCATGAT 240
181 AGGCAAAAGTTGCGCGTTGAAATTTGACAGCAAAAGACACCGTCTGTTATGCAATGTCATGAT 240
241 CAAATTTGATCCCATGTTAGGTTGAAATTTGAGAGTGGAGATAGTCTCTTTAGAAATGTCCTCA 300
241 CAAATTTGATCCCATGTTAGGTTGAAATTTGAGAGTGGAGATAGTCTCTTTAGAAATGTCCTCA 300
301 TTCCACCCCTATCATAGGCTTTCTGCAATATCCCAATTTTAAAGACAGCCCGGAAATGACGTCT 360
301 TTCCACCCCTATCATAGGCTTTCTGCAATATCCCAATTTTAAAGACAGCCCGGAAATGACGTCT 360
361 ACAATTTCTGACTTTAAATTTGATGTAGAAACCTCTTAGACATAATAAAATATTTGCTGTAAT 420
361 ACAATTTCTGACTTTAAATTTGATGTAGAAACCTCTTAGACATAATAAAATATTTGCTGTAAT 420
421 TTGACGTCCTCACTGACAAAAGCGCTTTGCTCTGGAATAAAGTACAGGACAGTGGGCTT 480
421 TTGACGTCCTCACTGACAAAAGCGCTTTGCTCTGGAATAAAGTACAGGACAGTGGGCTT 480
481 AAGCGAATTTGGCAATCACTTTAGAAATGATCTTATATGCGTAATTAACAAGACTGATGGG 540
481 AAGCGAATTTGGCAATCACTTTAGAAATGATCTTATATGCGTAATTAACAAGACTGATGGG 540
541 GCGGTATTTGCTCTAAATTTGTTTCAAGATGTGTTACCTTTGGGTATTTAGGGCTATGATGGTTCCG 600
541 GCGGTATTTGCTCTAAATTTGTTTCAAGATGTGTTACCTTTGGGTATTTAGGGCTATGATGGTTCCG 600
601 ATTGAGATTTGCGGTGATGATGACCAATTTAAAGAAAGTCTGACATGATGAGAAATGATTC 660
601 ATTGAGATTTGCGGTGATGATGACCAATTTAAAGAAAGTCTGACATGATGAGAAATGATTC 660
661 ATCTCGAGTATATPCCCAATGATGCTGGTGAAGAGTCCATCAAGCCATCTGGACCCGGG 720
661 ATCTCGAGTATATPCCCAATGATGCTGGTGAAGAGTCCATCAAGCCATCTGGACCCGGG 720
721 GGCCTTGGTAAAGTCCCAAGTTGGAAGTAGCTCTTAACTTCTTGGTAAACAGGAGC 780
721 GGCCTTGGTAAAGTCCCAAGTTGGAAGTAGCTCTTAACTTCTTGGTAAACAGGAGC 780
781 TATTAGGACATATTCATCTCATTAGTAAACAACTAAGGACACTGGTTTCAAGATAGGCAAA 840
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CC production of genetic constructs, used for modifying gene expression in a
CC target organism, in particular a plant. The method is useful for
CC modifying expression of a polynucleotide that comprises an intron
CC sequence, through removal of the intron sequence. The method is useful
CC for modifying growth and development of plants, and cellular responses to
CC external stimulus, such as environmental factors and disease pathogens.
CC The sequences are useful in genome and physical mapping, in positional
CC cloning of genes, in various assays to determine biological activity, to
CC raise antibodies, to isolate corresponding interacting proteins and other
CC compounds, and to quantitatively determine levels of interacting proteins
CC or other compounds. Sequences ABK17016-ABK17125 represent pinus radiata
CC and Eucalyptus grandis polynucleotides and PCR primers used in the method
CC of the invention
XX

SQ Sequence 661 BP; 192 A; 145 C; 150 G; 174 T; 0 U; 0 Other;

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Best Local Similarity 99.7%; Pred. No. 1.3e-126;
Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1416 GAGAGAGAGAGAGAGAGAGAG 1438
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Job time : 2758 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: OLIGO_NUC

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Searched: 48236798 seqs, 27959665780 residues

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 13	37	1.2	456	11	AA955639 UI-R-B1-f
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C 33	36	1.2	367	11	AZ349069
C 34	36	1.2	430	5	CF115975 et2-95.z1
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C 45	36	1.2	637	2	BJ749391 BJ749391

ALIGNMENTS

RESULT 1
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VERSION CB967579.1 GI:30229714
KEYWORDS EST.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
REFERENCE 1 (bases 1 to 344)
AUTHORS Kirst,M., Kirst,M.E., Gurgel,G.P., Myburg,A.A., Whetten,R. and Sederoff,R.
TITLE Gene Discovery in Eucalyptus grandis Xylem
JOURNAL Unpublished (2003)
COMMENT Contact: Kirst, Matias
NCSU
Tel: 919 513 0015
Fax: 919 515 7801
Email: mkirst@unity.ncsu.edu
Seq primer: T3.

FEATURES

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Best Local Similarity 100.0%; Pred. No. 4.8e-124;

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ACCESSION BZ103309
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1 (bases 1 to 430).
Geer, K.,
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G.,
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, P., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-152B20.TJB

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(<http://www.chori.org/bacpac/rat330.htm>) : rat_bac_end@mail.chor.org availability, please contact Pieter de Jong (pdejong@mail.chor.org) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or_eing_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 152 row: B column: 20 Seq primer: T7
 Class: RAC ends.

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S4	143	CNGCCTGACAGACAGACAGACAGACAGATTTTCTCT	181		

1 (bases 1 to 446)
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H.
and Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
10920195
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 67 row: F column: 23
Seq primer: SP6
Class: BAC ends
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urchin, sperm genomic BAC library"
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DH10B"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy - 1408 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTCTC 1445
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Db 433 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTCTC 396

RESULT 6
CB915484 536 bp mRNA linear EST 25-APR-2003
LOCUS VVD123B02.368629 An expressed sequence tag database for abiotic
DEFINITION stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
cDNA clone VVD123B02.5, mRNA sequence.
CB915484
CB915484.1 GI:30130145
EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 536)
Cushman,J.C.
An expressed sequence tag database for abiotic stressed berries of
Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 123 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 536.

ORIGIN

TITLE	JOURNAL	PUBLISHED	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shiroishi, T.							
Contribution of Asian mouse subspecies <i>Mus musculus molossinus</i> to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis	Genome Res.	14 (12), 2439-2447 (2004)	15574823				
2 (bases 1 to 895)							
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.							
Direct Submission							
Submitted (17-NOV-2003) Mashira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/ , Tel: 81-45-503-9111, Fax: 81-45-503-9170)							
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).							
Tsukuba Institute, Bio Resource Center, Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan							
phone: 81-298-36-9189, fax: 81-298-36-9199							
e-mail: abe@rtc.riken.jp							
PRIMERS							

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Query Match          1.2%; Score 38; DB 14; Length 895;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
1408 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTCTC 1445
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Db      194 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTCTC 231

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RESULT 11	
LOCUS	BQ568480/c
DEFINITION	403 bp mRNA linear EST 19-JUN-2002 gi108hl0.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cdNA clone gi108hl0 5', mRNA sequence.
ACCESSION	BQ568480
VERSION	BQ568480
KEYWORDS	BQ568480.1 GI:21471797
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 403) Kachar,B. EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing Unpublished (2002) Contact: Kachar,B. Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 Fax: 301-402-1765
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Email: kacharb@nidcd.nih.gov
 Plate: 108 row: h column: 10
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers
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 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watlham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

ORIGIN

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RESULT 15
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LOCUS       0241-38 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION   mRNA sequence.
ACCESSION   BG803750
VERSION     BG803750.1 GI:17950659
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 600)
AUTHORS    Wu,X.,Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TITLE       Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
JOURNAL     Nucleic Acids Res. 29 (24), 4983-4993 (2001)
PUBMED     11812828
COMMENT     Contact: Klein WH
            Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.

FEATURES             source
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ORIGIN
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Best Local Similarity 100.0%; Pred.No. 7.5e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1408 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGATTTTCT 1444
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Db       22 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGATTTTCT 58

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Job time : 13816 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 11:40:17 ; Search time 548 Seconds
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 93554401 residues

Word size : 20

Total number of hits satisfying chosen parameters: 2875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 3: /EMC Celerra_SID33/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC Celerra_SID33/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC Celerra_SID33/ptodata/2/ina/7 COMB.seq:*
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- 9: /EMC Celerra_SID33/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC Celerra_SID33/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3070	100.0	3070	3	US-09-598-401C-113
2	1255	40.9	2096	3	US-09-598-401C-60
3	774	25.2	1630	3	US-09-615-192A-107
4	774	25.2	1630	3	US-09-169-789-107
5	272	8.9	661	3	US-09-276-599-12
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7	111	3.6	407	3	US-09-615-192A-106
8	111	3.6	407	3	US-09-169-789-106
9	111	3.6	421	2	US-08-975-316-24
10	111	3.6	421	3	US-09-615-192A-24
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12	35	1.1	537	3	US-10-101-464A-299
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	27	34	1.1	607	3	US-09-169-789-23	Sequence 37, Appl
	28	34	1.1	376	3	US-09-244-805-37	Sequence 4, Appl
C	29	34	1.1	8779	2	US-08-750-703-4	Sequence 91, Appl
	30	34	1.1	12730	3	US-09-004-838-91	Sequence 15083, A
	31	34	1.1	50850	3	US-09-949-016-15083	Sequence 15084, A
	32	34	1.1	50850	3	US-09-949-016-15084	Sequence 15085, A
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	38	34	1.1	254964	3	US-09-949-016-11973	Sequence 12583, A
	39	34	1.1	254964	3	US-09-949-016-17392	Sequence 17392, A
	40	34	1.1	611587	4	US-09-531-120-209	Sequence 209, App
C	41	34	1.1	414	2	US-08-975-316-18	Sequence 18, Appl
C	42	33	1.1	414	3	US-09-615-192A-18	Sequence 18, Appl
C	43	33	1.1	414	3	US-09-615-192A-403	Sequence 403, App
C	44	33	1.1	414	3	US-09-325-932A-203	Sequence 203, App
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ALIGNMENTS

RESULT 1
US-09-598-401C-113
; Sequence 113, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C2
; CURRENT APPLICATION NUMBER: US/09/598,401C
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-113

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			Indels	0;
			Gaps	0;
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Db	1261	CATCAACAGATCGGCAGTAAAGGTTAATTAATTTAAACAAATAGCTCTTGTACCGGAA	1320	Db	2341	TCAATGAAAGGATCAACTTTGACCCCGCCCAAGGATTCAGACGCCCCCACTTCCTG	2400
				QY	2401	GTGTCAAGCAGCTCGGAGGCGACATGTTGCTGACGCTTCCAAAGGAGATGCCATTTTCA	2460

Best Local Similarity		99.4%;	Pred.No. 0;	Matches 1194;		Conservative	Mismatches		6;	Indels	1;	Gaps	1;
QY	1864	CAGTCCCGGACCCAGAACCCGAGGCA	CCCGTCA	GTCTCGACCGATCTTTCGGGCTGCTG	1923								
Db	264	CAGTCCCGACCCAGAACCCGAGGCA	CCCGTCA	GTCTCGACCGATCTTTCGGGCTGCTG	323								
QY	1924	GCAGCTACTCCGTGCTCAGGTGCAC	CCCTCCG	AGCTCCCGATGGCAAGGTTCGAGCGG	1983								
Db	324	GCCAGCTACTCCGTGCTCAGTGCAC	CCCTCCG	AGCTCCCGATGGCAAGGTTCGAGCGG	383								
QY	1984	CTCTACGGCTTAGCGCCGGTGTGCA	AGTCTT	TCGGTCAAGAACGAGACGGGTCTCCATC	2043								
Db	384	CTCTACGGCTTAGCGCCGGTGTGCA	AGTCTT	TCGGTCAAGAACGAGACGGGTCTCCATC	443								
QY	2044	GCCGCACTCAACTTGTATGAACAC	AGGCAAA	ATCTCATGGAAGCTGGTATTACCTGAA	2103								
Db	444	GCCGCACTCAACTTGTATGAACAC	AGGCAAA	ATCTCATGGAAGCTGGTATTACCTGAA	503								
QY	2104	GATCGGTCTTGAAGCGGGAATCCCA	ATTCAA	CAGGCGTACGGGATGACCGGTTCGAG	2163								
Db	504	GATCGGTCTTGAAGCGGGAATCCCA	ATTCAA	CAGGCGTACGGGATGACCGGTTCGAG	563								
QY	2164	TATCATGCGACCGACCCCGGATTC	CAACA	AGATCTTTAACCGGGGAATGTCTGATCACTCC	2223								
Db	564	TATCATGCGACCGACCCCGGATTC	CAACA	AGATCTTTAACCGGGGAATGTCTGATCACTCC	623								
QY	2224	ACCATTACTATGAAGAAGATACTG	GAACA	CATACAAAGGCTTCGAGGCGCTCGAGACCGTG	2283								
Db	624	ACCATTACTATGAAGAAGATACTG	GAACA	CATACAAAGGCTTCGAGGCGCTCGAGACCGTG	683								
QY	2284	GTTCGATGTCGAGGCGGCACTTGG	GGCCGTGT	CAGCATGATCGTTGCCAATACCCATCA	2343								
Db	684	GTTCGATGTCGAGGCGGCACTTGG	GGCCGTGT	CAGCATGATCGTTGCCAATACCCATCG	743								
QY	2344	ATGAAGGGATCAACTTCGACGC	-GCC	CCAAACGGATTTGAAGACGCCCCACCCCTTCCTGGT	2402								
Db	744	ATGAAGGGATCAACTTCGACGC	-GCC	CCAAACGGATTTGAAGACGCCCTTCCTGGT	803								
QY	2403	GTCAAGACGTCGGAGGCGCAATG	TTGTC	TGACGTTCCAAAGGAGATGCCATTTTCATG	2462								
Db	804	GTCAAGACGTCGGAGGCGCAATG	TTGTC	TGACGTTCCAAAGGAGATGCCATTTTCATG	863								
QY	2463	AACTGGATATGCCATGACTGGAGT	GACAC	CAATTCGCGGAAAGTTCTCTCAAGAATCTCTAC	2522								
Db	864	AACTGGATATGCCATGACTGGAGT	GACAC	CAATTCGCGGAAAGTTCTCTCAAGAATCTCTAC	923								
QY	2523	GATCGCTTCCCAACAATCGAAAG	GTGAT	CTGTTGCAGAGTGGTACTCCCTGTGTACCCA	2582								
Db	924	GATCGCTTCCCAACAATCGAAAG	GTGAT	CTGTTGCAGAGTGGTACTCCCTGTGTACCCA	983								
QY	2583	GACACGAGCTAGCGACGAGATGT	GATCC	ACATCGACTGATCATGTGTGCCCACACAC	2642								
Db	984	GACACGAGCTAGCGACGAGATGT	GATCC	ACATCGACTGATCATGTGTGCCCACACAC	1043								
QY	2643	CCAGGCGGGAAGAGAGGAGACAC	AGAAG	GTGTTGAGGCAATGGCCMAAGGGCCGGATTT	2702								
Db	1044	CCAGGCGGGAAGAGAGGAGACAC	AGAAG	GTGTTGAGGCAATGGCCMAAGGGCCGGATTT	1103								
QY	2703	CAGGGCTTCCAAGTCAATGCTG	CTCGCTT	TCGGCACTCAGTCTATGAGTTCCTCTGAAGACC	2762								
Db	1104	CAGGGCTTCCAAGTCAATGCTG	CTCGCTT	TCGGCACTCAGTCTATGAGTTCCTCTGAAGACC	1163								
QY	2763	GCTTGATCTGCTCTCTGTGGT	GATGTT	CTATGTTTGAAGAGTCTGTGAAGGA	2822								
Db	1164	GCTTGATCTGCTCTCTGTGGT	GATGTT	CTATGTTTGAAGAGTCTGTGAAGGA	1223								
QY	2823	GCCCTTTTCTCAGTGTGGCTTC	GGCAT	ACCAAGTTCCTCTCATATAAAGGAAACAATAAG	2882								
Db	1224	GCCCTTTTCTCAGTGTGGCTTC	GGCAT	ACCAAGTTCCTCTCATATAAAGGAAACAATAAG	1283								
QY	2883	AAGCGACTGTATGATGGCGCA	AGTGA	AGTTGATTTGTTTATGTTCTATTAAG	2942								

Qy	2428	TCGTCAGCGTCCAAAGGAGGATGCCATTTTCATGAATGGAATATGCCATGCATCGAGTG	2487
Db	1454	TCGTGACGGTTCCAAAGGAGATGCCATTTTCATGAATGGATATGCCATGCATCGAGTG	1513
Qy	2488	ACGACCAATTGCGGGAAGTTCTCCTCAAGAACTGCTACGATCGGCTTCCCAACAATGAAAGG	2547
Db	1514	ACGACCAATTGCGGGAAGTTCTCCTCAAGAACTGCTACGATCGGCTTCCCAACAATGAAAGG	1573
Qy	2548	TGATCGTTGCAGAGTGGCTACTCCCTGTGTACCCAGACACGAGCCTAGCGACCAAGAAATG	2607
Db	1574	TGATCGTTGCAGAGTGGCTACTCCCTGTGTACCCAGACACGAGCCTAGCGACCAAGAAATG	1633
Qy	2608	TGATCCACATCGACTGCGATCATGTTGGCCCAACAACCCAGCGCGGAAGAGAGACACAGA	2667
Db	1634	TGATCCACATCGACTGCGATCATGTTGGCCCAACAACCCAGCGCGGAAGAGAGACACAGA	1693
Qy	2668	AGGAGTTTCGAGGCCATTGGCCCAAAGGGGCCGGATTTTCAGGGCTTCCAAAGTCATGTGCTGG	2727
Db	1694	AGGAGTTTCGAGGCCATTGGCCCAAAGGGGCCGGATTTTCAGGGCTTCCAAAGTCATGTGCTGG	1753
Qy	2728	CTTTTCGGCACA CTCACGTCATGAGGTTCTGTAAGACCGCTTCGATCTGCTCCCTCTGTGTGAT	2787
Db	1754	CTTTTCGGCACA CTCACGTCATGAGGTTCTGTAAGACCGCTTCGATCTGCTCCCTCTGTGTGAT	1813
Qy	2788	GTTTCATGGTTCTTCGATTTGAAAGGTCGTGAAAGGAGGCCCTTTTCTCACAGTTGGCTTCGG	2847
Db	1814	GTTTCATGGTTCTTCGATTTGAAAGGTCGTGAAAGGAGGCCCTTTTCTCACAGTTGGCTTCGG	1873
Qy	2848	CATACCAAGTTCTTCTCATAAAGGAACATTAAGACGCACTGTATGATGGCGCAAGTG	2907
Db	1874	CATACCAAGTTCTTCTCATAAAGGAACATTAAGACGCACTGTATGATGGCGCAAGTG	1933
Qy	2908	GAAGTTACAAGATTTGTTGTTTTATGTCCTATAAAGTTTTGAGTCTTCTGCACTACTGATTT	2967
Db	1934	GAAGTTACAAGATTTGTTGTTTTATGTCCTATAAAGTTTTGAGTCTTCTGCACTACTGATTT	1993
Qy	2968	CACAGAATGCTGAACGAACCGCTATATGGATGTGCTGAATGATGGAAATTTGTGATAT	3027
Db	1994	CACAGAATGCTGAACGAACCGCTATATGGATGTGCTGAATGATGGAAATTTGTGATAT	2053
Qy	3028	TCGTCTTCTTTTTTCAGTAAATTCATCTCGAACAAAAA	3070
Db	2054	TCGTCTTCTTTTTTCAGTAAATTCATCTCGAACAAAAA	2096

```

RESULT 3
US-09-615-192A-107
; Sequence 107, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-107

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Query Match 25.2%; Score 774; DB 3; Length 1630;

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Db      1284  AAGCGACTGTATGATGCGCGCAAGTGAAGTTTACAAGATTGTTGTTTATGCTATAAAG 1343
Qy      2943  TTTTGAGTCTTTCGCACTACTGATTTTACAGAAATGTGTAAAGAAACCGCGTATATGATGT 3002
Db      1344  TTTTGAGTCTTTCGCACTACTGATTTTACAGAAATGTGTAAAGAAACCGCGTATATGATGT 1403
Qy      3003  GCCTGAATGATGGAATTTGTGATATTTCTGTCTTCTTTTTCAGTAAATCACTTCGAACAAA 3062
Db      1404  GCCTGAATGATGGAATTTGTGATATTTCTGTCTTCTTTTTCAGTAAATCACTTCGAACAAA 1463
Qy      3063  A 3063
Db      1464  A 1464

RESULT 4
US-09-169-789-107
; Sequence 107, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Blokeberg, Leonard N.
; APPLICANT: Havukala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; EARLIER FILING DATE: 1998-10-09
; EARLIER FILING DATE: 1997-11-21
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-107

Query Match      25.2%; Score 774; DB 3; Length 1630;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy      1864  CAGCTCCCGACCCAGAACCCCGAGGACCCCGTATGCTGACCGGATCTTCGGGCTGCTG 1923
Db      264  CAGCTCCCGACCCAGAACCCCGAGGACCCCGTATGCTGACCGGATCTTCGGGCTGCTG 323
Qy      1924  GCAGGTACTCCGTGCTCAGTGTGACCTCCCGACCTCCCGATGGCAAGGTGCGAGCGG 1983
Db      324  GCAGGTACTCCGTGCTCAGTGTGACCTCCCGACCTCCCGATGGCAAGGTGCGAGCGG 383
Qy      1984  CTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGGACGGGGTCTCCATC 2043
Db      384  CTCTACGGCTTAGCGCGGTGTGCAAGTTCTTGGTCAAGAACGAGGACGGGGTCTCCATC 443
Qy      2044  GCGGCACTCACTGTATGACACGAGCAAAATCTCATGAAAGCTGTTATACCTGAAA 2103
Db      444  GCGGCACTCACTGTATGACACGAGCAAAATCTCATGAAAGCTGTTATACCTGAAA 503
Qy      2104  GATGCGGTCTTGAAGCGGGAATCCCATTTCAACAGCGGTACCGGATGACCGGTTCCGAG 2163
Db      504  GATGCGGTCTTGAAGCGGGAATCCCATTTCAACAGCGGTACCGGATGACCGGTTCCGAG 563
Qy      2164  TATCATGGCACCGACCCCGGATTTCAACAGATCTTTAAACCGGGAATGTCTGATCACTCC 2223
Db      564  TATCATGGCACCGACCCCGGATTTCAACAGATCTTTAAACCGGGAATGTCTGATCACTCC 623
Qy      2224  ACCATTACTATGAAGAGACTGGAACATACAGGGCTTCGAGGCTTCGAGACCGGTG 2283
Db      624  ACCATTACTATGAAGAGACTGGAACATACAGGGCTTCGAGGCTTCGAGACCGGTG 683
Qy      2284  GTCGATGTCGGAGCGGCACTGGGGCGTCTCAGCATGATCGTTGCAAAATACCCATCA 2343

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Db      684  GTCGATGTCGGAGCGGCACTGGGGCGGTGCTCAGCATGATGCTTGTCCAAATACCCATCG 743
Qy      2344  ATGAAGGGATCAACTTTCGACC- GCCCAACGATTTGAAGACGCCGCCCTTCTCTGT 2402
Db      744  ATGAAGGGATCAACTTTCGACCCTCAGCTGATTTGAAGACGCTCCACCCCTTCTCTGT 803
Qy      2403  GTCAAGCAGCTCGGAGGCGACATGTTGTCAGCGTTTCAAAGGGAGATGCCATTTTCATG 2462
Db      804  GTCAAGCAGCTCGGAGGCGACATGTTGTCAGCGTTTCAAAGGGAGATGCCATTTTCATG 863
Qy      2463  AAGTGATATGCAATGACTGGAGTACGACCAATTTGGCGCAAGTTCTCAAGACTGCTAC 2522
Db      864  AAGTGATATGCAATGACTGGAGTACGACCAATTTGGCGCAAGTTCTCAAGACTGCTAC 923
Qy      2523  GATGCGCTTCCCAACAAATGGAAGGTGATGCTTGCAGAGTGGGTACTCTCCCTGTGTACCA 2582
Db      924  GATGCGCTTCCCAACAAATGGAAGGTGATGCTTGCAGAGTGGGTACTCTCCCTGTGTACCA 983
Qy      2583  GACAGAGCTTAGCGACCAAGAAATGTGATCCACATGCTGATCATGTTGGCCCAAC 2642
Db      984  GACAGAGCTTAGCGACCAAGAAATGTGATCCACATGCTGATCATGTTGGCCCAAC 1043
Qy      2643  CCAGCGGGAAGAGAGGACACAGAGGAGTTGCGAGGCAATGGCCAAAGGGCGCGATTT 2702
Db      1044  CCAGCGGGAAGAGAGGAGACACAGAGGAGTTGCGAGGCAATGGCCAAAGGGCGCGATTT 1103
Qy      2703  CAGGCTTCCAAAGTCAATGCTGCGCTTTTCGGCACCTCAGTCAATGAGTTCTTGAAGACC 2762
Db      1104  CAGGCTTCCAAAGTCAATGCTGCGCTTTTCGGCACCTCAGTCAATGAGTTCTTGAAGACC 1163
Qy      2763  GCTTGATCTGCTCCTCTGCTGCTGATGTTTCATGTTTCTTGGATTTGAAAGTCTGTAAGGA 2822
Db      1164  GCTTGATCTGCTCCTCTGCTGCTGATGTTTCATGTTTCTTGGATTTGAAAGTCTGTAAGGA 1223
Qy      2823  GCGCTTTCTCAGAGTTGCTGCGGATACCAAGTTCTTCTATAAAGAAACAATAAG 2882
Db      1224  GCGCTTTCTCAGAGTTGCTGCGGATACCAAGTTCTTCTATAAAGAAACAATAAG 1283
Qy      2883  AAGCGACTGATGATGCGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAAAG 2942
Db      1284  AAGCGACTGATGATGCGCGCAAGTGAAGTTTCAAGATTTGTTTATGCTATAAAG 1343
Qy      2943  TTTTGAGTCTTCTGCACTACTGATTTTCAAGAAATGTGTAACGAAACCGCGTATATGATGT 3002
Db      1344  TTTTGAGTCTTCTGCACTACTGATTTTCAAGAAATGTGTAACGAAACCGCGTATATGATGT 1403
Qy      3003  GCGTGAATGATGGAATTTGTGATTTCTGCTCTTCTTTTTCAGTAAATCACTTCGAACAAA 3062
Db      1404  GCGTGAATGATGGAATTTGTGATTTCTGCTCTTCTTTTTCAGTAAATCACTTCGAACAAA 1463
Qy      3063  A 3063
Db      1464  A 1464

RESULT 5
US-09-276-599-12
; Sequence 12, Application US/09276599
; Patent No. 6380459
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Composition and methods for the
; FILE REFERENCE: 11000.1036
; CURRENT APPLICATION NUMBER: US/09/276,599
; CURRENT FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Eucalyptus grandis

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Thu Nov 2 13:35:49 2006

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;
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(654)
; NAME/KEY: TATA signal
; LOCATION: (537)...(543)
; NAME/KEY: CAAT signal
; LOCATION: (499)...(502)
;
US-09-276-599-12
    Query Match      8.9%; Score 272; DB 3; Length 661;
    Best Local Similarity 99.7%; Pred. No. 5.6e-127;
    Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1116 CATGTTGACAAAAGCGCTGATTAGTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT 1175
Db 98 CATGTTGACAAAAGCGCTGATTAGTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT 157

QY 1176 GACGATGGCCCTCAGGGAATTAAGCGCCCAACCCAGATTCGAAAGAGCA 1235
Db 158 GACGATGGCCCTCAGGGAATTAAGCGCCCAACCCAGATTCGAAAGAGCA 217

QY 1236 CGACCCCAACCTTCTTAAACAAGATCATCCAGATTCGCGCCAGTAAGGGTAATATTAATT 1295
Db 218 CGATCCCAACCTTCTTAAACAAGATCATCCAGATTCGCGCCAGTAAGGGTAATATTAATT 277

QY 1296 TAAACAATAGCTCTTGACGGGAATCCGTTATTTCTCTCATTCCATAAACCCCTGATT 1355
Db 278 TAAACAATAGCTCTTGACGGGAATCCGTTATTTCTCTCATTCCATAAACCCCTGATT 337

QY 1356 AATTGTTGGAAAGCGACAGCAACCCACAAAGGTTCAGATGTCTATCCACGAGAGAGA 1415
Db 338 AATTGTTGGAAAGCGACAGCAACCCACAAAGGTTCAGATGTCTATCCACGAGAGAGA 397

QY 1416 GAGAGAGAGAGAGAGAGAG 1438
Db 398 GAGAGAGAGAGAGAGAGAG 420

RESULT 6
US-09-598-401C-12
; Sequence 12, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c2
; CURRENT APPLICATION NUMBER: US/09/598.401C
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-12
    Query Match      8.9%; Score 272; DB 3; Length 661;
    Best Local Similarity 99.7%; Pred. No. 5.6e-127;
    Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1116 CATGTTGACAAAAGCGCTGATTAGTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT 1175
Db 98 CATGTTGACAAAAGCGCTGATTAGTAGTATGATCTTGGAGTTGTTGGTGCAAAATTTGCAAGCT 157

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QY 1176 GACGATGGCCCTCAGGGAATTAAGCGCCCAACCCAGATTCGAAAGAGCA 1235
Db 158 GACGATGGCCCTCAGGGAATTAAGCGCCCAACCCAGATTCGAAAGAGCA 217

QY 1236 CGACCCCAACCTTCTTAAACAAGATCATCCAGATTCGCGCCAGTAAGGGTAATATTAATT 1295
Db 218 CGATCCCAACCTTCTTAAACAAGATCATCCAGATTCGCGCCAGTAAGGGTAATATTAATT 277

QY 1296 TAAACAATAGCTCTTGACGGGAATCCGTTATTTCTCTCATTCCATAAACCCCTGATT 1355
Db 278 TAAACAATAGCTCTTGACGGGAATCCGTTATTTCTCTCATTCCATAAACCCCTGATT 337

QY 1356 AATTGTTGGAAAGCGACAGCAACCCACAAAGGTTCAGATGTCTATCCACGAGAGAGA 1415
Db 338 AATTGTTGGAAAGCGACAGCAACCCACAAAGGTTCAGATGTCTATCCACGAGAGAGA 397

QY 1416 GAGAGAGAGAGAGAGAGAG 1438
Db 398 GAGAGAGAGAGAGAGAGAG 420

RESULT 7
US-09-615-192A-106
; Sequence 106, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615.192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-106
    Query Match      3.6%; Score 111; DB 3; Length 407;
    Best Local Similarity 100.0%; Pred. No. 1.6e-45;
    Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1897 ATGCTCGACCGGATCTTCGGCTGCTGGCCAGTACTCCGTGCTCACGTGACACCCCTCGC 1956
Db 297 ATGCTCGACCGGATCTTCGGCTGCTGGCCAGTACTCCGTGCTCACGTGACACCCCTCGC 356

QY 1957 GACCTCCCCGATGGCAAGGTTCGAGCGGCTCTACGGCTTAGCGCCGGTGTGC 2007
Db 357 GACCTCCCCGATGGCAAGGTTCGAGCGGCTCTACGGCTTAGCGCCGGTGTGC 407

RESULT 8
US-09-169-789-106
; Sequence 106, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316

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EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: US 08/713,000
EARLIER FILING DATE: 1996-09-11
NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 106
LENGTH: 407
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-169-789-106

Query Match 3.6%; Score 111; DB 3; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.6e-45;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1897 ATGCTCGACCGGATCTTCGGCTGCGGCGCTGAGTCTTACGGCTTAGCGCGCGGTGTGC 1956
D 297 ATGCTCGACCGGATCTTCGGCTGCGGCGCTGAGTCTTACGGCTTAGCGCGCGGTGTGC 356
Y 1957 GACCTCCCGATGCGCAAGTTCGAGCGGCTTACGGCTTAGCGCGCGGTGTGC 2007
D 357 GACCTCCCGATGCGCAAGTTCGAGCGGCTTACGGCTTAGCGCGCGGTGTGC 407

RESULT 9
US-08-975-316-24
Sequence 24, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-24

Query Match 3.6%; Score 111; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.6e-45;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1897 ATGCTCGACCGGATCTTCGGCTGCGGCGCTGAGTCTTACGGCTTAGCGCGCGGTGTGC 1956
D 311 ATGCTCGACCGGATCTTCGGCTGCGGCGCTGAGTCTTACGGCTTAGCGCGCGGTGTGC 370
Y 1957 GACCTCCCGATGCGCAAGTTCGAGCGGCTTACGGCTTAGCGCGCGGTGTGC 2007
D 371 GACCTCCCGATGCGCAAGTTCGAGCGGCTTACGGCTTAGCGCGCGGTGTGC 421

RESULT 10
US-09-615-192A-24
Sequence 24, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003C4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 421
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-615-192A-24

Query Match 3.6%; Score 111; DB 3; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.6e-45;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1897 ATGCTCGACCGGATCTTCGGCTGCGGCGCTGAGTCTTACGGCTTAGCGCGCGGTGTGC 1956
D 311 ATGCTCGACCGGATCTTCGGCTGCGGCGCTGAGTCTTACGGCTTAGCGCGCGGTGTGC 370
Y 1957 GACCTCCCGATGCGCAAGTTCGAGCGGCTTACGGCTTAGCGCGCGGTGTGC 2007
D 371 GACCTCCCGATGCGCAAGTTCGAGCGGCTTACGGCTTAGCGCGCGGTGTGC 421

RESULT 11
US-09-169-789-24
Sequence 24, Application US/09169789
Patent No. 6653528
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003C2
CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: US 08/713,000
EARLIER FILING DATE: 1996-09-11
NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 421
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-169-789-24

Query Match 3.6%; Score 111; DB 3; Length 421;

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Query Match      1.18; Score 35; DB 3; Length 537;
Best Local Similarity 100.0%; Prad. No. 4.6e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1408 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1442
          |||||
          20 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 54

RESULT 13
US-10-101-464A-871
; Sequence 871, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FASTSEQ for Windows Version 4.0

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RESULT 15
US-09-949-016-16813
; Sequence 16813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16813

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GenCore version 5.1.9
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(without alignments)

10563.719 Million cell updates/sec

Title: US-10-702-319A-113

Perfect score: 3070

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Gapop 60.0 , Gapext 60.0

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- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
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- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3070	100.0	3070	9	US-10-702-319A-113
3	3070	100.0	3070	10	US-10-927-641-113
4	1255	40.9	2096	6	US-10-137-036-60
5	1255	40.9	2096	9	US-10-702-319A-60
6	1255	40.9	2096	10	US-10-927-641-60
7	774	25.2	1630	8	US-10-174-693-107
8	534	17.4	534	8	US-10-703-091-1
9	485	15.8	485	8	US-10-703-091-2
10	306	10.0	306	8	US-10-703-091-3
11	293	9.5	293	8	US-10-703-091-4
12	272	8.9	661	6	US-10-137-036-12
13	272	8.9	661	9	US-10-702-319A-12
14	272	8.9	661	10	US-10-927-641-12
15	119	3.9	119	8	US-10-703-091-5
16	111	3.6	407	7	US-10-174-693-106
17	111	3.6	421	7	US-10-174-693-24

18	98	3.2	98	8	US-10-703-091-6	Sequence 6, Appli
19	66	2.1	66	8	US-10-703-091-7	Sequence 7, Appli
20	41	1.3	354	10	US-10-779-543-10544	Sequence 1, Appli
21	37	1.2	578	12	US-10-301-480-589546	Sequence 589546
22	37	1.2	578	12	US-10-301-480-1202955	Sequence 1202955
23	37	1.2	15050	11	US-10-893-483-113	Sequence 113, App
24	36	1.2	398	9	US-10-674-124A-1893	Sequence 1893, Ap
25	36	1.2	989	12	US-10-301-480-562402	Sequence 562402
26	36	1.2	989	12	US-10-301-480-1175811	Sequence 1175811
27	36	1.2	96600	3	US-09-997-722-85	Sequence 85, Appl
28	36	1.2	123192	6	US-10-175-523-71	Sequence 71, Appl
29	36	1.2	123192	13	US-11-099-266-71	Sequence 71, Appl
30	36	1.2	157875	3	US-09-935-464-1	Sequence 1, Appli
31	36	1.2	157875	6	US-10-125-835-1	Sequence 18188, A
32	35	1.1	266	9	US-10-425-115-18188	Sequence 29684, A
33	35	1.1	271	8	US-10-242-535A-23684	Sequence 23684, A
34	35	1.1	271	8	US-10-085-783A-23684	Sequence 23684, A
35	35	1.1	356	6	US-10-062-727-156	Sequence 156, App
36	35	1.1	402	6	US-10-062-727-78	Sequence 78, Appl
37	35	1.1	404	10	US-10-779-543-9925	Sequence 9925, Ap
38	35	1.1	518	8	US-10-424-599-128495	Sequence 128495
39	35	1.1	529	8	US-10-437-963-3046	Sequence 3046, Ap
40	35	1.1	537	6	US-10-101-464A-239	Sequence 239, App
41	35	1.1	537	10	US-10-864-252-239	Sequence 299, App
42	35	1.1	567	8	US-10-424-599-110277	Sequence 110277
43	35	1.1	807	6	US-10-027-632-8139	Sequence 8139, Ap
44	35	1.1	807	7	US-10-027-632-8139	Sequence 8139, Ap
45	35	1.1	1262	7	US-10-369-493-30442	Sequence 30442, A

ALIGNMENTS

RESULT 1

US-10-137-036-113
; Sequence 113, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-113

Query Match 100.0%; Score 3070; DB 6; Length 3070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Db 2161 GAGTATCATGCCACCGCCGCGATTCAACAAGATCTTTAAACCGGGAATGTCTGATCAC 2220
Qy 2221 TCACACATTACTAGAGAGATCTCGAACAATACAAAGGCTTCGAGGCGCTCGAGACC 2280
Db 2221 TCACACATTACTAGAGAGATCTCGAACAATACAAAGGCTTCGAGGCGCTCGAGACC 2280
Qy 2281 GTGGTCGATGTCGAGAGCGGCACCTGGGCGCGTGTCTCAGCATGATGCTGTGCAAAATACCCA 2340
Db 2281 GTGGTCGATGTCGAGAGCGGCACCTGGGCGCGTGTCTCAGCATGATGCTGTGCAAAATACCCA 2340
Qy 2341 TCAATGAAAGGGATCAACTTCGACCGCCCAACGGAATGGAAGCGCCCAACCCCTTCCTG 2400
Db 2341 TCAATGAAAGGGATCAACTTCGACCGCCCAACGGAATGGAAGCGCCCAACCCCTTCCTG 2400
Qy 2401 GTGTCAGACGCTCGGAGGCGACATGTCGTCTCAGCGTTCCAAAGGGAGATGCCATTTTCA 2460
Db 2401 GTGTCAGACGCTCGGAGGCGACATGTCGTCTCAGCGTTCCAAAGGGAGATGCCATTTTCA 2460
Qy 2461 TGAAGTGGATATGCCATGACTGGAGTGACGACCAATTCGCGGAAGTTCTTCAAGAACTGCT 2520
Db 2461 TGAAGTGGATATGCCATGACTGGAGTGACGACCAATTCGCGGAAGTTCTTCAAGAACTGCT 2520
Qy 2521 ACATGCGCTTCCCAACAATGGAAGGTGATGCTGTCAGAGTGCCTACTCCCTGTGPAAC 2580
Db 2521 ACATGCGCTTCCCAACAATGGAAGGTGATGCTGTCAGAGTGCCTACTCCCTGTGPAAC 2580
Qy 2581 CAGACAGCGCTAGCAGCAAGATGTCATGATCCATCGACTGCTGCTGCGCCACA 2640
Db 2581 CAGACAGCGCTAGCAGCAAGATGTCATGATCCATCGACTGCTGCTGCGCCACA 2640
Qy 2641 ACCAGCGCGGAAAGAGAGACACAGAAAGGATTCGAGGCAATTCGCCAAAGGGCGCGAT 2700
Db 2641 ACCAGCGCGGAAAGAGAGACACAGAAAGGATTCGAGGCAATTCGCCAAAGGGCGCGAT 2700
Qy 2701 TTCAGGCGCTTCCAAGTCATGCTGCTTCGCGCTTCGCGACTCAAGTACGAGTTCCTGAAGA 2760
Db 2701 TTCAGGCGCTTCCAAGTCATGCTGCTTCGCGCTTCGCGACTCAAGTACGAGTTCCTGAAGA 2760
Qy 2761 CCGCTTGATCTGCTCCTCTGCTGCTGATGTCATGCTTCGAGTTTGAAGGCTCGTGAAG 2820
Db 2761 CCGCTTGATCTGCTCCTCTGCTGCTGATGTCATGCTTCGAGTTTGAAGGCTCGTGAAG 2820
Qy 2821 GAGCGCTTTTCTACAGTTGCTTTCGCGCATACCAAGTTCCTCTCAAAAAGGAAACAATA 2880
Db 2821 GAGCGCTTTTCTACAGTTGCTTTCGCGCATACCAAGTTCCTCTCAAAAAGGAAACAATA 2880
Qy 2881 AGAAGCGACTGTATGATGCGCGCAAGTGGAAAGTTCAAGATTTGTTTATGCTATAA 2940
Db 2881 AGAAGCGACTGTATGATGCGCGCAAGTGGAAAGTTCAAGATTTGTTTATGCTATAA 2940
Qy 2941 AGTTTGAAGTCTTCTGCTACTGATTTTCACAGATGTTTCAAGAAACGGCGGTATATGGAT 3000
Db 2941 AGTTTGAAGTCTTCTGCTACTGATTTTCACAGATGTTTCAAGAAACGGCGGTATATGGAT 3000
Qy 3001 GTGCTCAATGATGGAATTTGATATTTCTGCTTCTTTTTCAGTAAATCACTTCGAACA 3060
Db 3001 GTGCTCAATGATGGAATTTGATATTTCTGCTTCTTTTTCAGTAAATCACTTCGAACA 3060
Qy 3061 AAAAAAAAAA 3070
Db 3061 AAAAAAAAAA 3070
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RESULT 2

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US-10-702-319A-113
; Sequence 113, Application US/10702319A
; Publication No. US20050026162A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Bagleton, Clare
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
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; FILE REFERENCE: 11000.1036C5
; CURRENT APPLICATION NUMBER: US/10/702,319A
; PRIOR FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: U.S. No. 10/291,447
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 60/425,087
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: U.S. No. 10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. Patent No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 3070
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-702-319A-113
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Query Match 100.0%; Score 3070; DB 9; Length 3070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCACCATCAGCAAAAAATAGATGGATAGAGTGGGACACCACCTGTTCAGTTTGTATTC 60

Qy 61 CTTGAGATGACCTACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 61 CTTGAGATGACCTACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

Qy 121 GATAAAAAGTAGGAGATAGGGATCTCCCGTCTGATGCTCGGCTAGGTTGAAAATA 180
Db 121 GATAAAAAGTAGGAGATAGGGATCTCCCGTCTGATGCTCGGCTAGGTTGAAAATA 180

Qy 181 AGSCAAAAGTTCGCGCTGTAATTTGACAGCAAAAGACACCGTCTGATGATGATGATGAT 240
Db 181 AGSCAAAAGTTCGCGCTGTAATTTGACAGCAAAAGACACCGTCTGATGATGATGATGAT 240

Qy 241 CCATTGTACCCATGTAGGGTGAATCCTAGAGTGAGGAGATAGTCCCTTTAGAAAAGTCCCA 300
Db 241 CCATTGTACCCATGTAGGGTGAATCCTAGAGTGAGGAGATAGTCCCTTTAGAAAAGTCCCA 300

Qy 301 TTCACCCCTATCATAGGCTTTCTGCAATATCCATTTTAAGAACAGCCGGAATTCAGCTCT 360
Db 301 TTCACCCCTATCATAGGCTTTCTGCAATATCCATTTTAAGAACAGCCGGAATTCAGCTCT 360

Qy 361 ACATTTTCTGACTTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 ACATTTTCTGACTTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

Qy 421 TTGACGCTCCACTGACAAAAGCGCTTTGCTCTCGGAAAAATAAGTACAGGCAAGTAGGGCTT 480
Db 421 TTGACGCTCCACTGACAAAAGCGCTTTGCTCTCGGAAAAATAAGTACAGGCAAGTAGGGCTT 480

Qy 481 AAGCGGATGGCAATCACCTTAGAATGATCTTATATGCGTAATACAAAGACTGATGGG 540
Db 481 AAGCGGATGGCAATCACCTTAGAATGATCTTATATGCGTAATACAAAGACTGATGGG 540

Qy 541 GCGGTATGCTCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 GCGGTATGCTCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

Qy 601 ATTGAGATTCGGTGTATGATGCCAGAAATTAATAAAGTGTCTGCACTGATGAGAAATAGTTC 660
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Qy	2881	AGAACGCACGTATGATGGCGCAAGTTCGAAGTTACAGATTTGTTGTTTATGTCTATAA	2940
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Db	2941	AGTTTTCGAGTCTTCTGCATATCTGATTTTCACAGAAATGTGAACGAAACGGCGTATATGGAT	3000
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RESULT 3

US-10-927-641-113

; Sequence 113, Application US/10927641

; Publication No. US20050244968A1

; GENERAL INFORMATION:

; APPLICANT: Perera, Ranjan

; APPLICANT: Rice, Stephen

; APPLICANT: Eagleton, Clare

; APPLICANT: Lasham, Annette

; APPLICANT: Wood, Marion

; APPLICANT: Visser, Elizabeth

; TITLE OF INVENTION: Compositions and Methods for the

; TITLE OF INVENTION: Modification of Gene Expression

; FILE REFERENCE: 11000.1036c4

; CURRENT APPLICATION NUMBER: US/10/927,641

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036

; PRIOR FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401

; PRIOR FILING DATE: 2000-06-20

; PRIOR APPLICATION NUMBER: PCT/NZ00/00018

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599

; PRIOR FILING DATE: 1999-03-25

; NUMBER OF SEQ ID NOS: 143

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 113

; LENGTH: 3070

; TYPE: DNA

; ORGANISM: Eucalyptus grandis

US-10-927-641-113

Query Match 100.0%; Score 3070; DB 10; Length 3070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	AGCACCATCAGCAAAAAATAGATGGGATAGATGGGACACCACTGTTTCAGTTGATTC	60
Qy	61	CTTGAGATGACCTACAGTGTAGCTTCGATGAATAAGATGGGATTAAGATTCACGAGG	120
Db	61	CTTGAGATGACCTACAGTGTAGCTTCGATGAATAAGATGGGATTAAGATTCACGAGG	120
Qy	121	GATAAAAAGGTGAGGAGATGGGATCTCCCGTCTGATCGCTCGGATGGTTGAAAAATA	180

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Db 1381 CCCACAAAAGGTGAGATGTCATCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATT 1440
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Db 1441 TTCTCTATATTTCTGGTTCACCGGTGGAGTCAATGGCATGCGTGACGAAATGTACATAT 1500
QY 1501 TGGGTAGGGTCCAAATATTTTGGGGAGGGTGGTGAACCGCAAGTTTCTTATATATCGA 1560
Db 1501 TGGGTAGGGTCCAAATATTTTGGGGAGGGTGGTGAACCGCAAGTTTCTTATATATCGA 1560
QY 1561 ACCTCCACCAACCATCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGCTT 1620
Db 1561 ACCTCCACCAACCATCTCACTTCAATCCCAACCATTTATCCGTTTATTTCTCTGCTT 1620
QY 1621 TCCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGATGGTTCGACC 1680
Db 1621 TCCTTTGCTCGAGTCTCGGGAAGAGAGAGAGAGAGAGAGAGAGAGATGGTTCGACC 1680
QY 1681 GGCTCCGAGACCCAGATGACCCGACCCAGATCTCGAGACGAGCGCAACCTTTCGCG 1740
Db 1681 GGCTCCGAGACCCAGATGACCCGACCCAGATCTCGAGACGAGCGCAACCTTTCGCG 1740
QY 1741 ATGCAGTGGCGAGCGCTCCGTCTCCCATGGTCTTAAGCCGCCATCGAGATCGAC 1800
Db 1741 ATGCAGTGGCGAGCGCTCCGTCTCCCATGGTCTTAAGCCGCCATCGAGATCGAC 1800
QY 1801 CTCTCGAGATCATGGCCAAAGAGCGGCCCGGGCGGTCTCTTCCACGGGGGAATTCGG 1860
Db 1801 CTCTCGAGATCATGGCCAAAGAGCGGCCCGGGCGGTCTCTTCCACGGGGGAATTCGG 1860
QY 1861 GCACAGTCCCGACCCAGAACCCCGAGCCACCGTCTCATGCTCGACCGGATCTTCGGCTG 1920
Db 1861 GCACAGTCCCGACCCAGAACCCCGAGCCACCGTCTCATGCTCGACCGGATCTTCGGCTG 1920
QY 1921 CTGGCCAGCTACTCCGTCTCACTGCAACCTCGCGACCTCCCGAGTGGCAAGTTCGAG 1980
Db 1921 CTGGCCAGCTACTCCGTCTCACTGCAACCTCGCGACCTCCCGAGTGGCAAGTTCGAG 1980
QY 1981 CGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGGTCAAGAACGAGGACGGGTCTCC 2040
Db 1981 CGGCTCTACGGCTTAGCGCGGTGTGCAAGTCTTGGTCAAGAACGAGGACGGGTCTCC 2040
QY 2041 ATCCCGGCACTCAACTTTGATGAACAGGACCAAAATCTCTATGGAAGCTGTATTACCTG 2100
Db 2041 ATCCCGGCACTCAACTTTGATGAACAGGACCAAAATCTCTATGGAAGCTGTATTACCTG 2100
QY 2101 AAAGATCGGCTCTTTGAAGCGGGAATCCCATTTCAACAAAGCGTACGGGATGACCGCGTTC 2160
Db 2101 AAAGATCGGCTCTTTGAAGCGGGAATCCCATTTCAACAAAGCGTACGGGATGACCGCGTTC 2160
QY 2161 GAGTATCATGGCAGCCGCGGATTCACAAAGATCTTTAACCGGGGAATGTCTGTATCAC 2220
Db 2161 GAGTATCATGGCAGCCGCGGATTCACAAAGATCTTTAACCGGGGAATGTCTGTATCAC 2220
QY 2221 TCCACATTAATGAGAGAGATCTGGAACATACAGGGCTTCGAGGGCTTCGAGACC 2280
Db 2221 TCCACATTAATGAGAGAGATCTGGAACATACAGGGCTTCGAGGGCTTCGAGACC 2280
QY 2281 GTGGTGTGATGCGGAGCGGCACTGGGGCCGTGTCTAGCATGATCGTTGCCAATATCCCA 2340
Db 2281 GTGGTGTGATGCGGAGCGGCACTGGGGCCGTGTCTAGCATGATCGTTGCCAATATCCCA 2340
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QY 2341 TCAATGAAAGGATCAACTTCGACCGCCCAACGGGATTTGAAGACGCCCAACCCCTTCTCTG 2400
Db 2341 TCAATGAAAGGATCAACTTCGACCGCCCAACGGGATTTGAAGACGCCCAACCCCTTCTCTG 2400
QY 2401 GTGTCAAGCAGCTCGGAGGCGACATGTTCTGACGGTTCAAAAGGGAGATGCCATTTTCA 2460
Db 2401 GTGTCAAGCAGCTCGGAGGCGACATGTTCTGACGGTTCAAAAGGGAGATGCCATTTTCA 2460
QY 2461 TGAAGTGGATATGCAATGCTGGAGTGACGACCATTCGCGGAAGTTTCTCAAGAACTGCT 2520
Db 2461 TGAAGTGGATATGCAATGCTGGAGTGACGACCATTCGCGGAAGTTTCTCAAGAACTGCT 2520
QY 2521 ACAGTACGCTTCCCAACAATGGAAGTGTGTTGAGAGTGGTACTCCCTGTGTACC 2580
Db 2521 ACAGTACGCTTCCCAACAATGGAAGTGTGTTGAGAGTGGTACTCCCTGTGTACC 2580
QY 2581 CAGACAGAGCTTAGCAGCAGCAAGATGTGATCCATCGATCGATCATGTTTGGCCACA 2640
Db 2581 CAGACAGAGCTTAGCAGCAGCAAGATGTGATCCATCGATCGATCATGTTTGGCCACA 2640
QY 2641 ACCAGGCGGGAAGAGAGGACACAGAAAGGATTCGAGGCAATTCGCAAGGGGCCCGAT 2700
Db 2641 ACCAGGCGGGAAGAGAGGACACAGAAAGGATTCGAGGCAATTCGCAAGGGGCCCGAT 2700
QY 2701 TTCAGGGCTTCCAAAGTCAATGTGCTGCGCTTTCGGCACTCAGTCAATGGAGTTCCTGAAGA 2760
Db 2701 TTCAGGGCTTCCAAAGTCAATGTGCTGCGCTTTCGGCACTCAGTCAATGGAGTTCCTGAAGA 2760
QY 2761 CGCTTGTATGCTCTCTGTTGGTGTGATGTTCACTGGTCTTGGATTTGAAAGTCTGTAAG 2820
Db 2761 CGCTTGTATGCTCTCTGTTGGTGTGATGTTCACTGGTCTTGGATTTGAAAGTCTGTAAG 2820
QY 2821 GAGCCCTTTCTCAGAGTGGCTTCGGCATACCAAGTCTTCTCATAAAAGGAAACAATA 2880
Db 2821 GAGCCCTTTCTCAGAGTGGCTTCGGCATACCAAGTCTTCTCATAAAAGGAAACAATA 2880
QY 2881 AGAAGCGACTGTGATGATGCGCAAGTGAAGTTCAAGATTTGTTTATGTCATAA 2940
Db 2881 AGAAGCGACTGTGATGATGCGCAAGTGAAGTTCAAGATTTGTTTATGTCATAA 2940
QY 2941 AGTTTGTAGTCTTCGCACTACTGATTTTCAAGATGTTCAAGAAACGCGGTATATGAT 3000
Db 2941 AGTTTGTAGTCTTCGCACTACTGATTTTCAAGATGTTCAAGAAACGCGGTATATGAT 3000
QY 3001 GTGCTGTGAATGATGAAATTTGATATTTCTGTTCTTTTTCAGTAAATCACTTCGAACA 3060
Db 3001 GTGCTGTGAATGATGAAATTTGATATTTCTGTTCTTTTTCAGTAAATCACTTCGAACA 3060
QY 3061 AAAAAAAAAA 3070
Db 3061 AAAAAAAAAA 3070
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RESULT 4
US-10-137-036-60
; Sequence 60, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-29
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Db	2054	TCTGTCCTCTCTTTTTCAGTAAATCACTTCGAAACAAAAA	2096
Db	804	GTCAAGCAGTTCGAGGCGACATGTTTCGTTCAGGTTCCAAAGGAGATGCCATTTTCATG	863
Qy	2463	AAGTGGATATGCCATGACTGGAGTGACGACCATTTGGCGGAGCTTCTCAAGAACTGCTAC	2522
Db	864	AAGTGGATATGCCATGACTGGAGTGACGACCATTTGGCGGAGCTTCTCAAGAACTGCTAC	923
Qy	2523	GATGCGCTTCCCAACCAATGAAAGTGATGCTGTTGACAGTGGCTATCTCCCTGTGTACCCA	2582
Db	924	GATGCGCTTCCCAACCAATGAAAGTGATGCTGTTGACAGTGGCTATCTCCCTGTGTACCCA	983
Qy	2583	GACAGGAGCTTACGAGCAAGAAATGATTCACATCGATCGATCGATCGATCGATCGATCGAT	2642
Db	984	GACAGGAGCTTACGAGCAAGAAATGATTCACATCGATCGATCGATCGATCGATCGATCGAT	1043
Qy	2643	CCAGGCGGGAAGAGAGGACACAGAAAGGAGTTCCAGGCAATGCGCCAAAGGGGCGGATTT	2702
Db	1044	CCAGGCGGGAAGAGAGGACACAGAAAGGAGTTCCAGGCAATGCGCCAAAGGGGCGGATTT	1103
Qy	2703	CAGGCTTCCAAAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2762
Db	1104	CAGGCTTCCAAAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1163
Qy	2763	GCTTGAATCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2822
Db	1164	GCTTGAATCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1223
Qy	2823	GCCCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTCTTCTCTATAAAAGGAAACAATAAG	2882
Db	1224	GCCCTTTTCTCACAGTTGGCTTCGGCATACCAAGTTCTTCTCTATAAAAGGAAACAATAAG	1283
Qy	2883	AAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2942
Db	1284	AAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1343
Qy	2943	TTTTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3002
Db	1344	TTTTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1403
Qy	3003	GCCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3062
Db	1404	GCCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1463
Qy	3063	A 3063	
Db	1464	A 1464	
RESULT 8			
US-10-703-091-1			
; Sequence 1, Application US/10703091			
; Publication NO. US20040146904A1			
; GENERAL INFORMATION:			
; APPLICANT: PHILLIPS, JONATHAN			
; APPLICANT: EAGLETON, CLARE			
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF			
; FILE REFERENCE: 044463-0263			
; CURRENT APPLICATION NUMBER: US/10/703,091			
; CURRENT FILING DATE: 2003-11-07			
; PRIOR APPLICATION NUMBER: 60/425,087			
; PRIOR FILING DATE: 2002-11-08			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: PatentIn Ver. 3.2			
; SEQ ID NO 1			
; LENGTH: 534			
; TYPE: DNA			
; ORGANISM: Eucalyptus grandis			
US-10-703-091-1			
Query Match 17.4%; Score 534; DB 8; Length 534;			
Best Local Similarity 100.0%; Pred. No. 3.9e-274;			
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

1110 ATGGCGCATGTTGACAAAAGGCTGATTTAGTATGATCTTGGAGTGTGGTGCATAATTG 1169
Db
1 ATGCGCCATGTTGACAAAAGGCTGATTTAGTATGATCTTGGAGTGTGGTGCATAATTG 60
1170 CAAGCTGACGATGGCCCTCAGGGAATTAAGCGGCCAACCCAGATTGCAAGAGCACAA 1229
Db
61 CAAGCTGACGATGGCCCTCAGGGAATTAAGCGGCCAACCCAGATTGCAAGAGCACAA 120
1230 AGAGCAGGCCAACCTTTCTTAAACAAGATCATCACCAGATCGGCCAGTAAGGGTAATA 1289
Db
121 AGAGCAGGCCAACCTTTCTTAAACAAGATCATCACCAGATCGGCCAGTAAGGGTAATA 180
1290 TTAATTTAAACAATAGCTCTTGACCGGGAACCTCCGTTATTTCTCTCACTTCCATAAACCC 1349
Db
181 TTAATTTAAACAATAGCTCTTGACCGGGAACCTCCGTTATTTCTCTCACTTCCATAAACCC 240
1350 CTGATTTAATTTGGTGGGAAGCAGCAGCCAAACCCAAAGGTCAGATGTCATCCACGA 1409
Db
241 CTGATTTAATTTGGTGGGAAGCAGCAGCCAAACCCAAAGGTCAGATGTCATCCACGA 300
1410 GAG 1469
Db
301 GAG 360
1470 AGTCAATGGCATCGTGACGAATGTACATATTTGGTGTAGGGTCCAATATTTTGGCGGAGG 1529
Db
361 AGTCAATGGCATCGTGACGAATGTACATATTTGGTGTAGGGTCCAATATTTTGGCGGAGG 420
1530 GTTGTGGAACCGCAAGTTCCTATATATATATATATATATATATATATATATATATATAT 1589
Db
421 GTTGTGGAACCGCAAGTTCCTATATATATATATATATATATATATATATATATATATAT 480
1590 CCACCATTTATCGTTTATTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCT 1643
Db
481 CCACCATTTATCGTTTATTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCT 534

RESULT 9
US-10-703-091-2
; Sequence 2, Application US/10703091
; Publication No. US20040146904A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE REFERENCE: 04463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; PRIOR FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-2

Query Match 15.8%; Score 485; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.8e-248;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1159 GTGCAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGCGGCCAACCCAGATTGC 1218
Db
1 GTGCAATTTGCAAGCTGACGATGGCCCTCAGGGAATTAAGCGGCCAACCCAGATTGC 60
1219 AAAGACACAAAGAGCAGCAGCCAACTTCTTAAACAAGATCATCACCAGATCGGCCAG 1278
Db
61 AAAGACACAAAGAGCAGCAGCCAACTTCTTAAACAAGATCATCACCAGATCGGCCAG 120
1279 TAAGGGTAATTTAATTTAAACAATAGCTCTGTACCGGGAATCTCCGTTATTTCTCTCACT 1338
Db
121 TAAGGGTAATTTAATTTAAACAATAGCTCTGTACCGGGAATCTCCGTTATTTCTCTCACT 180

1339 TCATATAAACCCCTGATTTAATTTGGTGGAAAGCGACAGCAACCCCAAAAAGGTCAAGT 1398
Db
181 TCATATAAACCCCTGATTTAATTTGGTGGAAAGCGACAGCAACCCCAAAAAGGTCAAGT 240
1399 TCATCCACGAG 1458
Db
241 TCATCCACGAG 300
1459 TCACCGTTGGAGTCAATGGCATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATAT 1518
Db
301 TCACCGTTGGAGTCAATGGCATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATAT 360
1519 TTTGGCGGAGGGTTGGTGAACCGCAAGTTCCTATATATATATATATATATATATATATAT 1578
Db
361 TTTGGCGGAGGGTTGGTGAACCGCAAGTTCCTATATATATATATATATATATATATATAT 420
1579 CACTTCAATCCCAACCATTTATTCGGTTTATTTCTCTGCTTCTCTGCTTCTCTGCTGAGTCTCG 1638
Db
421 CACTTCAATCCCAACCATTTATTCGGTTTATTTCTCTGCTTCTCTGCTTCTCTGCTGAGTCTCG 480
1639 CGGAA 1643
Db
481 CGGAA 485

RESULT 10
US-10-703-091-3
; Sequence 3, Application US/10703091
; Publication No. US20040146904A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE REFERENCE: 04463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; PRIOR FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-3

Query Match 10.0%; Score 306; DB 8; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.7e-152;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1338 TTCATATAAACCCCTGATTTAATTTGGTGGAAAGCGACAGCAACCCCAAAAAGGTCAAGT 1397
Db
1 TTCATATAAACCCCTGATTTAATTTGGTGGAAAGCGACAGCAACCCCAAAAAGGTCAAGT 60
1398 GTCATCCACGAG 1457
Db
61 GTCATCCACGAG 120
1458 TTCACCGTTGGAGTCAATGGCATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATA 1517
Db
121 TTCACCGTTGGAGTCAATGGCATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATA 180
1518 TTTTGGCGGAGGGTTGGTGAACCGCAAGTTCCTATATATATATATATATATATATATATAT 1577
Db
181 TTTTGGCGGAGGGTTGGTGAACCGCAAGTTCCTATATATATATATATATATATATATATAT 240
1578 TCACTTCAATCCCAACCATTTATTCGGTTTATTTCTCTGCTTCTCTGCTTCTCTGCTGAGTCTC 1637
Db
241 TCACTTCAATCCCAACCATTTATTCGGTTTATTTCTCTGCTTCTCTGCTTCTCTGCTGAGTCTC 300
1638 CGGAA 1643
Db
481 CGGAA 485


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; LENGTH: 661
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-702-319A-12

Query Match      8.9%;   Score 172;   DB 9;   Length 661;
Best Local Similarity 99.7%;   Pred. No. 7,7e-134;
Matches 322;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1116  CATGTTGACAAAAGGCTGATTAGTATGATCTTGGAGTCTTGTCGTCGAAATTTGCAAGCT 1175
Db      98   CATGTTGACAAAAGGCTGATTAGTATGATCTTGGAGTCTTGTCGTCGAAATTTGCAAGCT 157

Qy      1176  GACGATGGCCCTCAGGGAAATTAAGCGGCCAACCCAGATTGCAAAAGAGCACAAAGAGCA 1235
Db      158  GACGATGGCCCTCAGGGAAATTAAGCGGCCAACCCAGATTGCAAAAGAGCACAAAGAGCA 217

Qy      1236  CGACCCAAACCTTTCCCTTAAACAAGATCATCACAGATCGGCCAGTAAAGGGTAATTAATT 1295
Db      218  CGATCCAACTTTCCCTTAAACAAGATCATCACAGATCGGCCAGTAAAGGGTAATTAATT 277

Qy      1296  TAACAATAGCTCTTGTAACGGGAACCTCCGTATTTCTCTCACTTCCATAAACCCCTGATT 1355
Db      278  TAACAATAGCTCTTGTAACGGGAACCTCCGTATTTCTCTCACTTCCATAAACCCCTGATT 337

Qy      1356  AATTTGGTGGGAAGCGACAGCCCAACCCACAAGAAGTCAGATGTCATCCACGAGAGAGA 1415
Db      338  AATTTGGTGGGAAGCGACAGCCCAACCCACAAGAAGTCAGATGTCATCCACGAGAGAGA 397

Qy      1416  GAGAGAGAGAGAGAGAGAG 1438
Db      398  GAGAGAGAGAGAGAGAGAG 420

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RESULT 14
US-10-927-641-12
; Sequence 12, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleston, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-12

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	Best Local Similarity	99.7%; Matches	Pred. No. 7.7e-134; Conservative	0; Mismatches	Indels	0;	Gaps	0;
QY	1116	CATGTTGCACAAAAGCGCTGAATTAGTATGATCTTTGGAGTTGTTCGGTGCAAAATTTGCCAAGCT	1175					
Dd	98	CATGTTGCACAAAAGCGCTGAATTAGTAGATCTTTGGAGTTGTTCGGTGCAAAATTTGCCAAGCT	157					
QY	1176	GACGATGGCCCTCAGGGAAATTAAGGCGCCAACCAGATGTGCAAAGAGCACAAAGACA	1235					
Dd	158	GACGATGGCCCTCAGGGAAATTAAGGCGCCAACCAGATGTGCAAAGAGCACAAAGACA	217					
QY	1236	CGACCCAAACTTTCTTTAACAGATCATCACAGATCGGCAGTAAAGGGTAAATTAAATT	1295					
Dd	218	CGATCCAACTTTCTTTAACAGATCATCACAGATCGGCAGTAAAGGGTAAATTAAATT	277					
QY	1296	TACAAATAAGCTCTTTGACGGGAACTCCGTAATTTCTCTCACATTCATATAACCCCTGATT	1355					
Dd	278	TACAAATAAGCTCTTTGACGGGAACTCCGTAATTTCTCTCACATTCATATAACCCCTGATT	337					
QY	1356	AATTTGTTGGGAAGCGACAGCCAAACCCACAAAAGGTTCAGATCTCATCCACAGAGAGA	1415					
Dd	338	AATTTGTTGGGAAGCGACAGCCAAACCCACAAAAGGTTCAGATCTCATCCACAGAGAGA	397					
QY	1416	GAGAGAGAGAGAGAGAGAG	1438					
Dd	398	GAGAGAGAGAGAGAGAGAG	420					

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RESULT 15
US-10-703-091-5
; Sequence 5, Application US/10703091
; Publication No. US20040146904A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTER SEQUENCES AND USES THEREOF
; FILE OF INVENTION: 044463-0263
; CURRENT APPLICATION NUMBER: US/10/703,091
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/425,087
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 5
; LENGTH: 119
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-703-091-5

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Search completed: November 1, 2006, 13:32:37
Job time : 3575 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	774	25.2	1630	7	US-11-397-533-107	Sequence 107, App
2	485	15.8	485	8	US-11-229-856-78	Sequence 78, Appl
3	306	10.0	306	8	US-11-229-856-80	Sequence 80, Appl
4	111	3.6	407	7	US-11-397-533-106	Sequence 106, App
5	111	3.6	421	7	US-11-397-533-24	Sequence 24, Appl
6	35	1.1	601	8	US-11-266-748A-215547	Sequence 215547,
c 7	35	1.1	601	8	US-11-266-748A-237674	Sequence 237674,
c 8	35	1.1	1148	9	US-11-218-305-5916	Sequence 5916, Ap
c 9	35	1.1	1413	9	US-11-218-305-11276	Sequence 11276, A
c 10	35	1.1	2002	6	US-10-449-902-18409	Sequence 18409, A
c 11	35	1.1	2168	6	US-10-449-902-24951	Sequence 24951, A
c 12	35	1.1	2411	6	US-10-612-783-3402	Sequence 3402, Ap
c 13	35	1.1	120502	6	US-10-669-920-321	Sequence 321, App
c 14	35	1.1	215126	6	US-10-540-898-339	Sequence 339, App
c 15	34	1.1	584	6	US-10-449-902-10915	Sequence 10915, A
c 16	34	1.1	594	7	US-11-397-533-105	Sequence 105, App
17	34	1.1	607	7	US-11-397-533-23	Sequence 23, Appl
18	34	1.1	1587	6	US-10-449-902-7413	Sequence 7413, Ap
19	34	1.1	1642	9	US-11-218-305-18848	Sequence 18848, A
c 20	34	1.1	2103	9	US-11-218-305-6138	Sequence 6138, Ap
21	34	1.1	2115	8	US-11-216-545-2471	Sequence 2471, Ap
c 22	34	1.1	2455	6	US-10-449-902-14341	Sequence 14341, A
c 23	34	1.1	22582	6	US-10-669-920-226	Sequence 226, App

Thu Nov 2 13:35:50 2006

Db 384 CTCTACGGCTTAGCGCGGTGTGCAAGTCTTGTGTTCAAGAACGAGGACGGGTCTCCATC 443
QY 2044 GCGCACTCAACTGTATGAAACAGAGCAAAATCTCTCTGGAAGCTGTATTACTGAAA 2103
Db 444 GCGCACTCAACTGTATGAAACAGAGCAAAATCTCTCTGGAAGCTGTATTACTGAAA 503
QY 2104 GATCGGCTCTTGAAGCGGATCCCATTAACAAGGCGTACGGATGACCGCGTTCGAG 2163
Db 504 GATCGGCTCTTGAAGCGGATCCCATTAACAAGGCGTACGGATGACCGCGTTCGAG 563
QY 2164 TATCATGGACCGACCGCGGATTCACAAAGATCTTTAAACCGGGGAATGTGTATCACTCC 2223
Db 564 TATCATGGACCGACCGCGGATTCACAAAGATCTTTAAACCGGGGAATGTGTATCACTCC 623
QY 2224 ACCATTACTAAGAAAGTACTGGAACATACAAAGGCTTCAGGGCTTCGAGACCGTG 2283
Db 624 ACCATTACTAAGAAAGTACTGGAACATACAAAGGCTTCAGGGCTTCGAGACCGTG 683
QY 2284 GTCGATCTCGAGCGGCACTGGGCGGTCTCAGCATGATCGTTGCCAAATACCATCG 743
Db 684 GTCGATCTCGAGCGGCACTGGGCGGTCTCAGCATGATCGTTGCCAAATACCATCG 743
QY 2344 ATGAAAGGATCAACTTCGACC-GCCCCAAGGATTAAGACGCCGCCCTCTCTGTT 2402
Db 744 ATGAAAGGATCAACTTCGACCCTCCTCAGCTGATTTGAAGACGCTCCACCCCTTCTGTT 803
QY 2403 GTCAAGCAGCTCGAGCGGCACTGTCGAGCTTCCAAAGGAGATGCCATTTTCATG 2462
Db 804 GTCAAGCAGCTCGAGCGGCACTGTCGAGCTTCCAAAGGAGATGCCATTTTCATG 863
QY 2463 AAGTGGATATGCATGACTGAGTGACGACCAATTCGCGGAAGTTCTCAAGACTGCTAC 2522
Db 864 AAGTGGATATGCATGACTGAGTGACGACCAATTCGCGGAAGTTCTCAAGACTGCTAC 923
QY 2523 GATCGCTTCCCAACATGGAAGGTGATCGTTCAGAGTGCCTACCTCTGTGACCCA 2582
Db 924 GATCGCTTCCCAACATGGAAGGTGATCGTTCAGAGTGCCTACCTCTGTGACCCA 983
QY 2583 GACAGAGCTAGCAGCAAGAAATGTGATCCACATCGACTGATGTTGGGCCCAAC 2642
Db 984 GACAGAGCTAGCAGCAAGAAATGTGATCCACATCGACTGATGTTGGGCCCAAC 1043
QY 2643 CCAGCGGGAAGAGAGACACAGAGAGTTGAGGCAATTCGCGCAAGGGCGCGATTT 2702
Db 1044 CCAGCGGGAAGAGAGACACAGAGAGTTGAGGCAATTCGCGCAAGGGCGCGATTT 1103
QY 2702 CAGGCTTCCAGTCAATGCTGCGCTTTCGGCACTCAGCTCATGGAGTTCTCTGAAGAC 2762
Db 1104 CAGGCTTCCAGTCAATGCTGCGCTTTCGGCACTCAGCTCATGGAGTTCTCTGAAGAC 1163
QY 2763 GCTTGATCTGCTCTCTGCTGATGTTCAAGGTTCTGATTTGAAAGGTCGTGAAGGA 1223
Db 1164 GCTTGATCTGCTCTCTGCTGATGTTCAAGGTTCTGATTTGAAAGGTCGTGAAGGA 1282
QY 2823 GCGCTTTTTCAGTTCGCTTCCGATACCAAGTCTTCTCATAAAGGAAACAATAAG 1283
Db 1224 GCGCTTTTTCAGTTCGCTTCCGATACCAAGTCTTCTCATAAAGGAAACAATAAG 1343
QY 2883 AAGCGCTGTATGATGGCGCAAGTGAAGTTACAGATTTGTTGTTATGTTCTATAAG 2942
Db 1284 AAGCGCTGTATGATGGCGCAAGTGAAGTTACAGATTTGTTGTTATGTTCTATAAG 1343
QY 2943 TTTTGAATCTTGCATGATTTACAGATTTGTTGTTATGTTCTATAAG 3002
Db 1344 TTTTGAATCTTGCATGATTTACAGATTTGTTGTTATGTTCTATAAG 1403
QY 3003 GCGTGAATGATGGAATTTGATATCTGTTCTTTTTCAGTAAATCACTTCGAAACAA 3062
Db 1404 GCGTGAATGATGGAATTTGATATCTGTTCTTTTTCAGTAAATCACTTCGAAACAA 1463
QY 3063 A 3063
Db 1464 A 1464

RESULT 2

US-11-229-856-78
; Sequence 78, Application US/11229856
; Publication No. US20060130183A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: ROTTMANN, WILLIAM H.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: SANDERS, PAUL
; APPLICANT: ZHANG, GARY
; APPLICANT: FITZGERALD, SANDRA JOANNE
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
; FILE REFERENCE: 04463-0441
; CURRENT APPLICATION NUMBER: US/11/229,856
; CURRENT FILING DATE: 2005-09-20
; PRIOR APPLICATION NUMBER: 10/946,650
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 10/946,644
; PRIOR FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 78
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-229-856-78

Query Match 15.8%; Score 485; DB 8; Length 485;

Best Local Similarity 100.0%; Pred. No. 6.6e-243; Indels 0; Gaps 0;

Matches 485; Conservative 0; Mismatches 0;

QY 1159 GTGCATAATTCGAAGTGCAGATGCGCCCTCAGGGAATTAAGGCGCAACCCAGATTGC 1218
Db 1 GTGCATAATTCGAAGTGCAGATGCGCCCTCAGGGAATTAAGGCGCAACCCAGATTGC 60
QY 1219 AAAGAGCAAAAGAGCAGACCCCAACCTTCTTAAAGATCATCAGAGATCGGCCAG 1278
Db 61 AAAGAGCAAAAGAGCAGACCCCAACCTTCTTAAAGATCATCAGAGATCGGCCAG 120
QY 1279 TAAGGGTAATTAATTTAAAGATAGCTCTTGTACCGGAACTCCGTAATTTCTCTCACT 1338
Db 121 TAAGGGTAATTAATTTAAAGATAGCTCTTGTACCGGAACTCCGTAATTTCTCTCACT 180
QY 1339 TCATAAAACCCCTGATTAAATTTGGTGGAAAGCGACGCCAACCCCAAAAAGGTCAGATG 1398
Db 181 TCATAAAACCCCTGATTAAATTTGGTGGAAAGCGACGCCAACCCCAAAAAGGTCAGATG 240
QY 1399 TCATCCCAAG 1458
Db 241 TCATCCCAAG 300
QY 1459 TCACCGTTGGAGTCAATGCGATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATAT 1518
Db 301 TCACCGTTGGAGTCAATGCGATGCGTACGAATGTACATATTTGGTGTAGGGTCCAATAT 360
QY 1519 TTTGCGGGAGGGTGTGTGAACCGCAAGTTCCTATATATCGAACTCCACACCACTACCT 1578
Db 361 TTTGCGGGAGGGTGTGTGAACCGCAAGTTCCTATATATCGAACTCCACACCACTACCT 420
QY 1579 CACTTCAATCCCAACCAATTTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 1638
Db 421 CACTTCAATCCCAACCAATTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 480
QY 1639 CGGAA 1643
Db 481 CGGAA 485

RESULT 3

US-11-229-856-80

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; PRIOR APPLICATION NUMBER: US 60/143,833
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/615,192
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 10/174,693
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 407
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-106

Query Match          3.6%; Score 111; DB 7; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.6e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1897 ATGCTCGACCGGATCTTCGGGTGTTGGCCAGCTACTCCGTGCTCAGTGCACCCCTCCGC 1956
DB      297 ATGCTCGACCGGATCTTCGGGTGTTGGCCAGCTACTCCGTGCTCAGTGCACCCCTCCGC 356

QY      1957 GACCTCCCGGATGGCAAGGTCAGCGGCTCTACGGCTTAGCGCCGGGTGTC 2007
DB      357 GACCTCCCGGATGGCAAGGTCAGCGGCTCTACGGCTTAGCGCCGGGTGTC 407

RESULT 5
US-11-397-533-24
; Sequence 24, Application US/11397533
; Publication No. US2006018389SAI
; GENERAL INFORMATION:
; APPLICANT: Boksberg, Leonard N.
; APPLICANT: Havukala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c6
; CURRENT APPLICATION NUMBER: US/11/397,533
; CURRENT FILING DATE: 2006-04-03
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/143,833
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/615,192
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 10/174,693
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 407
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-11-397-533-24

Query Match          3.6%; Score 111; DB 7; Length 421;
Best Local Similarity 100.0%; Pred. No. 3.6e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1897 ATGCTCGACCGGATCTTCGGGTGTTGGCCAGCTACTCCGTGCTCAGTGCACCCCTCCGC 1956
DB      311 ATGCTCGACCGGATCTTCGGGTGTTGGCCAGCTACTCCGTGCTCAGTGCACCCCTCCGC 370

QY      1957 GACCTCCCGGATGGCAAGGTCAGCGGCTCTACGGCTTAGCGCCGGGTGTC 2007
DB      371 GACCTCCCGGATGGCAAGGTCAGCGGCTCTACGGCTTAGCGCCGGGTGTC 421

RESULT 6

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US-11-266-748A-215547
; Sequence 215547, Application US/11266748A
; Publication NO. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 215547
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
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; LOCATION: (128)..(132)
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Query Match 1.1%; Score 35; DB 8; Length 601;
 Best Local Similarity 100.0%; Pred. No. 2.2e-07;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1408 GAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 1442
Db 75 GAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 109

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RESULT 7
 US-11-266-748A-237674/c
 ; Sequence 237674, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl

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; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: Methods of Using the Same
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 237674
; LENGTH: 601
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; TYPE: DNA
; ORGANISM: Homo Sapiens
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LOCATION: (179)..(179)
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; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5916
; LENGTH: 1148
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-5916

Query Match 1.1%; Score 35; DB 9; Length 1148;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1404 CCACGAGAGAGAGAGAGAGAGAGAGAGAG 1438
DB 204 CCACGAGAGAGAGAGAGAGAGAGAGAGAGAG 170

RESULT 9
US-11-218-305-11276/c
; Sequence 11276, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Mengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11276
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-11276

Query Match 1.1%; Score 35; DB 9; Length 1413;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1408 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 1442
DB 1375 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 1341

RESULT 10
US-10-449-902-18409/c
; Sequence 18409, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18409
; LENGTH: 2002
; TYPE: DNA

; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK068805
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18409

Query Match 1.1%; Score 35; DB 6; Length 2002;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1406 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 1440
DB 54 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 20

RESULT 11
US-10-449-902-24951/c
; Sequence 24951, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
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; SEQ ID NO 24951
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK100393
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24951

Query Match 1.1%; Score 35; DB 6; Length 2168;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1406 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 1440
DB 240 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 206

RESULT 12
US-10-612-783-3402/c
; Sequence 3402, Application US/10612783
; Publication No. US20060236419A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with
; FILE REFERENCE: 38-21(53373)A
; CURRENT APPLICATION NUMBER: US/10/612,783
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 7098
; SEQ ID NO 3402
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_75440C.1

US-10-612-783-3402

Query Match 1.1%; Score 35; DB 6; Length 2411;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1406 ACCGAGAGAGAGAGAGAGAGAGAGAGTT 1440
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Db 181 ACGAGAGAGAGAGAGAGAGAGAGAGAGTT 147

RESULT 13

US-10-669-920-321/c
; Sequence 321, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morits, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23

; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 120502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(120502)
; OTHER INFORMATION: n = A,T,C or G

US-10-669-920-321
Query Match 1.1%; Score 35; DB 6; Length 120502;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1407 CGAGAGAGAGAGAGAGAGAGAGAGAGTT 1441
|||||
Db 13904 CGAGAGAGAGAGAGAGAGAGAGAGAGTT 13870

RESULT 14

US-10-540-898-339/c
; Sequence 339, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morits
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
; CURRENT APPLICATION NUMBER: US/10/540,898
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/330,773
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 339

; LENGTH: 215126

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(215126)

; OTHER INFORMATION: n = A,T,C or G

US-10-540-898-339

Query Match 1.1%; Score 35; DB 6; Length 215126;

Best Local Similarity 100.0%; Pred. No. 2.5e-07;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1408 GAGAGAGAGAGAGAGAGAGAGAGAGTTT 1442

|||||

Db 87670 GAGAGAGAGAGAGAGAGAGAGAGAGTTT 87636

|||||

RESULT 15

US-10-449-902-10915/c

; Sequence 10915, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205V1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10915

; LENGTH: 584

; TYPE: DNA

; ORGANISM: Oryza sativa

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: AK108263

; DATABASE ENTRY DATE: 2002-08-28

US-10-449-902-10915

Query Match 1.1%; Score 34; DB 6; Length 584;

Best Local Similarity 100.0%; Pred. No. 7.2e-07;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1405 CACGAGAGAGAGAGAGAGAGAGAGAGAG 1438

|||||

Db 479 CACGAGAGAGAGAGAGAGAGAGAGAGAG 446

|||||

Search completed: November 1, 2006, 13:45:00

Job time : 740 secs